Supplementary material: Statistical analysis methods applied to early outpatient COVID-19 treatment case series data

Eleftherios Gkioulekas, Ph.D.

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1. Introduction

This document contains the computer code and the raw calculations for our paper "Statistical analysis methods applied to early outpatient COVID-19 treatment case series data". The results of the calculations are summarized in the main paper's tables. Also included is the code used to generate the plots reported in the paper as well as the *p*-value plots for each case series studied in the main paper.

2. Methods

2.1. The exact Fisher test and confidence intervals

Let N be the number of treated patients, a the number of treated patients with an adverse outcome (hospitalization or death), M the number of untreated patients in the control group, and b the number of untreated patients with an adverse outcome (hospitalization or death) in the control group. The odds ratio comparing the two groups is given by

$$R = \frac{a(M-b)}{b(N-a)}, \tag{1}$$

In the exact Fisher test, we assume that N, M, and $a+b$, are fixed numbers, and under the null hypothesis, we also assume that the distribution of the total $a+b$ patients with an adverse outcome between the treatment group and control group is random, with equal probability for every possible combination. It follows that under the null hypothesis, the probability of seeing a particular event (N, a, M, b) is given by

$$\mathrm{pr}(N, a, M, b) = \frac{\binom{a+b}{b}\binom{N+M-a-b}{N-a}}{\binom{N+M}{N}}. \tag{2}$$

Here, the denominator counts the total number of combinations for distributing a total of $N + M$ patients between the two groups so that N patients end up in the treatment group and the remaining M patients in the control group, resulting in all possible outcomes. The numerator counts only the number of combinations for distributing patients between the two groups that results in the particular macroscopic event (N, a, M, b). The first factor in the numerator counts the number of combinations for distributing the fixed total $a + b$ patients with an adverse outcome between the two groups, so that a patients end up in the treatment group and the remaining patients in the control group. Likewise, the second factor of the numerator counts the number of combinations for distributing the remaining $N + M - a - b$ patients between the two groups, so that the treatment group has an additional $N - a$ patients with no adverse outcome, to add up to the required total of N patients, and likewise for the control group. It follows that the product of the two factors on the numerator counts the total number of ways that patients can be distributed between the two groups, so that we see the event (N, a, M, b) while keeping constant the sizes N, M of the two groups and the total number $a + b$ of patients with an adverse outcome.

The corresponding *p*-value is the probability of observing the event (N, a, M, b) or any other less probable event, and it is given by

$$\mathrm{pr}(N, a, M, b) = \sum_{n=0}^{\min\{N, a+b\}} \mathrm{pr}(N, n, M, a+b-n) H(\mathrm{pr}(N, a, M, b) - \mathrm{pr}(N, n, M, a+b-n)), \tag{3}$$

where H is the modified Heaviside function given by

$$H(x) = \begin{cases} 1, & \text{if } x \geq 0 \\ 0, & \text{if } x < 0 \end{cases} . \tag{4}$$

We note that the summation variable n is restricted by both the total size N of the treatment group and the total number $a+b$ of the patients with an adverse outcome, so the permissible range for all possible events is $0 \leq n \leq \min\{N, a+b\}$.

The corresponding confidence interval for the odds ratio R is given by

$$R_{\text{low}} = \exp(\ln R - z\sigma), \tag{5}$$

$$R_{\text{high}} = \exp(\ln R + z\sigma), \tag{6}$$

with σ calculated via the Woolf formula [1, 2] as follows:

$$\sigma = \left(\frac{1}{a} + \frac{1}{b} + \frac{1}{N-a} + \frac{1}{M-b}\right)^{1/2} . \tag{7}$$

To obtain a 95% confidence interval, we use $z = 1.96$.

The following Maxima code has been used to implement these formulas. The function pfisher calculates the exact Fisher test p-value. The function oddratio calculates the odd ratio for an (N, a, M, b) event. The functions lowci and highci calculate the confidence interval for the oddratio.

```
heaviside(x) := if x >= 0 then 1 else 0;
fisher(N,a,M,b) := 100*(binomial(a+b,a)*binomial(N+M-a-b, N-a));
pfisher(N,a,M,b) := float(sum(
  fisher(N,n,M,a+b-n)*heaviside(fisher(N,a,M,b)-fisher(N,n,M,a+b-n)), n, 0, min(N, a+b))
  /binomial(N+M, N));
oddratio(N,a,M,b) := float((a*(M-b))/(b*(N-a)));
stderror(N,a,M,b) := float((1/a+1/b+1/(N-a)+1/(M-b))^(1/2));
lowci(N,a, M,b) := float(exp(log(oddratio(N,a,M,b))-1.96*stderror(N,a,M,b)));
highci(N,a, M,b) := float(exp(log(oddratio(N,a,M,b))+1.96*stderror(N,a,M,b)));
```

2.2. Comparing data with known mortality rates for untreated patients

Let N be the number of treated patients, a the number of treated patients with an adverse outcome (hospitalization or death). Let x be the probability of adverse outcome if the patient is untreated. We wish to reject the null hypothesis that the treatment is ineffective and that the event (N, a) just happened by chance. The p-value for rejecting the null hypothesis, as a function of x, is given by

$$p(N, a, x) = \sum_{n=0}^{N} \text{pr}(N, n|x)\ H(\text{pr}(N, a|x) - \text{pr}(N, n|x)), \tag{8}$$

with $\text{pr}(N, a|x)$ the probability of the specific outcome (N, a) given by

$$\text{pr}(N, a|x) = \binom{N}{a} x^a (1-x)^{N-a}. \tag{9}$$

We calculate the efficacy threshold x_0 via the equation

$$x_0(N, a, p_0) = \inf\{x \in [a/N, 1] \mid p(N, a, x) \leq p_0\}, \tag{10}$$

with $p_0 = 0.05$ for 95% confidence, $p_0 = 0.01$ for 99% confidence and $p_0 = 0.001$ for 99.9% confidence. The threshold corresponds to the upper endpoint of the Sterne interval [3]. An alternate estimate of x_0 can be approximated using the upper endpoint of the Clopper-Pearson interval [4], which reads:

$$x_0(N, a, p_0) = \inf\{x \in [a/N, 1] \mid \textstyle\sum_{n=0}^{a} \text{pr}(N, n|x) \leq p_0/2\}, \tag{11}$$

and whose calculation is computationally more efficient.

This calculation has been implemented using the following Maxima code:

```
heaviside(x) := if x >= 0 then 1 else 0;
distr(N,a,x) := 100*binomial(N,a)*(x^a)*(1-x)^(N-a);
pdistr(N,a,x) := float(sum(distr(N,n,x)*heaviside(distr(N,a,x)-distr(N,n,x)), n, 0, N));
pdistrcp(N,a, x) := float(2*sum(distr(N,n,x), n, 0, a));
```

2.3. Coverage for Sterne and Clopper-Pearson intervals

The actual coverage probability for a confidence interval $[p_1, p_2]$ with confidence p-value p_0 for a binomial proportion probability x over a sample with N events is given by

$$c(N, p_0|x) = \sum_{a=0}^{N} I(N, a, x, p_0)\ \mathrm{pr}(N, a|x), \tag{12}$$

according to Vollset [5], with $I(N, a, x, p_0)$ an indicator function given by

$$I(N, a, x, p_0) = \begin{cases} 1, & \text{if } x \in [p_1, p_2] \\ 0, & \text{if } x \notin [p_1, p_2] \end{cases}, \tag{13}$$

with p_0 the maximum tolerated p-value. We note that the indicator function for the Sterne interval is given by

$$I(N, a, x, p_0) = 1 \Longleftrightarrow p(N, a, x) \geq p_0 \tag{14}$$

$$\Longleftrightarrow \sum_{n=0}^{N} \mathrm{pr}(N, n|x) H(\mathrm{pr}(N, a|x) - \mathrm{pr}(N, n|x)) \geq p_0, \tag{15}$$

and for the Clopper-Pearson interval, it is given by

$$I(N, a, x, p_0) = 1 \Longleftrightarrow \begin{cases} x \geq a/N \\ \sum_{n=0}^{a} \mathrm{pr}(N, n|x) \geq p_0/2 \end{cases} \vee \begin{cases} x \leq a/N \\ \sum_{n=a}^{N} \mathrm{pr}(N, n|x) \geq p_0/2. \end{cases} \tag{16}$$

We implemented the calculation of the coverage probability using the functions and `coversterne` and `covercp`, given below:

```
indicatorsterne(N,a,x,p0) := if pdistr(N,a,x) >= 100*p0 then 1 else 0;
coversterne(x,N,p0) := float(sum(distr(N,a,x)*indicatorsterne(N,a,x,p0) , a, 0, N));
indicatorcp(N,a,x, p0) := if ((x >= a/N and 2*sum(distr(N,n,x), n, 0, a) >= 100*p0)
  or (x <= a/N and 2*sum(distr(N,n,x), n, a, N) >= 100*p0)) then 1 else 0;
covercp(x,N,p0) := float(sum(distr(N,a,x)*indicatorcp(N,a,x, p0) , a, 0, N));
```

- Coverage probability for the Sterne interval for $N = 20$ and $N = 100$ (Fig. 1).

  ```
  f(t) := coversterne(t, 20, 0.05);
  dat: makelist([float(t/100), f(t/100)], t, 1, 99, 1);
  f2(t) := coversterne(t, 100, 0.05);
  dat2: makelist([float(t/100), f2(t/100)], t, 1, 99, 1);
  line95: makelist([float(t/100), 95], t, 1, 99, 1);
  draw2d(
  grid=true,
  title="Coverage for Sterne interval for N=20 and N=100",
  xlabel="binomial trial probability",
  ylabel="coverage",
  xtics=0.1,
  ytics=0.2,
  point_type=dot,
  points_joined=true,
  color=black,
  points(dat),
  color=blue,
  points(dat2),
  points(line95)
  );
  ```

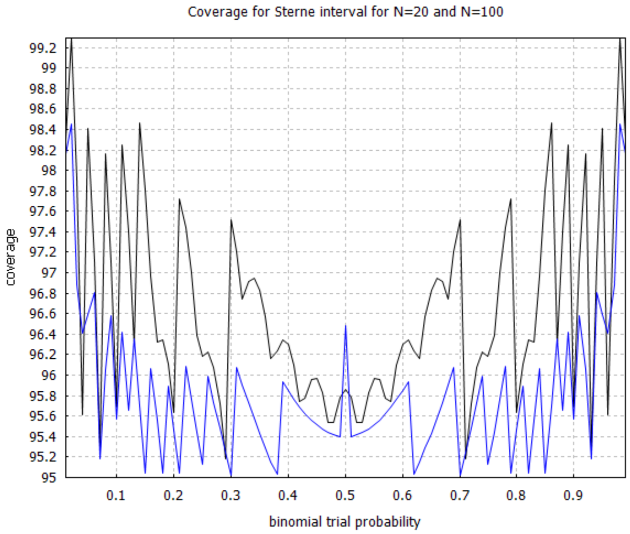

Figure 1: Coverage probability for the Sterne interval [3] with sample sizes $N = 20$ and $N = 100$. The black curve corresponds to $N = 20$ and the blue curve, which is situated below the black curve, corresponds to $N = 100$.

- Coverage probability for the Clopper-Pearson interval for $N = 20$ and $N = 100$ (Fig. 2)

```
f(t) := covercp(t, 20, 0.05);
dat: makelist([float(t/100), f(t/100)], t, 1, 99, 1);
f2(t) := covercp(t, 100, 0.05);
dat2: makelist([float(t/100), f2(t/100)], t, 1, 99, 1);
line95: makelist([float(t/100), 95], t, 1, 99, 1);
draw2d(
grid=true,
title="Coverage for Clopper-Pearson interval for N=20 and N=100",
xlabel="binomial trial probability",
ylabel="coverage",
xtics=0.1,
ytics=0.2,
point_type=dot,
points_joined=true,
color=black,
points(dat),
color=blue,
points(dat2),
points(line95)
);
```

- Coverage probability for the Sterne vs Clopper-Pearson interval for $N = 100$ (see Fig. 3)

```
f(t) := covercp(t, 100, 0.05);
dat: makelist([float(t/100), f(t/100)], t, 1, 99, 1);
f2(t) := coversterne(t, 100, 0.05);
dat2: makelist([float(t/100), f2(t/100)], t, 1, 99, 1);
line95: makelist([float(t/100), 95], t, 1, 99, 1);
draw2d(
grid=true,
```

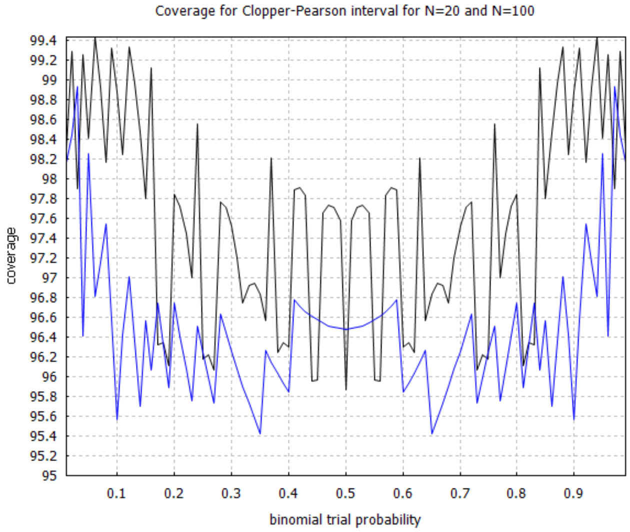

Figure 2: Coverage probability for the Clopper-Pearson interval [4] with sample sizes $N = 20$ and $N = 100$. The black curve corresponds to $N = 20$ and the blue curve, which is situated below the black curve, corresponds to $N = 100$.

```
    title="Coverage for Sterne vs Clopper-Pearson interval for N=100",
    xlabel="binomial trial probability",
    ylabel="coverage",
    xtics=0.1,
    ytics=0.2,
    point_type=dot,
    points_joined=true,
    color=black,
    points(dat),
    color=blue,
    points(dat2),
    points(line95)
    );
```

2.4. Bayesian factor analysis

Let N be the number of treated patients, a the number of treated patients with an adverse outcome (hospitalization or death). Let x be the probably of adverse outcome if the patient is untreated. We consider the null hypothesis $H_0 : x_0 < x < 1$ and the alternative hypothesis $H_1 : 0 < x \geq x_0$, using the following prior probability distributions:

$$\mathrm{pr}(x|H_0(x_0, p_2)) = \begin{cases} 1/(p_2 - x_0), & \text{if } x \in [x_0, p_2] \\ 0, & \text{if } x \in (p_2, 1], \end{cases} \tag{17}$$

$$\mathrm{pr}(x|H_1(x_0, t)) = \begin{cases} 1/t, & \text{if } x \in [0, t] \\ 0, & \text{if } x \in (t, x_0]. \end{cases} \tag{18}$$

As explained in our paper we calculate the metric $b(x_0, p_2)$ given by the equations

$$b(x_0, p_2) = \max_{t\in(0,x_0]} b_0(x_0, p_2, t), \tag{19}$$

$$b_0(x_0, p_2, t) = \log B(N, a|H_1(x_0, t), H_0(x_0, p_2)), \tag{20}$$

$$B(N, a|H_1(x_0, t), H_0(x_0, p_2)) = \frac{\mathrm{pr}(N, a|H_1(x_0, p_2))}{\mathrm{pr}(N, a|H_0(x_0, p_2))}, \tag{21}$$

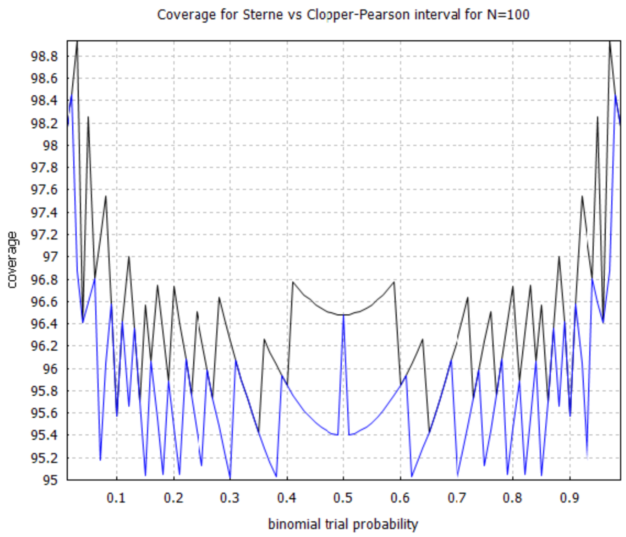

Figure 3: Comparison of the coverage probability for the Clopper-Pearson interval [4] versus the Sterne interval [3] with sample size $N = 100$. The black curve shows the coverage probability for the Clopper Pearson interval, and the blue curve, which is situated below the black curve, shows the coverage probability for the Sterne interval.

$$\mathrm{pr}(N, a|H_0(x_0, p_2)) = \frac{1}{p_2 - x_0}\binom{N}{a}\int_{x_0}^{p_2} x^a(1-x)^{N-a}\,\mathrm{d}x, \tag{22}$$

$$\mathrm{pr}(N, a|H_1(x_0, p_2)) = \frac{1}{t}\binom{N}{a}\int_0^t x^a(1-x)^{N-a}\,\mathrm{d}x. \tag{23}$$

For confidence p_0, we use the empirical thresholds given by

$$b(x_0, p_2) \geq \log\left(\frac{5(1-p_0)}{p_0}\right). \tag{24}$$

In particular we will identify the following thresholds:

$$p_0 = 0.05 \text{ requires } b(x_0, p_2) > 2, \tag{25}$$

$$p_0 = 0.01 \text{ requires } b(x_0, p_2) > 2.7, \tag{26}$$

$$p_0 = 0.001 \text{ requires } b(x_0, p_2) > 3.7. \tag{27}$$

We use the following code to implement the calculation of the Bayesian factor with exact symbolic integration:

```
bayesint(N,a,p,q) := integrate((x^a)*(1-x)^(N-a),x,p,q);
bayes(N,a,q,p1,p2) := float(((p2-p1)/q)*bayesint(N,a,0,q)/bayesint(N,a,p1,p2));
lbayes(N,a,q,p1,p2) := float(log(bayes(N,a,q,p1,p2))/log(10));
lbayesmax(N,a,q,p2) := lmax(makelist(lbayes(N,a,t,q,p2),t,q/100,q,q/100));
```

To use numerical instead of symbolic integration, one can instead use:

```
bayesint(N,a,p,q) := first(quad_qags((x^a)*(1-x)^(N-a),x,p,q));
```

Both seem to agree with each other, but numerical integration runs faster with negligible error.

2.5. CDC estimates for hospitalization and mortality rate risks

The CDC estimates [6] for hospitalization and mortality risk by age are shown in Fig. 4. The methodology for conductung the estimates is given in Refs [7, 8]. Based on this data, we have the following:

Age	Symptomatic illness	Hospitalizations	Deaths
0-17	22,030,307 (19,108,000–25,701,942)	266,597 (224,715–315,966)	645 (501–1,141)
18-49	64,029,542 (56,477,718–73,348,809)	1,996,830 (1,719,541–2,334,921)	60,355 (56,641–64,388)
50-64	23,378,591 (20,628,625–26,697,449)	2,009,141 (1,771,585–2,304,508)	159,489 (154,920–164,453)
65+	14,626,141 (12,913,173–16,745,092)	3,232,213 (2,864,006–3,683,201)	700,882 (688,959–713,090

Figure 4: Number of COVID-19 hospitalizations and deaths in the United States between February 2020 and September 2021, compared against symptomatic infections, as estimated by the CDC. Estimates are based on the CDC estimates for underreporting symptomatic illness, hospitalizations and deaths. 95% confidence intervals are given in parenthesis.

- Mortality rate for age range > 50

```
100*float((159489+700882)/(23378591+14626141));
2.263852301339738
```

- Mortality rate for age range > 50 lower bound

```
100*float((154920+688959)/(26697449+16745092));
1.942517588922803
```

- Mortality rate for age range > 50 upper bound

```
100*float((164453+713090)/(20628625+12913173));
2.616267023014091
```

- Mortality rate for age range > 65

```
100*float(700882/14626141);
4.791981699068812
```

- Mortality rate for age range > 65 lower bound

```
100*float(688959/16745092);
4.114393638446417
```

- Mortality rate for age range > 65 upper bound

```
100*float(713090/12913173);
5.522190402002669
```

- Hospitalization rate for age range > 50

```
100*float((2009141+3232213)/(23378591+14626141));
13.79131945990305
```

- Hospitalization rate for age range > 50 lower bound

```
100*float((1771585+2864006)/(26697449+16745092));
10.67062582734284
```

- Hospitalization rate for age range > 50 upper bound

```
100*float((2304508+3683201)/(20628625+12913173));
17.85148488462067
```

- Hospitalization rate for age range > 65

  ```
  100*float(3232213/14626141);
  22.09887761918882
  ```

- Hospitalization rate for age range > 65 lower bound

  ```
  100*float(2864006/16745092);
  17.103554880439
  ```

- Hospitalization rate for age range > 65 upper bound

  ```
  100*float(3683201/12913173);
  28.52281929468458
  ```

3. Analysis of Zelenko's paper data

Our analysis of Dr. Zelenko's data from his paper [9, 10] is as follows:

3.1. Exact Fisher test analysis

- Hospitalization rate reduction: Lab confirmed treated high risk group (141 patients with 4 hospitalizations) [10] against untreated control group (377 patients with 58 hospitalizations) [10].

  ```
  oddratio(141,4,377,58);
                           0.1605839416058394
  lowci(141,4,377,58);
                           0.05716811998545882
  highci(141,4,377,58);
                           0.4510766194205237
  pfisher(141,4,377,58);
                           0.002635139571703133
  ```

- Mortality rate reduction: Lab confirmed treated high risk group (141 patients with 1 death) [10] against untreated control group (377 patients with 13 deaths) [10] and (4179 patients with 143 deaths) [11].

  ```
  oddratio(141,1,377,13);
                                  0.2
  lowci(141,1,377,13);
                           0.02591989564984814
  highci(141,1,377,13);
                           1.54321608930684
  pfisher(141,1,377,13);
                           12.63672008711213
  oddratio(141,1,4179,143);
                           0.2015984015984016
  lowci(141,1,4179,143);
                           0.02800076895736154
  highci(141,1,4179,143);
                           1.451457122085408
  pfisher(141,1,4179,143);
                           9.113583261739734
  ```

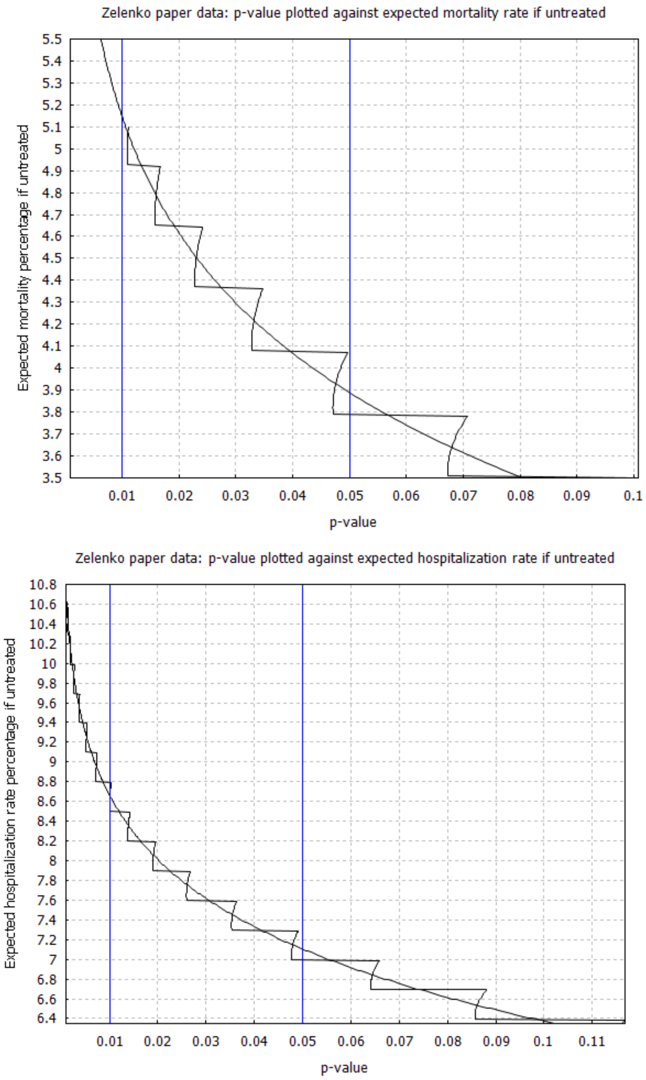

Figure 5: Relationship between *p*-value and expected mortality and hospitalization rate for high risk patients without early treatment, based on the case series data from the Scholz-Derwand-Zelenko study [10].

3.2. Frequentist efficacy threshold calculation for mortality rate reduction

- Mortality rate reduction: Lab confirmed treated high risk group (141 patients with 1 death) [10] against untreated mortality rates.

```
g(t) := pdistr(141,1,t);
xlist: makelist(t/1000,t,30,75,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.03 p-value =  13.61968166882261
x =  0.031 p-value =  13.81723967418287
x =  0.032 p-value =  14.1938521648013
x =  0.033 p-value =  9.60970628004097
x =  0.034 p-value =  9.772974256854047
x =  0.035 p-value =  10.07608218520726
x =  0.036 p-value =  6.756824621859506
```

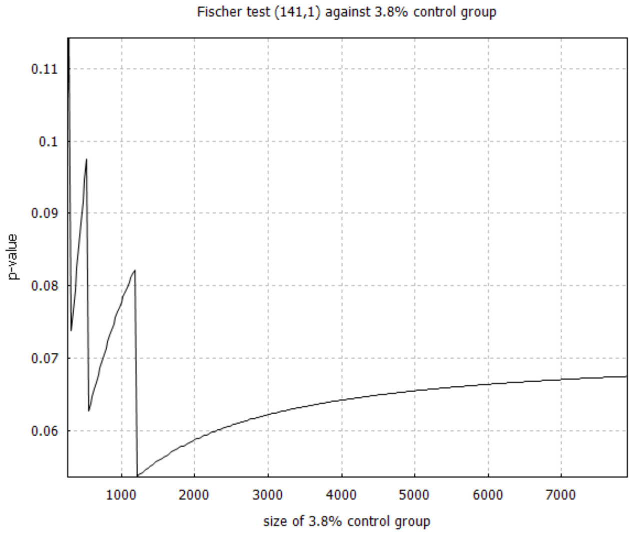

Figure 6: We plot the *p*-value calculated from an exact Fisher test that compares the treatment group from the DSZ study [10] (141 high-risk patients treated with 1 death) against an artificial control group with 3.8% mortality rate. Note that the exact *p*-value in the infinite control group limit should be 0.047, which is approached to three decimals when we get to control group size between 160,000 and 180,000

```
x =  0.037 p-value =  6.89076385444588
x =  0.038 p-value =  4.708618092902993
===========[ 95% threshold ]
x =  0.039 p-value =  4.735875389412373
x =  0.04 p-value =  4.844779413144026
x =  0.041 p-value =  3.28240505288532
x =  0.042 p-value =  3.309786131764296
x =  0.043 p-value =  3.397459700375322
x =  0.044 p-value =  2.281249136503831
x =  0.045 p-value =  2.306968781983206
x =  0.046 p-value =  2.376822290661623
x =  0.047 p-value =  1.581015765574308
x =  0.048 p-value =  1.60402251365917
x =  0.049 p-value =  1.659102596108932
x =  0.05 p-value =  1.092871971179575
x =  0.051 p-value =  1.112697731614994
x =  0.052 p-value =  1.155690851082285
x =  0.053 p-value =  0.7536079763242994
===========[ 99% threshold ]
x =  0.054 p-value =  0.7701946150702338
x =  0.055 p-value =  0.5165401422104255
x =  0.056 p-value =  0.5184732043301685
x =  0.057 p-value =  0.5320193527004696
x =  0.058 p-value =  0.3533071536489689
x =  0.059 p-value =  0.3559281648931398
x =  0.06 p-value =  0.366770858873634 8
x =  0.061 p-value =  0.2411021152768017
x =  0.062 p-value =  0.2438339492312386
x =  0.063 p-value =  0.2523654692652927
x =  0.064 p-value =  0.1641699737802234
```

```
x =  0.065 p-value =  0.1667067384113253
x =  0.066 p-value =  0.1733210714750937
x =  0.067 p-value =  0.1115489624096275
x =  0.068 p-value =  0.1137528405162266
x =  0.069 p-value =  0.1188146011665652
x =  0.07 p-value =  0.07563855870238759
===========[ 99.9% threshold ]
x =  0.071 p-value =  0.07747055115989582
x =  0.072 p-value =  0.0510393090330691
x =  0.073 p-value =  0.05118540375872668
x =  0.074 p-value =  0.05266042827415206
x =  0.075 p-value =  0.03432873246282359
```

- Selection bias threshold for 95% confidence (3.8% threshold)

```
g(t) := pdistr(141, ceiling(141*0.038), t);
xlist: makelist(t/1000, t, 80, 100);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.08 p-value =  11.89695937981814
x =  0.081 p-value =  11.99302505186626
x =  0.082 p-value =  9.160965010557694
x =  0.083 p-value =  9.17391815511646
x =  0.084 p-value =  9.246582340627757
x =  0.085 p-value =  7.023863973346787
x =  0.086 p-value =  7.02786224374162
x =  0.087 p-value =  7.081821443155382
x =  0.088 p-value =  5.351984869457466
x =  0.089 p-value =  5.350187715316618
x =  0.09 p-value =  5.389573948298094
x =  0.091 p-value =  5.469882003429634
x =  0.092 p-value =  4.048598101478344
=========[ 95% selection bias threshold ]
x =  0.093 p-value =  4.076877190496996
x =  0.094 p-value =  4.138519039371844
x =  0.095 p-value =  3.04599774945794
x =  0.096 p-value =  3.065974210765043
x =  0.097 p-value =  3.112819703528916
x =  0.098 p-value =  2.278935380378991
x =  0.099 p-value =  2.292814619905978
x =  0.1 p-value =  2.328093295682195
```

- Selection bias threshold for 99% confidence (5.3% threshold)

```
g(t) := pdistr(141, ceiling(141*0.053), t);
xlist: makelist(t/1000, t, 120, 135);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.12 p-value =  1.885027696518853
x =  0.121 p-value =  1.907212968555725
x =  0.122 p-value =  1.41309277449895
x =  0.123 p-value =  1.416576522567395
x =  0.124 p-value =  1.432569217576163
x =  0.125 p-value =  1.057450473189822
x =  0.126 p-value =  1.058958453585542
x =  0.127 p-value =  1.070319367146341
```

```
x =  0.128 p-value =  0.787321099427609
=========[ 99% selection bias threshold ]
x =  0.129 p-value =  0.7875698613731907
x =  0.13 p-value =  0.7955145311301319
x =  0.131 p-value =  0.5833043396738151
x =  0.132 p-value =  0.582801034478803
x =  0.133 p-value =  0.5882611407348382
x =  0.134 p-value =  0.4300658141465903
x =  0.135 p-value =  0.4291587855319338
```

- Selection bias threshold for 99.9% confidence (7% threshold)

```
g(t) := pdistr(141, ceiling(141*0.070), t);
xlist: makelist(t/1000, t, 140, 155);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.14 p-value =  1.489000320957836
x =  0.141 p-value =  1.491329096134713
x =  0.142 p-value =  1.505237547798424
x =  0.143 p-value =  1.127407398653966
x =  0.144 p-value =  1.12772159859056
x =  0.145 p-value =  1.137271826547533
x =  0.146 p-value =  0.8493198996330644
=========[ 99.9% selection bias threshold ]
x =  0.147 p-value =  0.8483783132437454
x =  0.148 p-value =  0.85474217984592
x =  0.149 p-value =  0.6366682100037645
x =  0.15 p-value =  0.6350156161460189
x =  0.151 p-value =  0.6390956853581093
x =  0.152 p-value =  0.4749525878122467
x =  0.153 p-value =  0.4729670186883305
x =  0.154 p-value =  0.4754458972950793
x =  0.155 p-value =  0.3526333730798296
```

- Plot code for Fig. 5

```
f(t) := pdistr(141, 1, t/100)/100;
g(t) := pdistrcp(141,1, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 350, 510, 1);
dat2: makelist([g(t/100), float(t/100)], t, 350, 550, 1);
draw2d(
grid=true,
title="Zelenko paper data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
ylabel="Expected mortality percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 3.5, 5.5),
parametric(0.01, x, x, 3.5, 5.5),
parametric(0.001, x, x, 3.5, 5.5)
);
```

- Validation of 3.8% threshold

```
xlist: makelist(2000*t, t, 1, 10);
h(t) := pfisher(141,1,t,round(t*0.038));
for t in xlist do print("control sample", t, "3.8% threshold -> ", h(t));
control sample 2000 3.8% threshold ->  5.871095516856185
control sample 4000 3.8% threshold ->  6.420932115216627
control sample 6000 3.8% threshold ->  6.638837478665079
control sample 8000 3.8% threshold ->  6.754759318247648
control sample 10000 3.8% threshold ->  6.826605475407994
control sample 12000 3.8% threshold ->  6.875473095923973
control sample 14000 3.8% threshold ->  6.910858404301216
control sample 16000 3.8% threshold ->  6.937661608848256
control sample 18000 3.8% threshold ->  6.958665913705388
control sample 20000 3.8% threshold ->  6.975568884844843
xlist: makelist(20000*t, t, 1, 10);
h(t) := pfisher(141,1,t,round(t*0.038));
for t in xlist do print("control sample", t, "3.8% threshold -> ", h(t));
control sample 20000 3.8% threshold ->  6.975568884844843
control sample 40000 3.8% threshold ->  4.672940319530953
control sample 60000 3.8% threshold ->  4.684683283122437
control sample 80000 3.8% threshold ->  4.69061069912564
control sample 100000 3.8% threshold ->  4.694185115215684
control sample 120000 3.8% threshold ->  4.69657556098076
control sample 140000 3.8% threshold ->  4.69828670148557
control sample 160000 3.8% threshold ->  4.699572070843199
control sample 180000 3.8% threshold ->  4.700572996866023
control sample 200000 3.8% threshold ->  4.701374490497547
```

- Plot code: p-value plotted in the limit of infinite control group with 3.8% mortality rate. See Fig. 6

```
f(t) := pfisher(141,1,t/0.038,t)/100;
dat1: makelist([t/0.038, f(t)], t, 10, 300, 1);
draw2d(
grid=true,
title="Fischer test (141,1) against 3.8% control group",
xlabel="size of 3.8% control group",
ylabel="p-value",
color=black,
point_type=dot,
points_joined=true,
points(dat1)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(141,1,t);
xlist: makelist(t/1000,t,30,75,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.03 p-value =  14.62433532579461
x =  0.031 p-value =  12.99870356511523
x =  0.032 p-value =  11.54411321554136
x =  0.033 p-value =  10.24407343005806
x =  0.034 p-value =  9.083436348618715
```

```
x =  0.035 p-value =  8.048331858566183
x =  0.036 p-value =  7.126096196577821
x =  0.037 p-value =  6.305197115281977
x =  0.038 p-value =  5.575157736042812
x =  0.039 p-value =  4.926480717243382
===========[ 95% threshold ]
x =  0.04 p-value =  4.350573966614928
x =  0.041 p-value =  3.839678801484502
x =  0.042 p-value =  3.38680119936293
x =  0.043 p-value =  2.985646572227928
x =  0.044 p-value =  2.630558332060168
x =  0.045 p-value =  2.316460385017131
x =  0.046 p-value =  2.038803590676994
x =  0.047 p-value =  1.793516145699922
x =  0.048 p-value =  1.576957793572451
x =  0.049 p-value =  1.385877720106969
x =  0.05 p-value =  1.217375964978937
x =  0.051 p-value =  1.068868160247167
x =  0.052 p-value =  0.9380533954109362
===========[ 99% threshold ]
x =  0.053 p-value =  0.8228850033803499
x =  0.054 p-value =  0.721544061354432
x =  0.055 p-value =  0.6324154038580729
x =  0.056 p-value =  0.5540659511453349
x =  0.057 p-value =  0.485225164075151
x =  0.058 p-value =  0.4247674457990083
x =  0.059 p-value =  0.3716963206859227
x =  0.06 p-value =  0.3251302314675493
x =  0.061 p-value =  0.2842898063194046
x =  0.062 p-value =  0.2484864582755632
x =  0.063 p-value =  0.2171121898325086
x =  0.064 p-value =  0.1896304857071589
x =  0.065 p-value =  0.1655681863851047
x =  0.066 p-value =  0.1445082442676454
x =  0.067 p-value =  0.126083272863341
x =  0.068 p-value =  0.1099698075527204
x =  0.069 p-value =  0.09588320397883429
===========[ 99.9% threshold ]
x =  0.07 p-value =  0.08357310708757096
x =  0.071 p-value =  0.07281943027419967
x =  0.072 p-value =  0.06342879000642435
x =  0.073 p-value =  0.05523134671337699
x =  0.074 p-value =  0.0480780076811879
x =  0.075 p-value =  0.04183795220734145
```

3.3. Frequentist efficacy threshold calculation for hospitalization rate reduction

- Hospitalization rate reduction: Lab confirmed treated high risk group (141 patients with 4 hospitalizations) [10] against untreated hosqitalization rates.

```
g(t) := pdistr(141,4,t);
xlist: makelist(t/1000,t,60,110,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.06 p-value =  15.20942433089376
x =  0.061 p-value =  11.39293388703001
```

```
x =  0.062 p-value =  11.41661153222707
x =  0.063 p-value =  11.52724345276485
x =  0.064 p-value =  8.578900316483553
x =  0.065 p-value =  8.592154273100734
x =  0.066 p-value =  8.677484192699449
x =  0.067 p-value =  6.418987487310412
x =  0.068 p-value =  6.425573441893508
x =  0.069 p-value =  6.4908484328797
x =  0.07 p-value =  4.773973729809336
===========[ 95% threshold ]
x =  0.071 p-value =  4.776552410756818
x =  0.072 p-value =  4.826194369613836
x =  0.073 p-value =  3.530159036141353
x =  0.074 p-value =  3.530514421877898
x =  0.075 p-value =  3.568109856453696
x =  0.076 p-value =  2.596073182768366
x =  0.077 p-value =  2.595337261154484
x =  0.078 p-value =  2.623722392944911
x =  0.079 p-value =  1.899080995728176
x =  0.08 p-value =  1.897928645524133
x =  0.081 p-value =  1.919308654121111
x =  0.082 p-value =  1.382162260434226
x =  0.083 p-value =  1.380964520147146
x =  0.084 p-value =  1.397034823539476
x =  0.085 p-value =  1.00101284777565
x =  0.086 p-value =  0.9999494604312827
x =  0.087 p-value =  1.012004256675268
x =  0.088 p-value =  0.7215286155937607
===========[ 99% threshold ]
x =  0.089 p-value =  0.7206661666119918
x =  0.09 p-value =  0.7296891380596094
x =  0.091 p-value =  0.5176807082690177
x =  0.092 p-value =  0.5170241412195732
x =  0.093 p-value =  0.5237611774699745
x =  0.094 p-value =  0.3697599761943005
x =  0.095 p-value =  0.3692847858589705
x =  0.096 p-value =  0.3743007866083736
x =  0.097 p-value =  0.2629521227465709
x =  0.098 p-value =  0.2626232535815236
x =  0.099 p-value =  0.2663457785279734
x =  0.1 p-value =  0.1861986780474471
x =  0.101 p-value =  0.1859807243005366
x =  0.102 p-value =  0.1887332177491757
x =  0.103 p-value =  0.1312983492057271
x =  0.104 p-value =  0.1311603575858887
x =  0.105 p-value =  0.1331873194912881
x =  0.106 p-value =  0.09220619147813443
===========[ 99.9% threshold ]
x =  0.107 p-value =  0.09212331866375502
x =  0.108 p-value =  0.09360934945214387
x =  0.109 p-value =  0.06449269742495857
x =  0.11 p-value =  0.06444618559003604
```

- Selection bias threshold for 95% confidence (7.0% threshold)

```
g(t) := pdistr(141, ceiling(141*0.070), t);
xlist: makelist(t/1000, t, 120, 135);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.12 p-value =  9.024871553273018
x =  0.121 p-value =  7.04269958743781
x =  0.122 p-value =  7.054900019638712
x =  0.123 p-value =  7.103917938588914
x =  0.124 p-value =  5.51804553271952
x =  0.125 p-value =  5.521895025809562
x =  0.126 p-value =  5.556949565612781
x =  0.127 p-value =  4.298413685898386
=========[ 95% selection bias threshold ]
x =  0.128 p-value =  4.296443760120598
x =  0.129 p-value =  4.320603894519128
x =  0.13 p-value =  3.32953331782783
x =  0.131 p-value =  3.323777296918492
x =  0.132 p-value =  3.339658420759492
x =  0.133 p-value =  2.564954168660576
x =  0.134 p-value =  2.556982926044823
x =  0.135 p-value =  2.56674311715464
```

- Selection bias threshold for 99% confidence (8.8% threshold)

```
g(t) := pdistr(141, ceiling(141*0.088), t);
xlist: makelist(t/1000, t, 165, 180);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.165 p-value =  1.700244070132663
x =  0.166 p-value =  1.698316961013533
x =  0.167 p-value =  1.707528054861051
x =  0.168 p-value =  1.30745863425927
x =  0.169 p-value =  1.303911978117307
x =  0.17 p-value =  1.309397273796566
x =  0.171 p-value =  1.000419567151308
x =  0.172 p-value =  0.9959967455921352
x =  0.173 p-value =  0.9988379095669602
x =  0.174 p-value =  1.008960912423464
x =  0.175 p-value =  0.7569982655229924
=========[ 99% selection bias threshold ]
x =  0.176 p-value =  0.758029185698173
x =  0.177 p-value =  0.7648709403872619
x =  0.178 p-value =  0.5725373637425463
x =  0.179 p-value =  0.5723859281781081
x =  0.18 p-value =  0.5768358549350348
```

- Selection bias threshold for 99.9% confidence (10.6% threshold)

```
g(t) := pdistr(141, ceiling(141*0.106), t);
xlist: makelist(t/1000, t, 205, 220);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.205 p-value =  0.2407878795253273
x =  0.206 p-value =  0.2391752143187225
x =  0.207 p-value =  0.2396042484728435
x =  0.208 p-value =  0.2420853546849055
x =  0.209 p-value =  0.1781425715791239
```

```
x =  0.21 p-value =  0.1780991704211251
x =  0.211 p-value =  0.1796439924690299
x =  0.212 p-value =  0.1320821331618274
x =  0.213 p-value =  0.1317594931755026
x =  0.214 p-value =  0.1326580122120174
x =  0.215 p-value =  0.09749511735646481
=========[ 99.9% selection bias threshold ]
x =  0.216 p-value =  0.09702685290831345
x =  0.217 p-value =  0.09749153935649497
x =  0.218 p-value =  0.07165081497521332
x =  0.219 p-value =  0.07112610269427266
x =  0.22 p-value =  0.0713097452909409
```

- Plot code for Fig. 5

```
f(t) := pdistr(141, 4, t/100)/100;
g(t) := pdistrcp(141,4, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 635, 1080, 1);
dat2: makelist([g(t/100), float(t/100)], t, 635, 1080, 1);
draw2d(
grid=true,
title="Zelenko paper data: p-value plotted against expected hospitalization rate if untreated",
xlabel="p-value",
ylabel="Expected hospitalization rate percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.2,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 6.35, 10.8),
parametric(0.01, x, x, 6.35, 10.8),
parametric(0.001, x, x, 6.35, 10.8)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(141,4,t);
xlist: makelist(t/1000,t,60,110,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.06 p-value =  14.01417207726254
x =  0.061 p-value =  12.82058563911107
x =  0.062 p-value =  11.71793995824317
x =  0.063 p-value =  10.70054028658583
x =  0.064 p-value =  9.762902381323551
x =  0.065 p-value =  8.899764002049045
x =  0.066 p-value =  8.106092977278516
x =  0.067 p-value =  7.377092249170433
x =  0.068 p-value =  6.708202278893366
x =  0.069 p-value =  6.09510116771335
x =  0.07 p-value =  5.533702821125297
x =  0.071 p-value =  5.020153455736973
x =  0.072 p-value =  4.550826721530986
```

```
===========[ 95% threshold ]
x =  0.073 p-value =  4.122317685897822
x =  0.074 p-value =  3.731435900694551
x =  0.075 p-value =  3.375197749718854
x =  0.076 p-value =  3.050818251521514
x =  0.077 p-value =  2.755702471491602
x =  0.078 p-value =  2.48743667767791
x =  0.079 p-value =  2.24377935686725
x =  0.08 p-value =  2.022652191008633
x =  0.081 p-value =  1.822131079115742
x =  0.082 p-value =  1.640437276246226
x =  0.083 p-value =  1.475928708981138
x =  0.084 p-value =  1.327091515938777
x =  0.085 p-value =  1.192531852176027
x =  0.086 p-value =  1.070967987775344
x =  0.087 p-value =  0.9612227234039108
===========[ 99% threshold ]
x =  0.088 p-value =  0.8622161390800891
x =  0.089 p-value =  0.7729586867098616
x =  0.09 p-value =  0.6925446320832227
x =  0.091 p-value =  0.6201458478715794
x =  0.092 p-value =  0.5550059556698874
x =  0.093 p-value =  0.4964348122132962
x =  0.094 p-value =  0.4438033325036691
x =  0.095 p-value =  0.3965386406470831
x =  0.096 p-value =  0.3541195376743891
x =  0.097 p-value =  0.3160722744426581
x =  0.098 p-value =  0.2819666168497223
x =  0.099 p-value =  0.2514121899950994
x =  0.1 p-value =  0.2240550875504172
x =  0.101 p-value =  0.1995747324268901
x =  0.102 p-value =  0.177680974815847
x =  0.103 p-value =  0.1581114138035182
x =  0.104 p-value =  0.1406289289990902
x =  0.105 p-value =  0.1250194089441055
x =  0.106 p-value =  0.1110896634729284
x =  0.107 p-value =  0.09866550765187754
===========[ 99.9% threshold ]
x =  0.108 p-value =  0.08759000542461151
x =  0.109 p-value =  0.07772186162122623
x =  0.11 p-value =  0.06893395153786698
```

3.4. Threshold calculation for control groups

- Control group

```
g(t) := pdistr(377,13,t);
xlist: makelist(t/1000,t,12,34,1);
for t in xlist do print("x = ",float(t), "p-value = ", g(t));
x =  0.012 p-value =  0.07715623731061237
x =  0.013 p-value =  0.1566930803447309
x =  0.014 p-value =  0.2948139492827936
x =  0.015 p-value =  0.5194169741235038
x =  0.016 p-value =  1.093028107364703
x =  0.017 p-value =  1.524206676824028
```

```
x =  0.018 p-value =  2.91267850734379
x =  0.019 p-value =  3.619601418828339
===========[ 95% threshold ]
x =  0.02 p-value =  6.128178803867998
x =  0.021 p-value =  7.186350178045584
x =  0.022 p-value =  11.0038356314035
x =  0.023 p-value =  16.40644015564414
x =  0.024 p-value =  17.64663048324744
x =  0.025 p-value =  24.40260188389401
x =  0.026 p-value =  32.71414547205467
x =  0.027 p-value =  33.91629616929241
x =  0.028 p-value =  43.21336706302784
x =  0.029 p-value =  53.63546662293978
x =  0.03 p-value =  54.59835524571509
x =  0.031 p-value =  65.4528992267622
x =  0.032 p-value =  76.85296111846735
x =  0.033 p-value =  77.3953643571547
x =  0.034 p-value =  88.69314072467424
```

- Control group

```
g(t) := pdistr(4179,143,t);
xlist: makelist(t/1000,t,20,34,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.02 p-value =  1.913244111333512E-7
x =  0.021 p-value =  4.219032249674979E-6
x =  0.022 p-value =  6.320019115283183E-5
x =  0.023 p-value =  5.265093164537755E-4
x =  0.024 p-value =  0.004991784112614881
x =  0.025 p-value =  0.02879806221500892
x =  0.026 p-value =  0.1312812146098234
x =  0.027 p-value =  0.5565110143022527
x =  0.028 p-value =  1.674309401277573
x =  0.029 p-value =  4.734760148631138
x =  0.03 p-value =  11.2338405615791
x =  0.031 p-value =  22.80701915993705
x =  0.032 p-value =  40.36837298412917
x =  0.033 p-value =  63.39800252603742
x =  0.034 p-value =  93.19472019790636
```

3.5. Bayesian factor analysis of efficacy thresholds for mortality rate reduction

Mortality rate reduction: Lab confirmed treated high risk group (141 patients with 1 death) [10] against untreated mortality rates. Integrals were calculated symbolically with exact arithmetic.

- Maximum high-risk cohort mortality rate $p_2 = 0.05$.

```
f(t) := lbayesmax(141, 1, t, 5/100);
g(t) := pdistr(141,1,t);
xlist: makelist(t/1000,t,30,49,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.03 log bayes =  1.113004396194256 p-value =  13.61968166882261
x =  0.031 log bayes =  1.147240116527225 p-value =  13.81723967418287
x =  0.032 log bayes =  1.181341192953928 p-value =  14.1938521648013
x =  0.033 log bayes =  1.215296403955267 p-value =  9.60970628004097
```

```
x =  0.034 log bayes =  1.249104631587378 p-value =  9.772974256854047
x =  0.035 log bayes =  1.282705022539335 p-value =  10.07608218520726
x =  0.036 log bayes =  1.316073211334553 p-value =  6.756824621859506
x =  0.037 log bayes =  1.349183141610838 p-value =  6.89076385444588
x =  0.038 log bayes =  1.382007060430614 p-value =  4.708618092902993
===========[ 95% threshold ]
x =  0.039 log bayes =  1.414532736953924 p-value =  4.735875389412373
x =  0.04 log bayes =  1.446760246658216 p-value =  4.844779413144026
x =  0.041 log bayes =  1.47863022354943 p-value =  3.28240505288532
x =  0.042 log bayes =  1.510109696903593 p-value =  3.309786131764296
x =  0.043 log bayes =  1.541173639598983 p-value =  3.397459700375322
x =  0.044 log bayes =  1.571904918428995 p-value =  2.281249136503831
x =  0.045 log bayes =  1.602164557566037 p-value =  2.306968781983206
x =  0.046 log bayes =  1.631959194700457 p-value =  2.376822290661623
x =  0.047 log bayes =  1.661359436542996 p-value =  1.581015765574308
x =  0.048 log bayes =  1.69020042864089 p-value =  1.60402251365917
x =  0.049 log bayes =  1.718654397299797 p-value =  1.659102596108932
```

- Maximum high-risk cohort mortality rate $p_2 = 0.10$.

```
f(t) := lbayesmax(141, 1, t, 10/100);
g(t) := pdistr(141,1,t);
xlist: makelist(t/1000,t,30,75,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.03 log bayes =  1.620152979158695 p-value =  13.61968166882261
x =  0.031 log bayes =  1.665525997803725 p-value =  13.81723967418287
x =  0.032 log bayes =  1.711151888767101 p-value =  14.1938521648013
x =  0.033 log bayes =  1.757031884280853 p-value =  9.60970628004097
x =  0.034 log bayes =  1.803177263160823 p-value =  9.772974256854047
x =  0.035 log bayes =  1.849539450104653 p-value =  10.07608218520726
x =  0.036 log bayes =  1.896106172153063 p-value =  6.756824621859506
x =  0.037 log bayes =  1.94286320850676 p-value =  6.89076385444588
x =  0.038 log bayes =  1.989794309011207 p-value =  4.708618092902993
===========[ 95% threshold ]
x =  0.039 log bayes =  2.036898333110309 p-value =  4.735875389412373
===========[ bayes 2 threshold ]
x =  0.04 log bayes =  2.084185951031351 p-value =  4.844779413144026
x =  0.041 log bayes =  2.131607810332404 p-value =  3.28240505288532
x =  0.042 log bayes =  2.179140285141837 p-value =  3.309786131764296
x =  0.043 log bayes =  2.22676693603539 p-value =  3.397459700375322
x =  0.044 log bayes =  2.274578371908685 p-value =  2.281249136503831
x =  0.045 log bayes =  2.322442426049101 p-value =  2.306968781983206
x =  0.046 log bayes =  2.370371527010143 p-value =  2.376822290661623
x =  0.047 log bayes =  2.418440972078091 p-value =  1.581015765574308
x =  0.048 log bayes =  2.466489419378419 p-value =  1.60402251365917
x =  0.049 log bayes =  2.514691357479947 p-value =  1.659102596108932
x =  0.05 log bayes =  2.5628512969426 p-value =  1.092871971179575
x =  0.051 log bayes =  2.611122435732586 p-value =  1.112697731614994
x =  0.052 log bayes =  2.659332721809562 p-value =  1.155690851082285
x =  0.053 log bayes =  2.70765258675927 p-value =  0.7536079763242994
===========[ 99% threshold ]
===========[ bayes 2.7 threshold ]
x =  0.054 log bayes =  2.755851419409188 p-value =  0.7701946150702338
x =  0.055 log bayes =  2.804188815452142 p-value =  0.5165401422104255
```

```
x =  0.056 log bayes =  2.852399616052845 p-value =  0.5184732043301685
x =  0.057 log bayes =  2.900625492518065 p-value =  0.5320193527004696
x =  0.058 log bayes =  2.948820016494387 p-value =  0.3533071536489689
x =  0.059 log bayes =  2.99685813293926 p-value =  0.3559281648931398
x =  0.06 log bayes =  3.044989527802275 p-value =  0.3667708588736348
x =  0.061 log bayes =  3.092962037249195 p-value =  0.2411021152768017
x =  0.062 log bayes =  3.140768529642268 p-value =  0.2438339492312386
x =  0.063 log bayes =  3.188638727532369 p-value =  0.2523654692652927
x =  0.064 log bayes =  3.236305178137612 p-value =  0.1641699737802234
x =  0.065 log bayes =  3.283757756099742 p-value =  0.1667067384113253
x =  0.066 log bayes =  3.331226680159258 p-value =  0.1733210714750937
x =  0.067 log bayes =  3.378489535260566 p-value =  0.1115489624096275
x =  0.068 log bayes =  3.425502567992218 p-value =  0.1137528405162266
x =  0.069 log bayes =  3.472352157292819 p-value =  0.1188146011665652
x =  0.07 log bayes =  3.519099619550358 p-value =  0.07563855870238759
===========[ 99.9% threshold ]
x =  0.071 log bayes =  3.565556209010824 p-value =  0.07747055115989582
x =  0.072 log bayes =  3.611707765738182 p-value =  0.0510393090330691
x =  0.073 log bayes =  3.657658855361628 p-value =  0.05118540375872668
x =  0.074 log bayes =  3.703427381133177 p-value =  0.05266042827415206
===========[ bayes 3.7 threshold ]
x =  0.075 log bayes =  3.748842999180289 p-value =  0.03432873246282359
```

3.6. Bayesian factor analysis of efficacy thresholds for hospitalization rate reduction

Hospitalization rate reduction: Lab confirmed treated high risk group (141 patients with 4 hospitalizations) [10] against untreated hosqitalization rates. Integrals were calculated symbolically with exact arithmetic. Integrals were calculated numerically.

- Maximum high-risk cohort hospitalization rate $p_2 = 0.10$.

```
f(t) := lbayesmax(141, 4, t, 10/100);
g(t) := pdistr(141,4,t);
xlist: makelist(t/1000,t,60,99,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.06 log bayes =  1.012769922682152 p-value =  15.20942433089376
x =  0.061 log bayes =  1.041510033560858 p-value =  11.39293388703001
x =  0.062 log bayes =  1.070423486299256 p-value =  11.41661153222707
x =  0.063 log bayes =  1.099498435339457 p-value =  11.52724345276485
x =  0.064 log bayes =  1.128722391646731 p-value =  8.578900316483553
x =  0.065 log bayes =  1.158082231249699 p-value =  8.592154273100734
x =  0.066 log bayes =  1.187564199591675 p-value =  8.677484192699449
x =  0.067 log bayes =  1.217153911968357 p-value =  6.418987487310412
x =  0.068 log bayes =  1.246836350280866 p-value =  6.425573441893508
x =  0.069 log bayes =  1.276595856288581 p-value =  6.4908484328797
x =  0.07 log bayes =  1.306416121502387 p-value =  4.773973729809336
===========[ 95% threshold ]
x =  0.071 log bayes =  1.336280173814931 p-value =  4.776552410756818
x =  0.072 log bayes =  1.366170360919329 p-value =  4.826194369613836
x =  0.073 log bayes =  1.39606833052014 p-value =  3.530159036141353
x =  0.074 log bayes =  1.425955007289862 p-value =  3.530514421877898
x =  0.075 log bayes =  1.455810566468936 p-value =  3.568109856453696
x =  0.076 log bayes =  1.485664552267269 p-value =  2.596073182768366
x =  0.077 log bayes =  1.515471730193222 p-value =  2.595337261154484
x =  0.078 log bayes =  1.545195116851633 p-value =  2.623722392944911
```

```
x =  0.079 log bayes =  1.574812365124318 p-value =  1.899080995728176
x =  0.08 log bayes =  1.604378555432692 p-value =  1.897928645524133
x =  0.081 log bayes =  1.633824747373811 p-value =  1.919308654121111
x =  0.082 log bayes =  1.663106532756831 p-value =  1.382162260434226
x =  0.083 log bayes =  1.692277990031316 p-value =  1.380964520147146
x =  0.084 log bayes =  1.721293511824247 p-value =  1.397034823539476
x =  0.085 log bayes =  1.750082793552904 p-value =  1.00101284777565
x =  0.086 log bayes =  1.778753727493018 p-value =  0.9999494604312827
x =  0.087 log bayes =  1.80717825963781 p-value =  1.012004256675268
x =  0.088 log bayes =  1.835379142822171 p-value =  0.7215286155937607
===========[ 99% threshold ]
x =  0.089 log bayes =  1.863377190230661 p-value =  0.7206661666119918
x =  0.09 log bayes =  1.891062498441527 p-value =  0.7296891380596094
x =  0.091 log bayes =  1.918572898781932 p-value =  0.5176807082690177
x =  0.092 log bayes =  1.945714839657761 p-value =  0.5170241412195732
x =  0.093 log bayes =  1.972661559308689 p-value =  0.5237611774699745
x =  0.094 log bayes =  1.999217539559729 p-value =  0.3697599761943005
x =  0.095 log bayes =  2.025543675158659 p-value =  0.3692847858589705
===========[ bayes 2 threshold ]
x =  0.096 log bayes =  2.05145610233538 p-value =  0.3743007866083736
x =  0.097 log bayes =  2.077125519117913 p-value =  0.2629521227465709
x =  0.098 log bayes =  2.102339525456614 p-value =  0.2626232535815236
x =  0.099 log bayes =  2.127320483013288 p-value =  0.2663457785279734
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.15$.

```
f(t) := lbayesmax(141, 4, t, 15/100);
g(t) := pdistr(141,4,t);
xlist: makelist(t/1000,t,60,126,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.06 log bayes =  1.358252697901071 p-value =  15.20942433089376
x =  0.061 log bayes =  1.392499312273745 p-value =  11.39293388703001
x =  0.062 log bayes =  1.427081608088926 p-value =  11.41661153222707
x =  0.063 log bayes =  1.46199375687778 p-value =  11.52724345276485
x =  0.064 log bayes =  1.497229493885939 p-value =  8.578900316483553
x =  0.065 log bayes =  1.532782128120214 p-value =  8.592154273100734
x =  0.066 log bayes =  1.568644547368408 p-value =  8.677484192699449
x =  0.067 log bayes =  1.604809218353459 p-value =  6.418987487310412
x =  0.068 log bayes =  1.641268182129878 p-value =  6.425573441893508
x =  0.069 log bayes =  1.678013044779007 p-value =  6.4908484328797
x =  0.07 log bayes =  1.715034963409778 p-value =  4.773973729809336
===========[ 95% threshold ]
x =  0.071 log bayes =  1.752324627422483 p-value =  4.776552410756818
x =  0.072 log bayes =  1.789872234943723 p-value =  4.826194369613836
x =  0.073 log bayes =  1.827667464290568 p-value =  3.530159036141353
x =  0.074 log bayes =  1.865699440270457 p-value =  3.530514421877898
x =  0.075 log bayes =  1.903956695069212 p-value =  3.568109856453696
x =  0.076 log bayes =  1.942477271743003 p-value =  2.596073182768366
x =  0.077 log bayes =  1.98122455930436 p-value =  2.595337261154484
x =  0.078 log bayes =  2.020170302816973 p-value =  2.623722392944911
===========[ bayes 2 threshold ]
x =  0.079 log bayes =  2.059300966298462 p-value =  1.899080995728176
x =  0.08 log bayes =  2.098680499032615 p-value =  1.897928645524133
x =  0.081 log bayes =  2.138248859503998 p-value =  1.919308654121111
```

```
x =  0.082 log bayes =  2.17797053792745 p-value =  1.382162260434226
x =  0.083 log bayes =  2.217908477337153 p-value =  1.380964520147146
x =  0.084 log bayes =  2.25802586495722 p-value =  1.397034823539476
x =  0.085 log bayes =  2.298261081861691 p-value =  1.00101284777565
x =  0.086 log bayes =  2.338730555383194 p-value =  0.9999494604312827
x =  0.087 log bayes =  2.379314571728005 p-value =  1.012004256675268
x =  0.088 log bayes =  2.420043982438747 p-value =  0.7215286155937607
===========[ 99% threshold ]
x =  0.089 log bayes =  2.460947409036812 p-value =  0.7206661666119918
x =  0.09 log bayes =  2.501922415257724 p-value =  0.7296891380596094
x =  0.091 log bayes =  2.543113905962691 p-value =  0.5176807082690177
x =  0.092 log bayes =  2.58433495574386 p-value =  0.5170241412195732
x =  0.093 log bayes =  2.625764927071242 p-value =  0.5237611774699745
x =  0.094 log bayes =  2.667213868989176 p-value =  0.3697599761943005
x =  0.095 log bayes =  2.708847631422429 p-value =  0.3692847858589705
===========[ bayes 2.7 threshold ]
x =  0.096 log bayes =  2.75048663922612 p-value =  0.3743007866083736
x =  0.097 log bayes =  2.792305159031902 p-value =  0.2629521227465709
x =  0.098 log bayes =  2.834093587470561 p-value =  0.2626232535815236
x =  0.099 log bayes =  2.876076261157404 p-value =  0.2663457785279734
x =  0.1 log bayes =  2.918015972863797 p-value =  0.1861986780474471
x =  0.101 log bayes =  2.96009487373799 p-value =  0.1859807243005366
x =  0.102 log bayes =  3.002164135464247 p-value =  0.1887332177491757
x =  0.103 log bayes =  3.044289633423265 p-value =  0.1312983492057271
x =  0.104 log bayes =  3.08646321509741 p-value =  0.1311603575858887
x =  0.105 log bayes =  3.128583336030617 p-value =  0.1331873194912881
x =  0.106 log bayes =  3.170833970284446 p-value =  0.09220619147813443
===========[ 99.9% threshold ]
x =  0.107 log bayes =  3.21299517245273 p-value =  0.09212331866375502
x =  0.108 log bayes =  3.255190557879395 p-value =  0.09360934945214387
x =  0.109 log bayes =  3.297382690218559 p-value =  0.06449269742495857
x =  0.11 log bayes =  3.339461583492099 p-value =  0.06444618559003604
x =  0.111 log bayes =  3.38162968349817 p-value =  0.06553040855523729
x =  0.112 log bayes =  3.423687403586287 p-value =  0.04493022114611908
x =  0.113 log bayes =  3.465632456302403 p-value =  0.0449065933832548
x =  0.114 log bayes =  3.507631590027047 p-value =  0.04569359909978657
x =  0.115 log bayes =  3.549469065696426 p-value =  0.03117947191605835
x =  0.116 log bayes =  3.591178722985914 p-value =  0.03116946935942665
x =  0.117 log bayes =  3.632894477076287 p-value =  0.0317376407295453
x =  0.118 log bayes =  3.674415213489259 p-value =  0.02155374506721887
x =  0.119 log bayes =  3.715752740883101 p-value =  0.021551282229512
===========[ bayes 3.7 threshold ]
x =  0.12 log bayes =  3.757081377307389 p-value =  0.02195914021089236
x =  0.121 log bayes =  3.798177712261807 p-value =  0.01484291972092138
x =  0.122 log bayes =  3.839029469712094 p-value =  0.01484418431475297
x =  0.123 log bayes =  3.879818479594503 p-value =  0.01513523121000046
x =  0.124 log bayes =  3.920371493121382 p-value =  0.01018297832573744
x =  0.125 log bayes =  3.960637469034146 p-value =  0.01018571550698967
x =  0.126 log bayes =  4.000694831533672 p-value =  0.01039213248538565
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.20$.

  ```
  f(t) := lbayesmax(141, 4, t, 20/100);
  g(t) := pdistr(141,4,t);
  ```

```
xlist: makelist(t/1000,t,60,115,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.06 log bayes =  1.550126841636672 p-value =  15.20942433089376
x =  0.061 log bayes =  1.586111651326605 p-value =  11.39293388703001
x =  0.062 log bayes =  1.622464382245621 p-value =  11.41661153222707
x =  0.063 log bayes =  1.659180119493077 p-value =  11.52724345276485
x =  0.064 log bayes =  1.696253546647043 p-value =  8.578900316483553
x =  0.065 log bayes =  1.733678957444961 p-value =  8.592154273100734
x =  0.066 log bayes =  1.771450262525927 p-value =  8.677484192699449
x =  0.067 log bayes =  1.809560991400887 p-value =  6.418987487310412
x =  0.068 log bayes =  1.848004289764211 p-value =  6.425573441893508
x =  0.069 log bayes =  1.886772912208824 p-value =  6.4908484328797
x =  0.07 log bayes =  1.925859210357697 p-value =  4.773973729809336
===========[ 95% threshold ]
x =  0.071 log bayes =  1.965255116375491 p-value =  4.776552410756818
x =  0.072 log bayes =  2.004952121775286 p-value =  4.826194369613836
===========[ bayes 2 threshold ]
x =  0.073 log bayes =  2.044941251385406 p-value =  3.530159036141353
x =  0.074 log bayes =  2.085213032290319 p-value =  3.530514421877898
x =  0.075 log bayes =  2.12575745750566 p-value =  3.568109856453696
x =  0.076 log bayes =  2.166614092411372 p-value =  2.596073182768366
x =  0.077 log bayes =  2.20774791294149 p-value =  2.595337261154484
x =  0.078 log bayes =  2.249132318954114 p-value =  2.623722392944911
x =  0.079 log bayes =  2.290755500589968 p-value =  1.899080995728176
x =  0.08 log bayes =  2.332683208230443 p-value =  1.897928645524133
x =  0.081 log bayes =  2.374857280277956 p-value =  1.919308654121111
x =  0.082 log bayes =  2.417244169741142 p-value =  1.382162260434226
x =  0.083 log bayes =  2.45990886959997 p-value =  1.380964520147146
x =  0.084 log bayes =  2.502816708683322 p-value =  1.397034823539476
x =  0.085 log bayes =  2.545908306077576 p-value =  1.00101284777565
x =  0.086 log bayes =  2.589302428536343 p-value =  0.9999494604312827
x =  0.087 log bayes =  2.63288180835985 p-value =  1.012004256675268
x =  0.088 log bayes =  2.676679855395955 p-value =  0.7215286155937607
===========[ 99% threshold ]
x =  0.089 log bayes =  2.720727867505368 p-value =  0.7206661666119918
===========[ bayes 2.7 threshold ]
x =  0.09 log bayes =  2.764926208914395 p-value =  0.7296891380596094
x =  0.091 log bayes =  2.809422715548108 p-value =  0.5176807082690177
x =  0.092 log bayes =  2.854033530370235 p-value =  0.5170241412195732
x =  0.093 log bayes =  2.898941228585681 p-value =  0.5237611774699745
x =  0.094 log bayes =  2.94395922372015 p-value =  0.3697599761943005
x =  0.095 log bayes =  2.989256889642104 p-value =  0.3692847858589705
x =  0.096 log bayes =  3.034658342664367 p-value =  0.3743007866083736
x =  0.097 log bayes =  3.080341716778753 p-value =  0.2629521227465709
x =  0.098 log bayes =  3.126101460601934 p-value =  0.2626232535815236
x =  0.099 log bayes =  3.172166156413697 p-value =  0.2663457785279734
x =  0.1 log bayes =  3.218303045701933 p-value =  0.1861986780474471
x =  0.101 log bayes =  3.26469894106383 p-value =  0.1859807243005366
x =  0.102 log bayes =  3.311209898333404 p-value =  0.1887332177491757
x =  0.103 log bayes =  3.357906909973487 p-value =  0.1312983492057271
x =  0.104 log bayes =  3.404787183943708 p-value =  0.1311603575858887
x =  0.105 log bayes =  3.45175479031463 p-value =  0.1331873194912881
x =  0.106 log bayes =  3.498999582520731 p-value =  0.09220619147813443
===========[ 99.9% threshold ]
```

```
x =  0.107 log bayes =  3.546307770255944 p-value =  0.09212331866375502
x =  0.108 log bayes =  3.5938094105863 p-value =  0.09360934945214387
x =  0.109 log bayes =  3.641473806336267 p-value =  0.06449269742495857
x =  0.11 log bayes =  3.689198018807797 p-value =  0.06444618559003604
x =  0.111 log bayes =  3.737191859574112 p-value =  0.06553040855523729
===========[ bayes 3.7 threshold ]
x =  0.112 log bayes =  3.785263436236275 p-value =  0.04493022114611908
x =  0.113 log bayes =  3.833418493500452 p-value =  0.0449065933832548
x =  0.114 log bayes =  3.881832158534729 p-value =  0.04569359909978657
x =  0.115 log bayes =  3.930297425511096 p-value =  0.03117947191605835
```

4. Analysis of Zelenko's April 2020 data

Our analysis of Dr. Zelenko's April data [9] is as follows:

4.1. Exact Fisher test analysis

- Hospitalization rate reduction: Lab confirmed and clinically diagnosed treated high risk group through April 28 2020 (405 patients with 6 hospitalizations) [9] against untreated control group (377 patients with 58 hospitalizations) [10].

  ```
  oddratio(405,6,377,58);
                         0.08270676691729323
  lowci(405,6,377,58);
                         0.03523259194983845
  highci(405,6,377,58);
                         0.1941500444716169
  pfisher(405,6,377,58);
                         1.245012713216156E-11
  ```

- Mortality rate reduction: Lab confirmed and clinically diagnosed treated high risk group through April 28 2020 (405 patients with 2 deaths) [9] against untreated control group (377 patients with 13 deaths) [10] and (4179 patients with 143 deaths) [11].

  ```
  oddratio(405,2,377,13);
                          0.1389578163771712
  lowci(405,2,377,13);
                          0.03114683401766284
  highci(405,2,377,13);
                          0.6199434177278393
  pfisher(405,2,377,13);
                          0.295697673142659
  oddratio(405,2,4179,143);
                          0.1400683683562096
  lowci(405,2,4179,143);
                          0.03456328503047134
  highci(405,2,4179,143);
                          0.567629720284816
  pfisher(405,2,4179,143);
                          0.02711480854385587
  ```

4.2. Frequentist efficacy threshold calculation for mortality rate reduction

- Mortality rate reduction: Lab confirmed and clinically diagnosed treated high risk group through April 28, 2020 (405 patients with 2 deaths) [9] against untreated mortality rates.

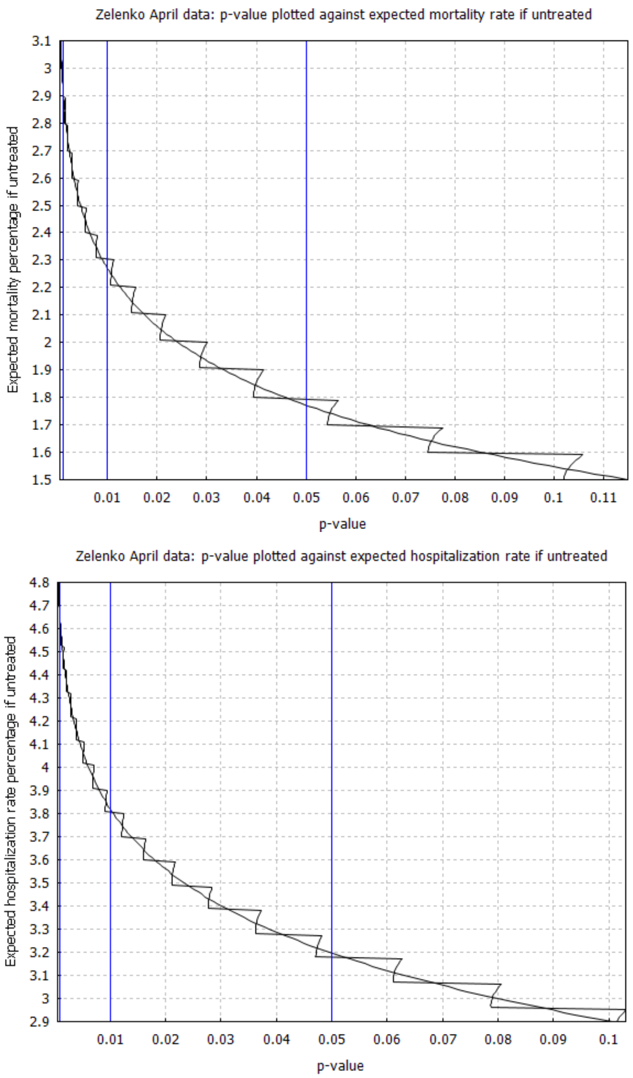

Figure 7: Relationship between *p*-value and expected mortality and hospitalization rate for high risk patients without early treatment, based on the case series data from the complete April 2020 Zelenko data set [9].

```
g(t) := pdistr(405,2,t);
xlist: makelist(t/1000,t,12,34,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.012 p-value =  25.32636212574359
x =  0.013 p-value =  18.79280670007152
x =  0.014 p-value =  13.87213142993775
x =  0.015 p-value =  10.1922934062546
x =  0.016 p-value =  7.457132266029055
x =  0.017 p-value =  5.435030355957899
x =  0.018 p-value =  3.947262120144083
===========[ 95% threshold ]
x =  0.019 p-value =  4.146847838803229
x =  0.02 p-value =  3.006168613400072
x =  0.021 p-value =  2.173113260523502
x =  0.022 p-value =  1.566854233875139
```

```
x =  0.023 p-value =  1.127042874355033
x =  0.024 p-value =  0.5446776986243319
===========[ 99% threshold ]
x =  0.025 p-value =  0.3881835338217826
x =  0.026 p-value =  0.2760740698510672
x =  0.027 p-value =  0.1959537370140917
x =  0.028 p-value =  0.138824250778621
x =  0.029 p-value =  0.09817520798331068
===========[ 99.9% threshold ]
x =  0.03 p-value =  0.06931075739392051
x =  0.031 p-value =  0.04885358905933861
x =  0.032 p-value =  0.03438122511711495
x =  0.033 p-value =  0.02416044070293476
x =  0.034 p-value =  0.01695408413469226
```

- Selection bias threshold for 95% confidence (threshold 1.8%)

```
g(t) := pdistr(405, ceiling(405*0.018), t);
xlist: makelist(t/1000, t, 35, 45);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.035 p-value =  10.38142870824139
x =  0.036 p-value =  8.235751248077618
x =  0.037 p-value =  6.503732350669575
x =  0.038 p-value =  5.113849044104118
x =  0.039 p-value =  5.227849188703664
x =  0.04 p-value =  4.083004605013183
=========[ 95% selection bias threshold ]
x =  0.041 p-value =  3.175541750223769
x =  0.042 p-value =  2.459982845053716
x =  0.043 p-value =  1.898490741753277
x =  0.044 p-value =  1.459905228494951
x =  0.045 p-value =  1.118796095367163
```

- Selection bias threshold for 99% confidence (threshold 2.4%)

```
g(t) := pdistr(405, ceiling(405*0.024), t);
xlist: makelist(t/1000, t, 45, 55);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.045 p-value =  5.362892236136537
x =  0.046 p-value =  4.248457716922166
x =  0.047 p-value =  3.352067795428997
x =  0.048 p-value =  2.634677989274764
x =  0.049 p-value =  2.063251278756205
x =  0.05 p-value =  1.610113163670263
x =  0.051 p-value =  1.252287919995525
x =  0.052 p-value =  0.9708538369648964
=========[ 99% selection bias threshold ]
x =  0.053 p-value =  0.7503412444537928
x =  0.054 p-value =  0.5781867082019758
x =  0.055 p-value =  0.4442492720169026
```

- Selection bias threshold for 99.9% confidence (threshold 2.9%)

```
g(t) := pdistr(405, ceiling(405*0.029), t);
```

```
xlist: makelist(t/1000, t, 60, 72);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.06 p-value =  0.8426217639321205
x =  0.061 p-value =  0.6551049775145751
x =  0.062 p-value =  0.5077900563891244
x =  0.063 p-value =  0.3924624123061612
x =  0.064 p-value =  0.3024787717044182
x =  0.065 p-value =  0.2324952893723579
x =  0.066 p-value =  0.1782348549793458
x =  0.067 p-value =  0.1362902132406009
x =  0.068 p-value =  0.1039590550486054
x =  0.069 p-value =  0.07910711875312489
=========[ 99.9% selection bias threshold ]
x =  0.07 p-value =  0.06005545335058995
x =  0.071 p-value =  0.04548825181256182
x =  0.072 p-value =  0.03437799931779614
```

- Plot code for Fig. 7.

```
f(t) := pdistr(405, 2, t/100)/100;
g(t) := pdistrcp(405, 2, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 150, 310, 1);
dat2: makelist([g(t/100), float(t/100)], t, 150, 310, 1);
draw2d(
grid=true,
title="Zelenko April data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
ylabel="Expected mortality percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 1.5, 3.1),
parametric(0.01, x, x, 1.5, 3.1),
parametric(0.001, x, x, 1.5, 3.1)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(405,2,t);
xlist: makelist(t/1000,t,12,34,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.012 p-value =  27.07479556030049
x =  0.013 p-value =  20.50213009174926
x =  0.014 p-value =  15.39886007379204
x =  0.015 p-value =  11.48162223628762
x =  0.016 p-value =  8.504639795076695
x =  0.017 p-value =  6.262009507439473
x =  0.018 p-value =  4.585707467082885
===========[ 95% threshold ]
x =  0.019 p-value =  3.341431819522845
```

```
x =  0.02 p-value =  2.423626086283392
x =  0.021 p-value =  1.75047938618141
x =  0.022 p-value =  1.259331946113436
x =  0.023 p-value =  0.9026790175934897
===========[ 99% threshold ]
x =  0.024 p-value =  0.6448241644143023
x =  0.025 p-value =  0.4591533117381149
x =  0.026 p-value =  0.3259616319851599
x =  0.027 p-value =  0.230750696536117
x =  0.028 p-value =  0.1629128691986474
x =  0.029 p-value =  0.1147268865448581
x =  0.03 p-value =  0.08059876832110366
===========[ 99.9% threshold ]
x =  0.031 p-value =  0.05649316658908524
x =  0.032 p-value =  0.03951065700887107
x =  0.033 p-value =  0.02757566327890085
x =  0.034 p-value =  0.01920746800481487
```

4.3. Frequentist efficacy threshold calculation for hospitalization rate reduction

- Hospitalization rate reduction: Lab confirmed and clinically diagnosed treated high risk group through April 28 2020 (405 patients with 6 hospitalizations) [9] against untreated hospitalization rates.

  ```
  g(t) := pdistr(405,6,t);
  xlist: makelist(t/1000,t,28,50,1);
  for t in xlist do print("x = ", float(t), "p-value = ", g(t));
  x =  0.028 p-value =  12.9626516129443
  x =  0.029 p-value =  10.14145238186383
  x =  0.03 p-value =  7.893908094320398
  x =  0.031 p-value =  6.115337524649429
  x =  0.032 p-value =  4.716464480198675
  ===========[ 95% threshold ]
  x =  0.033 p-value =  3.622391137524796
  x =  0.034 p-value =  2.771135487297536
  x =  0.035 p-value =  2.111996074850005
  x =  0.036 p-value =  1.6039127423954
  x =  0.037 p-value =  1.213924178672344
  x =  0.038 p-value =  1.254523357128454
  x =  0.039 p-value =  0.9443312819863021
  ===========[ 99% threshold ]
  x =  0.04 p-value =  0.7085545605201414
  x =  0.041 p-value =  0.5300148571746954
  x =  0.042 p-value =  0.3952985802318654
  x =  0.043 p-value =  0.2939926037375726
  x =  0.044 p-value =  0.2180561921752901
  x =  0.045 p-value =  0.1613110921245292
  x =  0.046 p-value =  0.1190318531595799
  x =  0.047 p-value =  0.08761965272586508
  ===========[ 99.9% threshold ]
  x =  0.048 p-value =  0.06434467789485993
  x =  0.049 p-value =  0.04714410491802042
  x =  0.05 p-value =  0.03446469600650248
  ```

- Selection bias threshold for 95% confidence (threshold 3.2%)

```
g(t) := pdistr(405, ceiling(405*0.032), t);
xlist: makelist(t/1000, t, 50, 60);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.05 p-value =  10.95171108487981
x =  0.051 p-value =  8.957902999322604
x =  0.052 p-value =  7.296313021497818
x =  0.053 p-value =  5.91918567639156
x =  0.054 p-value =  4.783693131412254
=========[ 95% selection bias threshold ]
x =  0.055 p-value =  4.851574836709863
x =  0.056 p-value =  3.894703995371056
x =  0.057 p-value =  3.114646286370489
x =  0.058 p-value =  2.481746054632456
x =  0.059 p-value =  1.970547342208384
x =  0.06 p-value =  1.559405645773567
```

- Selection bias threshold for 99% confidence (threshold 3.9%)

```
g(t) := pdistr(405, ceiling(405*0.039), t);
xlist: makelist(t/1000, t,65, 75);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.065 p-value =  3.413335019964251
x =  0.066 p-value =  2.764132314236277
x =  0.067 p-value =  2.798523101424035
x =  0.068 p-value =  2.251527425103635
x =  0.069 p-value =  1.805422655069643
x =  0.07 p-value =  1.443074766506559
x =  0.071 p-value =  1.149896509292798
x =  0.072 p-value =  0.9135602228745013
=========[ 99% selection bias threshold ]
x =  0.073 p-value =  0.7237184481548476
x =  0.074 p-value =  0.5717403413862114
x =  0.075 p-value =  0.4504688627113032
```

- Selection bias threshold for 99.9% confidence (threshold 4.7%)

```
g(t) := pdistr(405, ceiling(405*0.047), t);
xlist: makelist(t/1000, t, 90, 100);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.09 p-value =  0.3013181291289431
x =  0.091 p-value =  0.2381241004158617
x =  0.092 p-value =  0.1877386008796764
x =  0.093 p-value =  0.1476749682164762
x =  0.094 p-value =  0.1159024559628444
x =  0.095 p-value =  0.09076923094641516
=========[ 99.9% selection bias threshold ]
x =  0.096 p-value =  0.07093674755699615
x =  0.097 p-value =  0.07233823092162993
x =  0.098 p-value =  0.05615898740876546
x =  0.099 p-value =  0.04350254929228897
x =  0.1 p-value =  0.03362640763375089
```

- Plot code for Fig. 7.

```
f(t) := pdistr(405, 6, t/100)/100;
```

```
g(t) := pdistrcp(405,6, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 290, 480, 1);
dat2: makelist([g(t/100), float(t/100)], t, 290, 480, 1);
draw2d(
grid=true,
title="Zelenko April data: p-value plotted against expected hospitalization rate if untreated",
xlabel="p-value",
ylabel="Expected hospitalization rate percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 2.90, 4.80),
parametric(0.01, x, x, 2.90, 4.80),
parametric(0.001, x, x, 2.90, 4.80)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(405,6,t);
xlist: makelist(t/1000,t,28,50,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.028 p-value =  12.61011541658185
x =  0.029 p-value =  10.06841921562306
x =  0.03 p-value =  7.993317486621558
x =  0.031 p-value =  6.311521860801765
x =  0.032 p-value =  4.957835086661905
===========[ 95% threshold ]
x =  0.033 p-value =  3.875281931523924
x =  0.034 p-value =  3.014832497129215
x =  0.035 p-value =  2.334859766224291
x =  0.036 p-value =  1.800442913838316
x =  0.037 p-value =  1.382600316698581
x =  0.038 p-value =  1.05751246765921
x =  0.039 p-value =  0.8057755439574652
===========[ 99% threshold ]
x =  0.04 p-value =  0.6117110721961452
x =  0.041 p-value =  0.462745567801239
x =  0.042 p-value =  0.3488656505034744
x =  0.043 p-value =  0.262148361528122
x =  0.044 p-value =  0.1963626714152317
x =  0.045 p-value =  0.146635971146625
x =  0.046 p-value =  0.1091782628688418
x =  0.047 p-value =  0.08105646956413204
===========[ 99.9% threshold ]
x =  0.048 p-value =  0.0600114999876161
x =  0.049 p-value =  0.04431123599778143
x =  0.05 p-value =  0.03263330861494943
```

4.4. Bayesian factor analysis of efficacy thresholds for mortality rate reduction

Mortality rate reduction: Lab confirmed and clinically diagnosed treated high risk group through April 28, 2020 (405 patients with 2 deaths) [9] against untreated mortality rates. Integrals were calculated symbolically with exact arithmetic.

- Maximum high-risk cohort mortality rate $p_2 = 0.02$

```
f(t) := lbayesmax(405, 2, t, 2/100);
g(t) := pdistr(405,2,t);
xlist: makelist(t/1000,t,6,19,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.006 log bayes =  0.2726065935809781 p-value =  100.0
x =  0.007 log bayes =  0.3520089592247723 p-value =  100.0
x =  0.008 log bayes =  0.4234612494031177 p-value =  77.71809331837703
x =  0.009 log bayes =  0.4916186932435405 p-value =  59.54455806557501
x =  0.01 log bayes =  0.5629588471589525 p-value =  45.1371478152323
x =  0.011 log bayes =  0.637040288965995 p-value =  33.9286482201045
x =  0.012 log bayes =  0.7129622108774006 p-value =  25.32636212574359
x =  0.013 log bayes =  0.7900007260481505 p-value =  18.79280670007152
x =  0.014 log bayes =  0.8674269355700555 p-value =  13.87213142993775
x =  0.015 log bayes =  0.9446531818891732 p-value =  10.1922934062546
x =  0.016 log bayes =  1.02111995176861 p-value =  7.457132266029055
x =  0.017 log bayes =  1.096304365914527 p-value =  5.435030355957899
x =  0.018 log bayes =  1.169747099468813 p-value =  3.947262120144083
===========[ 95% threshold ]
x =  0.019 log bayes =  1.241110541390543 p-value =  4.146847838803229
```

- Maximum high-risk cohort mortality rate $p_2 = 0.05$

```
f(t) := lbayesmax(405, 2, t, 5/100);
g(t) := pdistr(405,2,t);
xlist: makelist(t/1000,t,6,34,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.006 log bayes =  0.7605811859386633 p-value =  100.0
x =  0.007 log bayes =  0.8600945675311065 p-value =  100.0
x =  0.008 log bayes =  0.9532574964969315 p-value =  77.71809331837703
x =  0.009 log bayes =  1.044898226738949 p-value =  59.54455806557501
x =  0.01 log bayes =  1.141680886914091 p-value =  45.1371478152323
x =  0.011 log bayes =  1.243364015866416 p-value =  33.9286482201045
x =  0.012 log bayes =  1.349259050351099 p-value =  25.32636212574359
x =  0.013 log bayes =  1.458864433928199 p-value =  18.79280670007152
x =  0.014 log bayes =  1.571680254747588 p-value =  13.87213142993775
x =  0.015 log bayes =  1.687349745018568 p-value =  10.1922934062546
x =  0.016 log bayes =  1.805540103785351 p-value =  7.457132266029055
x =  0.017 log bayes =  1.925943715005332 p-value =  5.435030355957899
x =  0.018 log bayes =  2.048296909829392 p-value =  3.947262120144083
===========[ 95% threshold ]
===========[ bayes 2 threshold ]
x =  0.019 log bayes =  2.172429565126627 p-value =  4.146847838803229
x =  0.02 log bayes =  2.298076206728314 p-value =  3.006168613400072
x =  0.021 log bayes =  2.425096273260508 p-value =  2.173113260523502
x =  0.022 log bayes =  2.553322633813418 p-value =  1.566854233875139
x =  0.023 log bayes =  2.682558417341359 p-value =  1.127042874355033
x =  0.024 log bayes =  2.812709925063927 p-value =  0.5446776986243319
```

```
===========[ 99% threshold ]
===========[ bayes 2.7 threshold ]
x =  0.025 log bayes =  2.943583021917035 p-value =  0.3881835338217826
x =  0.026 log bayes =  3.075138075607018 p-value =  0.2760740698510672
x =  0.027 log bayes =  3.20714246536049 p-value =  0.1959537370140917
x =  0.028 log bayes =  3.33949076792749 p-value =  0.138824250778621
x =  0.029 log bayes =  3.47206514159958 p-value =  0.09817520798331068
===========[ 99.9% threshold ]
x =  0.03 log bayes =  3.60473392858113 p-value =  0.06931075739392051
x =  0.031 log bayes =  3.737349834981126 p-value =  0.04885358905933861
===========[ bayes 3.7 threshold ]
x =  0.032 log bayes =  3.869747668947878 p-value =  0.03438122511711495
x =  0.033 log bayes =  4.001741610564537 p-value =  0.02416044070293476
x =  0.034 log bayes =  4.13317125769011 p-value =  0.01695408413469226
```

- Maximum high-risk cohort mortality rate $p_2 = 0.10$

```
f(t) := lbayesmax(405, 2, t, 10/100);
g(t) := pdistr(405,2,t);
xlist: makelist(t/1000,t,6,34,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.006 log bayes =  1.09025618785821 p-value =  100.0
x =  0.007 log bayes =  1.195108846674017 p-value =  100.0
x =  0.008 log bayes =  1.293795767534885 p-value =  77.71809331837703
x =  0.009 log bayes =  1.391155426366655 p-value =  59.54455806557501
x =  0.01 log bayes =  1.493862974679422 p-value =  45.1371478152323
x =  0.011 log bayes =  1.601688857672108 p-value =  33.9286482201045
x =  0.012 log bayes =  1.713957395289867 p-value =  25.32636212574359
x =  0.013 log bayes =  1.830180996755337 p-value =  18.79280670007152
x =  0.014 log bayes =  1.949874918224084 p-value =  13.87213142993775
x =  0.015 log bayes =  2.072698898627418 p-value =  10.1922934062546
===========[ bayes 2 threshold ]
x =  0.016 log bayes =  2.198338137997716 p-value =  7.457132266029055
x =  0.017 log bayes =  2.326504693426462 p-value =  5.435030355957899
x =  0.018 log bayes =  2.456956445274193 p-value =  3.947262120144083
===========[ 95% threshold ]
x =  0.019 log bayes =  2.589546930062364 p-value =  4.146847838803229
x =  0.02 log bayes =  2.724036713691956 p-value =  3.006168613400072
===========[ bayes 2.7 threshold ]
x =  0.021 log bayes =  2.86031396693843 p-value =  2.173113260523502
x =  0.022 log bayes =  2.99824334359956 p-value =  1.566854233875139
x =  0.023 log bayes =  3.137663227508208 p-value =  1.127042874355033
x =  0.024 log bayes =  3.278519129323298 p-value =  0.5446776986243319
===========[ 99% threshold ]
x =  0.025 log bayes =  3.420660640221991 p-value =  0.3881835338217826
x =  0.026 log bayes =  3.564097023602393 p-value =  0.2760740698510672
x =  0.027 log bayes =  3.70865048087118 p-value =  0.1959537370140917
===========[ bayes 3.7 threshold ]
x =  0.028 log bayes =  3.85427721404794 p-value =  0.138824250778621
x =  0.029 log bayes =  4.000928821799619 p-value =  0.09817520798331068
===========[ 99.9% threshold ]
x =  0.03 log bayes =  4.148552064829207 p-value =  0.06931075739392051
x =  0.031 log bayes =  4.29708837363353 p-value =  0.04885358905933861
x =  0.032 log bayes =  4.446473088598543 p-value =  0.03438122511711495
```

```
x =  0.033 log bayes =  4.59663440751538 p-value =  0.02416044070293476
x =  0.034 log bayes =  4.747541272921352 p-value =  0.01695408413469226
```

4.5. Bayesian factor analysis of efficacy thresholds for hospitalization rate reduction

Hospitalization rate reduction: Lab confirmed and clinically diagnosed treated high risk group through April 28 2020 (405 patients with 6 hospitalizations) [9] against untreated hospitalization rates.

- Maximum high-risk cohort hospitalization rate $p_2 = 0.10$.

```
f(t) := lbayesmax(405, 6, t, 10/100);
g(t) := pdistr(405,6,t);
xlist: makelist(t/1000,t,28,50,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.028 log bayes =  1.619698771712726 p-value =  12.9626516129443
x =  0.029 log bayes =  1.711788849562016 p-value =  10.14145238186383
x =  0.03 log bayes =  1.806273684743185 p-value =  7.893908094320398
x =  0.031 log bayes =  1.903040717158227 p-value =  6.115337524649429
x =  0.032 log bayes =  2.001973761044478 p-value =  4.716464480198675
===========[ 95% threshold ]
===========[ bayes 2 threshold ]
x =  0.033 log bayes =  2.102950774347199 p-value =  3.622391137524796
x =  0.034 log bayes =  2.205886430160631 p-value =  2.771135487297536
x =  0.035 log bayes =  2.310688544149057 p-value =  2.111996074850005
x =  0.036 log bayes =  2.417257578220823 p-value =  1.6039127423954
x =  0.037 log bayes =  2.525504285550605 p-value =  1.213924178672344
x =  0.038 log bayes =  2.63543755666786 p-value =  1.254523357128454
x =  0.039 log bayes =  2.746841784333004 p-value =  0.9443312819863021
===========[ 99% threshold ]
===========[ bayes 2.7 threshold ]
x =  0.04 log bayes =  2.859808312754048 p-value =  0.7085545605201414
x =  0.041 log bayes =  2.974121670878566 p-value =  0.5300148571746954
x =  0.042 log bayes =  3.089822424048819 p-value =  0.3952985802318654
x =  0.043 log bayes =  3.206846105084106 p-value =  0.2939926037375726
x =  0.044 log bayes =  3.325089575195568 p-value =  0.2180561921752901
x =  0.045 log bayes =  3.444514356164539 p-value =  0.1613110921245292
x =  0.046 log bayes =  3.565080847240095 p-value =  0.1190318531595799
x =  0.047 log bayes =  3.686748297786747 p-value =  0.08761965272586508
===========[ 99.9% threshold ]
x =  0.048 log bayes =  3.809474730406961 p-value =  0.06434467789485993
===========[ bayes 3.7 threshold ]
x =  0.049 log bayes =  3.933216815376222 p-value =  0.04714410491802042
x =  0.05 log bayes =  4.057929696070883 p-value =  0.03446469600650248
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.15$.

```
f(t) := lbayesmax(405, 6, t, 15/100);
g(t) := pdistr(405,6,t);
xlist: makelist(t/1000,t,28,50,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.028 log bayes =  1.848726105932186 p-value =  12.9626516129443
x =  0.029 log bayes =  1.94331587112927 p-value =  10.14145238186383
x =  0.03 log bayes =  2.040356890738584 p-value =  7.893908094320398
===========[ bayes 2 threshold ]
x =  0.031 log bayes =  2.13973858776537 p-value =  6.115337524649429
```

```
x =  0.032 log bayes =  2.241346855583037 p-value =  4.716464480198675
===========[ 95% threshold ]
x =  0.033 log bayes =  2.345061833313996 p-value =  3.622391137524796
x =  0.034 log bayes =  2.450800483744624 p-value =  2.771135487297536
x =  0.035 log bayes =  2.558473027729204 p-value =  2.111996074850005
x =  0.036 log bayes =  2.667982455403858 p-value =  1.6039127423954
x =  0.037 log bayes =  2.779242179359434 p-value =  1.213924178672344
===========[ bayes 2.7 threshold ]
x =  0.038 log bayes =  2.892263889549469 p-value =  1.254523357128454
x =  0.039 log bayes =  3.006834927728905 p-value =  0.9443312819863021
===========[ 99% threshold ]
x =  0.04 log bayes =  3.123049747027593 p-value =  0.7085545605201414
x =  0.041 log bayes =  3.24069615651405 p-value =  0.5300148571746954
x =  0.042 log bayes =  3.359818185092527 p-value =  0.3952985802318654
x =  0.043 log bayes =  3.480355025924125 p-value =  0.2939926037375726
x =  0.044 log bayes =  3.602207411886973 p-value =  0.2180561921752901
x =  0.045 log bayes =  3.725340963639471 p-value =  0.1613110921245292
===========[ bayes 3.7 threshold ]
x =  0.046 log bayes =  3.84972042389151 p-value =  0.1190318531595799
x =  0.047 log bayes =  3.975309649082952 p-value =  0.08761965272586508
===========[ 99.9% threshold ]
x =  0.048 log bayes =  4.102071553385152 p-value =  0.06434467789485993
x =  0.049 log bayes =  4.229968006080473 p-value =  0.04714410491802042
x =  0.05 log bayes =  4.35895968224665 p-value =  0.03446469600650248
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.20$.

```
f(t) := lbayesmax(405, 6, t, 20/100);
g(t) := pdistr(405,6,t);
xlist: makelist(t/1000,t,28,50,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.028 log bayes =  1.997894722164983 p-value =  12.9626516129443
x =  0.029 log bayes =  2.093526611204977 p-value =  10.14145238186383
===========[ bayes 2 threshold ]
x =  0.03 log bayes =  2.19162456606923 p-value =  7.893908094320398
x =  0.031 log bayes =  2.292078330986514 p-value =  6.115337524649429
x =  0.032 log bayes =  2.394774130002772 p-value =  4.716464480198675
===========[ 95% threshold ]
x =  0.033 log bayes =  2.499592442715417 p-value =  3.622391137524796
x =  0.034 log bayes =  2.60645058255776 p-value =  2.771135487297536
x =  0.035 log bayes =  2.715259131589492 p-value =  2.111996074850005
===========[ bayes 2.7 threshold ]
x =  0.036 log bayes =  2.82592145211508 p-value =  1.6039127423954
x =  0.037 log bayes =  2.938351340279972 p-value =  1.213924178672344
x =  0.038 log bayes =  3.052560881421925 p-value =  1.254523357128454
x =  0.039 log bayes =  3.168337824974097 p-value =  0.9443312819863021
===========[ 99% threshold ]
x =  0.04 log bayes =  3.285777044525287 p-value =  0.7085545605201414
x =  0.041 log bayes =  3.404666782893872 p-value =  0.5300148571746954
x =  0.042 log bayes =  3.525051516559991 p-value =  0.3952985802318654
x =  0.043 log bayes =  3.646870900648152 p-value =  0.2939926037375726
x =  0.044 log bayes =  3.77002614497666 p-value =  0.2180561921752901
===========[ bayes 3.7 threshold ]
x =  0.045 log bayes =  3.894483362739824 p-value =  0.1613110921245292
```

```
x =  0.046 log bayes =  4.020207805429197 p-value =  0.1190318531595799
x =  0.047 log bayes =  4.147163855195378 p-value =  0.08761965272586508
===========[ 99.9% threshold ]
x =  0.048 log bayes =  4.27531496956801 p-value =  0.06434467789485993
x =  0.049 log bayes =  4.40462357959099 p-value =  0.04714410491802042
x =  0.05 log bayes =  4.53505094130233 p-value =  0.03446469600650248
```

5. Analysis of Zelenko's June 2020 data

Our analysis of Dr. Zelenko's June data [12] is as follows:

5.1. Exact Fisher test analysis

- Hospitalization rate reduction: Lab confirmed and clinically diagnosed treated high risk group through June 14, 2020 (800 patients with 12 hospitalizations) [12] against untreated control group (377 patients with 58 hospitalizations).

```
oddratio(800,12,377,58);
                          0.08375634517766498
lowci(800,12,377,58);
                          0.04438334272199264
highci(800,12,377,58);
                          0.1580576163778682
pfisher(800,12,377,58);
                          1.731217935934369E-17
```

- Mortality rate reduction: Lab confirmed and clinically diagnosed treated high risk group through June 14, 2020 (800 patients with 2 deaths) [12] against untreated control group (377 patients with 13 deaths) [10] and (4179 patients with 143 deaths)[11].

```
oddratio(800,2,377,13);
                         0.07017543859649122
lowci(800,2,377,13);
                         0.01575438913656422
highci(800,2,377,13);
                         0.3125854096608842
pfisher(800,2,377,13);
                         0.001713330005851432
oddratio(800,2,4179,143);
                         0.07073628126259705
lowci(800,2,4179,143);
                         0.01748436299679642
highci(800,2,4179,143);
                         0.2861769392329611
pfisher(800,2,4179,143);
                         5.685115008401689E-7
```

5.2. Frequentist efficacy threshold calculation for mortality rate reduction

- Mortality rate reduction: Lab confirmed and clinically diagnosed treated high risk group through June 14, 2020 (800 patients with 2 deaths) [12] against untreated mortality rates.

```
g(t) := pdistr(800,2,t);
xlist: makelist(t/1000,t,1,20,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
```

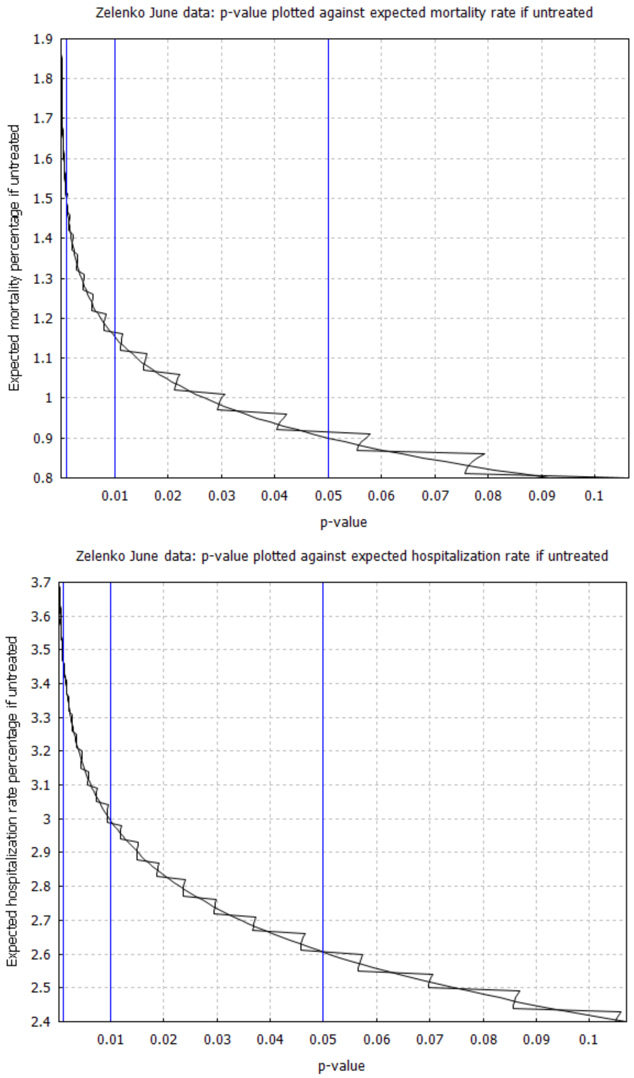

Figure 8: Relationship between *p*-value and expected mortality and hospitalization rate for high risk patients without early treatment, based on the case series data from the complete June 2020 Zelenko data set [12].

```
x =  0.001 p-value =  19.11718535039783
x =  0.002 p-value =  67.68363748520372
x =  0.003 p-value =  100.0
x =  0.004 p-value =  77.69711192391122
x =  0.005 p-value =  45.18462307844748
x =  0.006 p-value =  25.44402391878668
x =  0.007 p-value =  19.52313955172368
x =  0.008 p-value =  10.63740091933478
x =  0.009 p-value =  5.702329861935913
x =  0.01 p-value =  3.018401049036129
===========[ 95% threshold ]
x =  0.011 p-value =  1.581442969062921
x =  0.012 p-value =  0.8215294582765259
===========[ 99% threshold ]
x =  0.013 p-value =  0.4236831756966519
```

```
x =  0.014 p-value =  0.2171410923985604
x =  0.015 p-value =  0.1106817409556868
x =  0.016 p-value =  0.05614779050966141
===========[ 99.9% threshold ]
x =  0.017 p-value =  0.02836321921788459
x =  0.018 p-value =  0.01427419920752369
x =  0.019 p-value =  0.00715977351608265
x =  0.02 p-value =  0.003580566333983698
```

- Selection bias threshold for 95% confidence (threshold 1.0%)

```
g(t) := pdistr(800, ceiling(800*0.010), t);
xlist: makelist(t/1000, t, 15, 25);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.015 p-value =  30.69908248508675
x =  0.016 p-value =  20.44919878485689
x =  0.017 p-value =  16.82029060777186
x =  0.018 p-value =  10.80525893076907
x =  0.019 p-value =  6.809460626257609
x =  0.02 p-value =  4.220430902956585
=========[ 95% selection bias threshold ]
x =  0.021 p-value =  2.577699138348571
x =  0.022 p-value =  1.553918377737926
x =  0.023 p-value =  0.9257595138171845
x =  0.024 p-value =  0.7318551613054234
x =  0.025 p-value =  0.4264200711586395
```

- Selection bias threshold for 99% confidence (threshold 1.2%)

```
g(t) := pdistr(800, ceiling(800*0.012), t);
xlist: makelist(t/1000, t, 20, 30);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.02 p-value =  16.24225262874018
x =  0.021 p-value =  10.73135002865967
x =  0.022 p-value =  6.965714721534106
x =  0.023 p-value =  4.45137740163576
x =  0.024 p-value =  3.621784308401019
x =  0.025 p-value =  2.253820754612163
x =  0.026 p-value =  1.384432793611993
x =  0.027 p-value =  0.840457792486308
=========[ 99% selection bias threshold ]
x =  0.028 p-value =  0.504776968104228
x =  0.029 p-value =  0.3001917613423096
x =  0.03 p-value =  0.1769011488001782
```

- Selection bias threshold for 99.9% confidence (threshold 1.6%)

```
g(t) := pdistr(800, ceiling(800*0.016), t);
xlist: makelist(t/1000, t, 30, 40);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.03 p-value =  2.18029595816919
x =  0.031 p-value =  1.380672391053335
x =  0.032 p-value =  0.8645695606931342
x =  0.033 p-value =  0.5358515614054155
```

```
x =  0.034 p-value =  0.3289785652683334
x =  0.035 p-value =  0.2001994873058452
x =  0.036 p-value =  0.159757426613886
x =  0.037 p-value =  0.09531848454678325
=========[ 99.9% selection bias threshold ]
x =  0.038 p-value =  0.05641709171965808
x =  0.039 p-value =  0.03314173697276526
x =  0.04 p-value =  0.01933116975859409
```

- Plot code for Fig. 8.

```
f(t) := pdistr(800, 2, t/100)/100;
g(t) := pdistrcp(800, 2, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 80, 190, 1);
dat2: makelist([g(t/100), float(t/100)], t, 80, 190, 1);
draw2d(
grid=true,
title="Zelenko June data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
ylabel="Expected mortality percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 0.8, 1.9),
parametric(0.01, x, x, 0.8, 1.9),
parametric(0.001, x, x, 0.8, 1.9)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(800,2,t);
xlist: makelist(t/1000,t,1,20,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.001 p-value =  190.5327483493416
x =  0.002 p-value =  156.6924246401921
x =  0.003 p-value =  113.9103621220034
x =  0.004 p-value =  75.88036231079803
x =  0.005 p-value =  47.47382997386132
x =  0.006 p-value =  28.34831187538962
x =  0.007 p-value =  16.33146171436611
x =  0.008 p-value =  9.145135863840162
x =  0.009 p-value =  5.004348363906782
x =  0.01 p-value =  2.686672374150134
===========[ 95% threshold ]
x =  0.011 p-value =  1.419362755919675
x =  0.012 p-value =  0.7395919526792089
===========[ 99% threshold ]
x =  0.013 p-value =  0.3808092191316619
x =  0.014 p-value =  0.1940343543432836
x =  0.015 p-value =  0.09795497469437646
```

```
===========[ 99.9% threshold ]
x =  0.016 p-value =  0.04904341125116476
x =  0.017 p-value =  0.02437247116418766
x =  0.018 p-value =  0.01203054248776694
x =  0.019 p-value =  0.005901934980940605
x =  0.02 p-value =  0.002879037579065686
```

5.3. Frequentist efficacy threshold calculation for hospitalization rate reduction

- Hospitalization rate reduction: Lab confirmed and clinically diagnosed treated high risk group through June 14, 2020 (800 patients with 12 hospitalizations) [12] against untreated hosqitalization rates.

```
g(t) := pdistr(800,12,t);
xlist: makelist(t/1000,t,23,40,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.023 p-value =  15.54013045650735
x =  0.024 p-value =  10.4981160034363
x =  0.025 p-value =  6.977256773728229
x =  0.026 p-value =  5.744010066021493
x =  0.027 p-value =  3.713811001405364
===========[ 95% threshold ]
x =  0.028 p-value =  2.368631054308999
x =  0.029 p-value =  1.492162554770994
x =  0.03 p-value =  0.9295129602098239
===========[ 99% threshold ]
x =  0.031 p-value =  0.5730858984645315
x =  0.032 p-value =  0.4596197217292147
x =  0.033 p-value =  0.2773973209475854
x =  0.034 p-value =  0.1658903283945886
x =  0.035 p-value =  0.09836318158406657
===========[ 99.9% threshold ]
x =  0.036 p-value =  0.05785982432256075
x =  0.037 p-value =  0.03378029431625588
x =  0.038 p-value =  0.01958273723671357
x =  0.039 p-value =  0.01127628623826122
x =  0.04 p-value =  0.006451805449457608
```

- Selection bias threshold for 95% confidence (threshold 2.7%)

```
g(t) := pdistr(800, ceiling(800*0.027), t);
xlist: makelist(t/1000, t, 35, 45);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.035 p-value =  28.92463112980593
x =  0.036 p-value =  21.7362252221348
x =  0.037 p-value =  18.84213140384389
x =  0.038 p-value =  13.80215508078294
x =  0.039 p-value =  9.969717844011518
x =  0.04 p-value =  7.110017505346466
x =  0.041 p-value =  6.02475779231714
x =  0.042 p-value =  4.199642787750226
=========[ 95% selection bias threshold ]
x =  0.043 p-value =  2.894531922500901
x =  0.044 p-value =  1.974401650296473
x =  0.045 p-value =  1.647359178844403
```

- Selection bias threshold for 99% confidence (threshold 3.0%)

```
g(t) := pdistr(800, ceiling(800*0.030), t);
xlist: makelist(t/1000, t, 45, 55);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.045 p-value =  4.02332651006446
x =  0.046 p-value =  2.800853223051335
x =  0.047 p-value =  2.356321537996149
x =  0.048 p-value =  1.60698187616381
x =  0.049 p-value =  1.085495246769219
x =  0.05 p-value =  0.7267648168452615
=========[ 99% selection bias threshold ]
x =  0.051 p-value =  0.4826001438409527
x =  0.052 p-value =  0.3976506192166278
x =  0.053 p-value =  0.2591034229506757
x =  0.054 p-value =  0.1675422598580701
x =  0.055 p-value =  0.1075657046692324
```

- Selection bias threshold for 99.9% confidence (threshold 3.5%)

```
g(t) := pdistr(800, ceiling(800*0.035), t);
xlist: makelist(t/1000, t, 57, 70);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.057 p-value =  0.935044401027665
x =  0.058 p-value =  0.6380281446799202
x =  0.059 p-value =  0.531785495057672
x =  0.06 p-value =  0.3563665015591283
x =  0.061 p-value =  0.2370556780392855
x =  0.062 p-value =  0.1566071657925826
x =  0.063 p-value =  0.1027960620173094
x =  0.064 p-value =  0.08422932150655225
=========[ 99.9% selection bias threshold ]
x =  0.065 p-value =  0.05434223633582113
x =  0.066 p-value =  0.03484600629050099
x =  0.067 p-value =  0.02221636282656067
x =  0.068 p-value =  0.01408788825533577
x =  0.069 p-value =  0.01142268337923989
x =  0.07 p-value =  0.007124263152424046
```

- Plot code for Fig. 8.

```
f(t) := pdistr(800, 12, t/100)/100;
g(t) := pdistrcp(800, 12, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 240, 370, 1);
dat2: makelist([g(t/100), float(t/100)], t, 240, 370, 1);
draw2d(
grid=true,
title="Zelenko June data: p-value plotted against expected hospitalization rate if untreated",
xlabel="p-value",
ylabel="Expected hospitalization rate percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
```

```
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 2.4, 3.7),
parametric(0.01, x, x, 2.4, 3.7),
parametric(0.001, x, x, 2.4, 3.7)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(800,12,t);
xlist: makelist(t/1000,t,23,40,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.023 p-value =  15.10758501869266
x =  0.024 p-value =  10.69861416197628
x =  0.025 p-value =  7.450790144771532
x =  0.026 p-value =  5.107681443328172
x =  0.027 p-value =  3.44960563896216
===========[ 95% threshold ]
x =  0.028 p-value =  2.297156982323415
x =  0.029 p-value =  1.509433477775008
x =  0.03 p-value =  0.9793600702240108
===========[ 99% threshold ]
x =  0.031 p-value =  0.627851666340222
x =  0.032 p-value =  0.397941064763926
x =  0.033 p-value =  0.2494994191665769
x =  0.034 p-value =  0.1548225151558883
x =  0.035 p-value =  0.09513083442077559
===========[ 99.9% threshold ]
x =  0.036 p-value =  0.05790623005559061
x =  0.037 p-value =  0.03493227247926466
x =  0.038 p-value =  0.02089269129656085
x =  0.039 p-value =  0.01239324553446247
x =  0.04 p-value =  0.007293660695024255
```

5.4. Bayesian factor analysis of efficacy thresholds for mortality rate reduction

Mortality rate reduction: Lab confirmed and clinically diagnosed treated high risk group through June 14, 2020 (800 patients with 2 deaths) [12] against untreated mortality rates. Integrals were calculated symbolically with exact arithmetic.

- Maximum high-risk cohort mortality rate $p_2 = 0.02$

```
f(t) := lbayesmax(800,2, t, 2/100);
g(t) := pdistr(800,2,t);
xlist: makelist(t/1000,t,1,19,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.001 log bayes =  - 0.02360244357001934 p-value =  19.11718535039783
x =  0.002 log bayes =  0.397089728779972 p-value =  67.68363748520372
x =  0.003 log bayes =  0.6331158756155819 p-value =  100.0
x =  0.004 log bayes =  0.8173283057220773 p-value =  77.69711192391122
x =  0.005 log bayes =  0.9942764369960841 p-value =  45.18462307844748
x =  0.006 log bayes =  1.188653438743439 p-value =  25.44402391878668
x =  0.007 log bayes =  1.396412111547157 p-value =  19.52313955172368
x =  0.008 log bayes =  1.613969964415513 p-value =  10.63740091933478
```

```
x =  0.009 log bayes =  1.838559577085591 p-value =  5.702329861935913
x =  0.01 log bayes =  2.067925708887017 p-value =  3.018401049036129
===========[ 95% threshold ]
===========[ bayes 2 threshold ]
x =  0.011 log bayes =  2.300104395820878 p-value =  1.581442969062921
x =  0.012 log bayes =  2.533314454770625 p-value =  0.8215294582765259
===========[ 99% threshold ]
x =  0.013 log bayes =  2.765577662559006 p-value =  0.4236831756966519
===========[ bayes 2.7 threshold ]
x =  0.014 log bayes =  2.995126362169135 p-value =  0.2171410923985604
x =  0.015 log bayes =  3.219668614834722 p-value =  0.1106817409556868
x =  0.016 log bayes =  3.436850346970831 p-value =  0.05614779050966141
===========[ 99.9% threshold ]
x =  0.017 log bayes =  3.644350798167292 p-value =  0.02836321921788459
x =  0.018 log bayes =  3.839289003716655 p-value =  0.01427419920752369
===========[ bayes 3.7 threshold ]
x =  0.019 log bayes =  4.019717138624746 p-value =  0.00715977351608265
```

- Maximum high-risk cohort mortality rate $p_2 = 0.05$

```
f(t) := lbayesmax(800,2, t, 5/100);
g(t) := pdistr(800,2,t);
xlist: makelist(t/1000,t,1,20,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.001 log bayes =  0.3878335882261972 p-value =  19.11718535039783
x =  0.002 log bayes =  0.823050617366588 p-value =  67.68363748520372
x =  0.003 log bayes =  1.07475401479614 p-value =  100.0
x =  0.004 log bayes =  1.27594993242556 p-value =  77.69711192391122
x =  0.005 log bayes =  1.471371739356816 p-value =  45.18462307844748
x =  0.006 log bayes =  1.685934577284479 p-value =  25.44402391878668
x =  0.007 log bayes =  1.915861629195897 p-value =  19.52313955172368
x =  0.008 log bayes =  2.15790288872038 p-value =  10.63740091933478
===========[ bayes 2 threshold ]
x =  0.009 log bayes =  2.409703553895587 p-value =  5.702329861935913
x =  0.01 log bayes =  2.669524697562606 p-value =  3.018401049036129
===========[ 95% threshold ]
x =  0.011 log bayes =  2.93605260006106 p-value =  1.581442969062921
===========[ bayes 2.7 threshold ]
x =  0.012 log bayes =  3.208327743324983 p-value =  0.8215294582765259
===========[ 99% threshold ]
x =  0.013 log bayes =  3.485408663921015 p-value =  0.4236831756966519
x =  0.014 log bayes =  3.766824742509705 p-value =  0.2171410923985604
===========[ bayes 3.7 threshold ]
x =  0.015 log bayes =  4.051876859866955 p-value =  0.1106817409556868
x =  0.016 log bayes =  4.340104607626055 p-value =  0.05614779050966141
===========[ 99.9% threshold ]
x =  0.017 log bayes =  4.631325656492189 p-value =  0.02836321921788459
x =  0.018 log bayes =  4.924892149840545 p-value =  0.01427419920752369
x =  0.019 log bayes =  5.220925922494471 p-value =  0.00715977351608265
x =  0.02 log bayes =  5.51889732908614 p-value =  0.003580566333983698
```

- Maximum high-risk cohort mortality rate $p_2 = 0.10$

```
f(t) := lbayesmax(800,2, t, 10/100);
```

```
g(t) := pdistr(800,2,t);
xlist: makelist(t/1000,t,1,20,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.001 log bayes =  0.6932727027952328 p-value =  19.11718535039783
x =  0.002 log bayes =  1.133035455683495 p-value =  67.68363748520372
x =  0.003 log bayes =  1.389427891126667 p-value =  100.0
x =  0.004 log bayes =  1.595463333783553 p-value =  77.69711192391122
x =  0.005 log bayes =  1.795882830870318 p-value =  45.18462307844748
x =  0.006 log bayes =  2.015609754397986 p-value =  25.44402391878668
===========[ bayes 2 threshold ]
x =  0.007 log bayes =  2.250876122170239 p-value =  19.52313955172368
x =  0.008 log bayes =  2.498441425668022 p-value =  10.63740091933478
x =  0.009 log bayes =  2.755961089496922 p-value =  5.702329861935913
===========[ bayes 2.7 threshold ]
x =  0.01 log bayes =  3.021707215673925 p-value =  3.018401049036129
===========[ 95% threshold ]
x =  0.011 log bayes =  3.294377999679391 p-value =  1.581442969062921
x =  0.012 log bayes =  3.573026818858183 p-value =  0.8215294582765259
===========[ 99% threshold ]
x =  0.013 log bayes =  3.85672619247233 p-value =  0.4236831756966519
===========[ bayes 3.7 threshold ]
x =  0.014 log bayes =  4.14502069298538 p-value =  0.2171410923985604
x =  0.015 log bayes =  4.437227741229773 p-value =  0.1106817409556868
x =  0.016 log bayes =  4.732904976643285 p-value =  0.05614779050966141
===========[ 99.9% threshold ]
x =  0.017 log bayes =  5.031889808985547 p-value =  0.02836321921788459
x =  0.018 log bayes =  5.333556023894564 p-value =  0.01427419920752369
x =  0.019 log bayes =  5.63804924751887 p-value =  0.00715977351608265
x =  0.02 log bayes =  5.944866061317426 p-value =  0.003580566333983698
```

5.5. Bayesian factor analysis of efficacy thresholds for hospitalization rate reduction

Hospitalization rate reduction: Lab confirmed and clinically diagnosed treated high risk group through June 14, 2020 (800 patients with 12 hospitalizations) [12] against untreated hosqitalization rates.

- Maximum high-risk cohort hospitalization rate $p_2 = 0.10$.

```
f(t) := lbayesmax(800, 12, t, 10/100);
g(t) := pdistr(800,12,t);
xlist: makelist(t/1000,t,23,40,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.023 log bayes =  1.62405869904765 p-value =  15.54013045650735
x =  0.024 log bayes =  1.768648225238603 p-value =  10.4981160034363
x =  0.025 log bayes =  1.92041233340645 p-value =  6.977256773728229
x =  0.026 log bayes =  2.078970123408494 p-value =  5.744010066021493
===========[ bayes 2 threshold ]
x =  0.027 log bayes =  2.243931894140307 p-value =  3.713811001405364
===========[ 95% threshold ]
x =  0.028 log bayes =  2.414928189354164 p-value =  2.368631054308999
x =  0.029 log bayes =  2.591688816082273 p-value =  1.492162554770994
x =  0.03 log bayes =  2.773777522492486 p-value =  0.9295129602098239
===========[ 99% threshold ]
===========[ bayes 2.7 threshold ]
x =  0.031 log bayes =  2.961074917679372 p-value =  0.5730858984645315
x =  0.032 log bayes =  3.153214547587449 p-value =  0.4596197217292147
```

```
x =  0.033 log bayes =  3.349961639470907 p-value =  0.2773973209475854
x =  0.034 log bayes =  3.551088473390008 p-value =  0.1658903283945886
x =  0.035 log bayes =  3.756359128709967 p-value =  0.09836318158406657
===========[ 99.9% threshold ]
===========[ bayes 3.7 threshold ]
x =  0.036 log bayes =  3.965704783900136 p-value =  0.05785982432256075
x =  0.037 log bayes =  4.178806823484106 p-value =  0.03378029431625588
x =  0.038 log bayes =  4.395505974792782 p-value =  0.01958273723671357
x =  0.039 log bayes =  4.615706240957454 p-value =  0.01127628623826122
x =  0.04 log bayes =  4.839228976230477 p-value =  0.006451805449457608
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.15$.

```
f(t) := lbayesmax(800, 12, t, 15/100);
g(t) := pdistr(800,12,t);
xlist: makelist(t/1000,t,23,40,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.023 log bayes =  1.84137169483112 p-value =  15.54013045650735
x =  0.024 log bayes =  1.988205178075364 p-value =  10.4981160034363
x =  0.025 log bayes =  2.142261083022798 p-value =  6.977256773728229
===========[ bayes 2 threshold ]
x =  0.026 log bayes =  2.30316008883975 p-value =  5.744010066021493
x =  0.027 log bayes =  2.470514145459257 p-value =  3.713811001405364
===========[ 95% threshold ]
x =  0.028 log bayes =  2.643955523597636 p-value =  2.368631054308999
x =  0.029 log bayes =  2.823215837679643 p-value =  1.492162554770994
===========[ bayes 2.7 threshold ]
x =  0.03 log bayes =  3.007860728525842 p-value =  0.9295129602098239
===========[ 99% threshold ]
x =  0.031 log bayes =  3.197772788334638 p-value =  0.5730858984645315
x =  0.032 log bayes =  3.392587642187328 p-value =  0.4596197217292147
x =  0.033 log bayes =  3.59207269851625 p-value =  0.2773973209475854
x =  0.034 log bayes =  3.796002527075053 p-value =  0.1658903283945886
===========[ bayes 3.7 threshold ]
x =  0.035 log bayes =  4.00414361242072 p-value =  0.09836318158406657
===========[ 99.9% threshold ]
x =  0.036 log bayes =  4.216429661252723 p-value =  0.05785982432256075
x =  0.037 log bayes =  4.432544717513952 p-value =  0.03378029431625588
x =  0.038 log bayes =  4.652332307964707 p-value =  0.01958273723671357
x =  0.039 log bayes =  4.875699384733353 p-value =  0.01127628623826122
x =  0.04 log bayes =  5.102470411005076 p-value =  0.006451805449457608
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.20$.

```
f(t) := lbayesmax(800, 12, t, 20/100);
g(t) := pdistr(800,12,t);
xlist: makelist(t/1000,t,23,40,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.023 log bayes =  1.985541240236975 p-value =  15.54013045650735
x =  0.024 log bayes =  2.133347300771955 p-value =  10.4981160034363
===========[ bayes 2 threshold ]
x =  0.025 log bayes =  2.288389118701045 p-value =  6.977256773728229
x =  0.026 log bayes =  2.450287651960118 p-value =  5.744010066021493
x =  0.027 log bayes =  2.618655137148668 p-value =  3.713811001405364
```

```
===========[ 95% threshold ]
x =  0.028 log bayes =  2.793124139830436 p-value =  2.368631054308999
===========[ bayes 2.7 threshold ]
x =  0.029 log bayes =  2.973426577755345 p-value =  1.492162554770994
x =  0.03 log bayes =  3.159128403856494 p-value =  0.9295129602098239
===========[ 99% threshold ]
x =  0.031 log bayes =  3.350112531555775 p-value =  0.5730858984645315
x =  0.032 log bayes =  3.546014916607066 p-value =  0.4596197217292147
x =  0.033 log bayes =  3.746603307917665 p-value =  0.2773973209475854
===========[ bayes 3.7 threshold ]
x =  0.034 log bayes =  3.951652625888201 p-value =  0.1658903283945886
x =  0.035 log bayes =  4.160929716281008 p-value =  0.09836318158406657
===========[ 99.9% threshold ]
x =  0.036 log bayes =  4.374368657963939 p-value =  0.05785982432256075
x =  0.037 log bayes =  4.591653878434494 p-value =  0.03378029431625588
x =  0.038 log bayes =  4.812629299837162 p-value =  0.01958273723671357
x =  0.039 log bayes =  5.03720228197854 p-value =  0.01127628623826122
x =  0.04 log bayes =  5.265197708502766 p-value =  0.006451805449457608
```

6. Analysis of Procter’s data – 1st study

6.1. Frequentist efficacy threshold calculation for mortality rate reduction

- Mortality rate reduction: From Procter study [13], 320 high-risk patients treated with 1 death, against untreated mortality rates.

```
g(t) := pdistr(320,1,t);
xlist: makelist(t/1000,t,13,35,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.013 p-value =  13.91970464846517
x =  0.014 p-value =  14.43709057971318
x =  0.015 p-value =  10.10370958869166
x =  0.016 p-value =  7.072008175623298
x =  0.017 p-value =  4.958953725054154
===========[ 95% threshold ]
x =  0.018 p-value =  3.48764883806858
x =  0.019 p-value =  3.636716683421755
x =  0.02 p-value =  2.513152474416863
x =  0.021 p-value =  1.740532329913697
x =  0.022 p-value =  1.2092064358047
x =  0.023 p-value =  0.8432694395557437
===========[ 99% threshold ]
x =  0.024 p-value =  0.8872943936829412
x =  0.025 p-value =  0.6068957711007117
x =  0.026 p-value =  0.4163837491960345
x =  0.027 p-value =  0.2867438640397117
x =  0.028 p-value =  0.1983032132119638
x =  0.029 p-value =  0.211444602142885
x =  0.03 p-value =  0.1432404301496832
x =  0.031 p-value =  0.09738081326308919
===========[ 99.9% threshold ]
x =  0.032 p-value =  0.06647576084940104
x =  0.033 p-value =  0.04558499816313139
x =  0.034 p-value =  0.03141064302827002
```

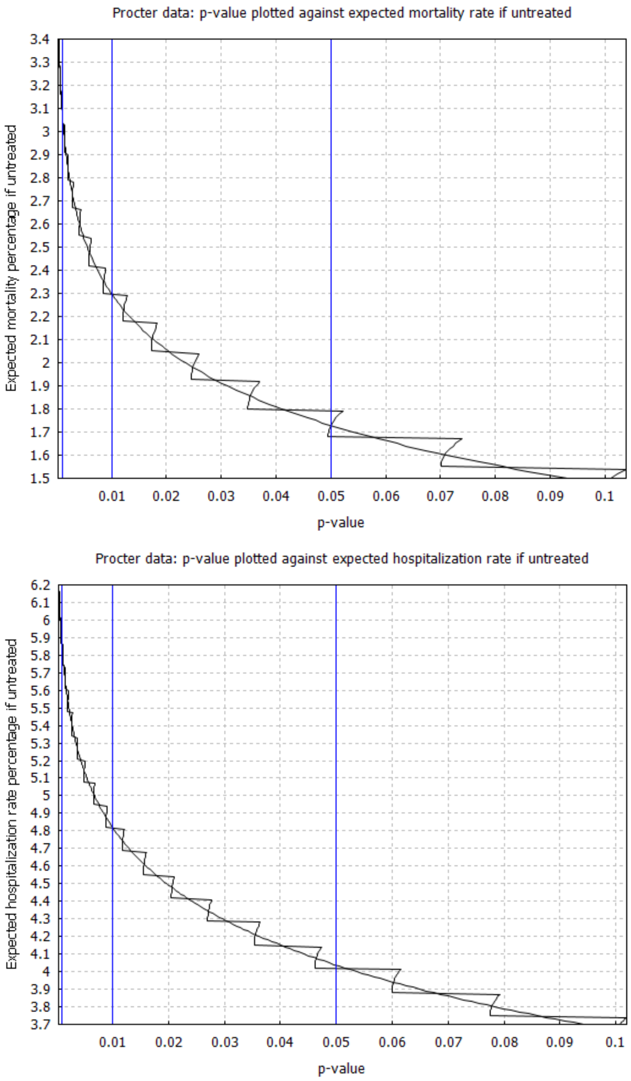

Figure 9: Relationship between *p*-value and expected mortality and hospitalization rate for high risk patients without early treatment, based on the case series data from Procter's dataset of 320 high-risk patients [13].

```
x =  0.035 p-value =  0.03316496316963895
```

- Selection bias threshold for 95% confidence (threshold 1.7%)

```
g(t) := pdistr(320, ceiling(320*0.017), t);
xlist: makelist(t/1000, t, 35, 45);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.035 p-value =  12.7532931285363
x =  0.036 p-value =  12.99892776641984
x =  0.037 p-value =  10.06751552424303
x =  0.038 p-value =  7.77527411245212
x =  0.039 p-value =  5.995878931138274
x =  0.04 p-value =  6.122271737867003
x =  0.041 p-value =  4.66327408784768
=========[ 95% selection bias threshold ]
```

```
x =  0.042 p-value =  3.547947269443758
x =  0.043 p-value =  2.699178732939873
x =  0.044 p-value =  2.7625598984677
x =  0.045 p-value =  2.074170478424906
```

- Selection bias threshold for 99% confidence (threshold 2.3%)

```
g(t) := pdistr(320, ceiling(320*0.023), t);
xlist: makelist(t/1000, t, 50, 60);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.05 p-value =  3.909803484278417
x =  0.051 p-value =  3.027882073013489
x =  0.052 p-value =  3.091596088235616
x =  0.053 p-value =  2.36595863783398
x =  0.054 p-value =  1.810043993987881
x =  0.055 p-value =  1.3854741564888
x =  0.056 p-value =  1.415810504979562
x =  0.057 p-value =  1.07005178005005
x =  0.058 p-value =  0.8092535340641899
=========[ 99% selection bias threshold ]
x =  0.059 p-value =  0.6128719513730921
x =  0.06 p-value =  0.627229598954903
```

- Selection bias threshold for 99.9% confidence (threshold 3.1%)

```
g(t) := pdistr(320, ceiling(320*0.031), t);
xlist: makelist(t/1000, t, 70, 80);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.07 p-value =  0.4152627852812387
x =  0.071 p-value =  0.3158683201390354
x =  0.072 p-value =  0.3222349744881794
x =  0.073 p-value =  0.241901675569567
x =  0.074 p-value =  0.1819345811355869
x =  0.075 p-value =  0.1371703274214665
x =  0.076 p-value =  0.1399926794878326
x =  0.077 p-value =  0.1040893388699597
x =  0.078 p-value =  0.07758600418075177
=========[ 99.9% selection bias threshold ]
x =  0.079 p-value =  0.05800631950496135
x =  0.08 p-value =  0.05925938258692712
```

- Plot code for Fig. 9

```
f(t) := pdistr(320, 1, t/100)/100;
g(t) := pdistrcp(320, 1, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 150, 340, 1);
dat2: makelist([g(t/100), float(t/100)], t, 150, 340, 1);
draw2d(
grid=true,
title="Procter data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
ylabel="Expected mortality percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
```

```
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 1.5, 3.4),
parametric(0.01, x, x, 1.5, 3.4),
parametric(0.001, x, x, 1.5, 3.4)
);
```

- Clopper-Pearson interval:

  ```
  g(t) := pdistrcp(320,1,t);
  xlist: makelist(t/1000,t,13,35,1);
  for t in xlist do print("x = ", float(t), "p-value = ", g(t));
  x =  0.013 p-value =  15.84002510343056
  x =  0.014 p-value =  12.17406144137323
  x =  0.015 p-value =  9.321609116578959
  x =  0.016 p-value =  7.113460433316616
  x =  0.017 p-value =  5.411779661180995
  x =  0.018 p-value =  4.105663463597442
  ===========[ 95% threshold ]
  x =  0.019 p-value =  3.106773280292748
  x =  0.02 p-value =  2.345332940875868
  x =  0.021 p-value =  1.766619421128715
  x =  0.022 p-value =  1.327977524479585
  x =  0.023 p-value =  0.9963355428930543
  ===========[ 99% threshold ]
  x =  0.024 p-value =  0.7461722249546294
  x =  0.025 p-value =  0.557874949772626
  x =  0.026 p-value =  0.4164279855683933
  x =  0.027 p-value =  0.3103737500663435
  x =  0.028 p-value =  0.2309964034117403
  x =  0.029 p-value =  0.1716842951576985
  x =  0.03 p-value =  0.1274348505325426
  x =  0.031 p-value =  0.09447194846060902
  ===========[ 99.9% threshold ]
  x =  0.032 p-value =  0.0699515108929298
  x =  0.033 p-value =  0.05173584196248539
  x =  0.034 p-value =  0.03822126445563505
  x =  0.035 p-value =  0.02820688095286836
  ```

6.2. Frequentist efficacy threshold calculation for hospitalization rate reduction

- Hospitalization rate reduction: From Procter study [13], 320 high-risk patients treated with 6 hospitalizations, against untreated mortality rates.

  ```
  g(t) := pdistr(320,6,t);
  xlist: makelist(t/1000,t,35,65,1);
  for t in xlist do print("x = ", float(t), "p-value = ", g(t));
  x =  0.035 p-value =  12.7532931285363
  x =  0.036 p-value =  12.99892776641984
  x =  0.037 p-value =  10.06751552424303
  x =  0.038 p-value =  7.77527411245212
  x =  0.039 p-value =  5.995878931138274
  ```

```
x =  0.04 p-value =  6.122271737867003
x =  0.041 p-value =  4.66327408784768
===========[ 95% threshold ]
x =  0.042 p-value =  3.547947269443758
x =  0.043 p-value =  2.699178732939873
x =  0.044 p-value =  2.7625598984677
x =  0.045 p-value =  2.074170478424906
x =  0.046 p-value =  1.557453739783845
x =  0.047 p-value =  1.170607013495124
x =  0.048 p-value =  1.202390260363017
x =  0.049 p-value =  0.8911814107362057
===========[ 99% threshold ]
x =  0.05 p-value =  0.6611825051739697
x =  0.051 p-value =  0.4914151719906096
x =  0.052 p-value =  0.5073769120364107
x =  0.053 p-value =  0.3715760087288503
x =  0.054 p-value =  0.2725860651910377
x =  0.055 p-value =  0.2004487955212581
x =  0.056 p-value =  0.2084014375883334
x =  0.057 p-value =  0.150895999792609
x =  0.058 p-value =  0.1095045062408967
x =  0.059 p-value =  0.07969825867093394
===========[ 99.9% threshold ]
x =  0.06 p-value =  0.05820540819801348
x =  0.061 p-value =  0.05986208366501996
x =  0.062 p-value =  0.04298571825714922
x =  0.063 p-value =  0.03096977558525352
x =  0.064 p-value =  0.02239863415163661
x =  0.065 p-value =  0.02325623551427935
```

- Selection bias threshold for 95% confidence (threshold 4.1%)

```
g(t) := pdistr(320, ceiling(320*0.041), t);
xlist: makelist(t/1000, t, 65, 75);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.065 p-value =  13.96618423682955
x =  0.066 p-value =  11.51395724973006
x =  0.067 p-value =  11.59550326388617
x =  0.068 p-value =  9.477114275911061
x =  0.069 p-value =  7.729232125407765
x =  0.07 p-value =  7.816094430031508
x =  0.071 p-value =  6.318128694053308
x =  0.072 p-value =  5.098491179890202
x =  0.073 p-value =  4.110349967790462
=========[ 95% selection bias threshold ]
x =  0.074 p-value =  4.144877230296738
x =  0.075 p-value =  3.309853509708569
```

- Selection bias threshold for 99% confidence (threshold 4.9%)

```
g(t) := pdistr(320, ceiling(320*0.049), t);
xlist: makelist(t/1000, t, 85, 95);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.085 p-value =  2.102991220556766
```

```
x =  0.086 p-value =  2.11945762865424
x =  0.087 p-value =  1.68500556187122
x =  0.088 p-value =  1.339740196933158
x =  0.089 p-value =  1.358726548132611
x =  0.09 p-value =  1.06971468104557
x =  0.091 p-value =  0.8424423670643589
=========[ 99% selection bias threshold ]
x =  0.092 p-value =  0.6640640932181312
x =  0.093 p-value =  0.6711297153426505
x =  0.094 p-value =  0.5234758964250854
x =  0.095 p-value =  0.4087549223470162
```

- Selection bias threshold for 99.9% confidence (threshold 5.9%)

```
g(t) := pdistr(320, ceiling(320*0.059), t);
xlist: makelist(t/1000, t, 105, 120);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.105 p-value =  0.6014898912290743
x =  0.106 p-value =  0.4757426988567413
x =  0.107 p-value =  0.4816292684176465
x =  0.108 p-value =  0.3771232995225856
x =  0.109 p-value =  0.2956429228048311
x =  0.11 p-value =  0.2321626786826054
x =  0.111 p-value =  0.2339549070745093
x =  0.112 p-value =  0.181760781415003
x =  0.113 p-value =  0.1414751063458982
x =  0.114 p-value =  0.1437287808966021
x =  0.115 p-value =  0.1106464584107458
x =  0.116 p-value =  0.08534928638402686
=========[ 99.9% selection bias threshold ]
x =  0.117 p-value =  0.06600092528205523
x =  0.118 p-value =  0.06674776769532378
x =  0.119 p-value =  0.05101630624381473
x =  0.12 p-value =  0.0390952745880248
```

- Plot code for Fig. 9

```
f(t) := pdistr(320, 6, t/100)/100;
g(t) := pdistrcp(320,6, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 370, 620, 1);
dat2: makelist([g(t/100), float(t/100)], t, 370, 620, 1);
draw2d(
grid=true,
title="Procter data: p-value plotted against expected hospitalization rate if untreated",
xlabel="p-value",
ylabel="Expected hospitalization rate percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 3.70, 6.20),
```

```
parametric(0.01, x, x, 3.70, 6.20),
parametric(0.001, x, x, 3.70, 6.20)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(320,6,t);
xlist: makelist(t/1000,t,35,65,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.035 p-value =  13.46776977035591
x =  0.036 p-value =  11.28320105890921
x =  0.037 p-value =  9.417786993379485
x =  0.038 p-value =  7.832599053488089
x =  0.039 p-value =  6.491734310020937
x =  0.04 p-value =  5.36250359081055
x =  0.041 p-value =  4.41547832646288
===========[ 95% threshold ]
x =  0.042 p-value =  3.624430309398063
x =  0.043 p-value =  2.966193848964016
x =  0.044 p-value =  2.42047499933185
x =  0.045 p-value =  1.969627952795471
x =  0.046 p-value =  1.59841450350767
x =  0.047 p-value =  1.293758790934348
x =  0.048 p-value =  1.044506365218682
x =  0.049 p-value =  0.8411939738840234
===========[ 99% threshold ]
x =  0.05 p-value =  0.6758343193988439
x =  0.051 p-value =  0.5417183323745894
x =  0.052 p-value =  0.4332361897803202
x =  0.053 p-value =  0.3457173235078597
x =  0.054 p-value =  0.2752889556067134
x =  0.055 p-value =  0.2187522104607538
x =  0.056 p-value =  0.1734745446632522
x =  0.057 p-value =  0.1372970621592962
x =  0.058 p-value =  0.1084552114342738
x =  0.059 p-value =  0.08551136515452167
===========[ 99.9% threshold ]
x =  0.06 p-value =  0.06729783814406887
x =  0.061 p-value =  0.0528689891050715
x =  0.062 p-value =  0.04146116133361279
x =  0.063 p-value =  0.03245933753355823
x =  0.064 p-value =  0.02536950616816381
x =  0.065 p-value =  0.01979585632987889
```

6.3. Bayesian factor analysis of efficacy thresholds for mortality rate reduction

Mortality rate reduction: From Procter study [13], 320 high-risk patients treated with 1 death, against untreated mortality rates. Integrals were calculated symbolically with exact arithmetic.

- Maximum high-risk cohort mortality rate $p_2 = 0.02$

```
f(t) := lbayesmax(320,1, t, 2/100);
g(t) := pdistr(320,1,t);
xlist: makelist(t/1000,t,10,19,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
```

```
x =  0.01 log bayes =  0.7861394157191933 p-value =  38.84303075052667
x =  0.011 log bayes =  0.8580924052693669 p-value =  27.62884497807075
x =  0.012 log bayes =  0.930152023979093 p-value =  19.60482195393931
x =  0.013 log bayes =  1.001910515307586 p-value =  13.91970464846517
x =  0.014 log bayes =  1.07296101011259 p-value =  14.43709057971318
x =  0.015 log bayes =  1.142958235486832 p-value =  10.10370958869166
x =  0.016 log bayes =  1.211641281115763 p-value =  7.072008175623298
x =  0.017 log bayes =  1.278701898510068 p-value =  4.958953725054154
===========[ 95% threshold ]
x =  0.018 log bayes =  1.343920347955987 p-value =  3.48764883806858
x =  0.019 log bayes =  1.407057341441779 p-value =  3.636716683421755
```

- Maximum high-risk cohort mortality rate $p_2 = 0.05$

```
f(t) := lbayesmax(320,1, t, 5/100);
g(t) := pdistr(320,1,t);
xlist: makelist(t/1000,t,10,35,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.01 log bayes =  1.357431539561896 p-value =  38.84303075052667
x =  0.011 log bayes =  1.454996273325203 p-value =  27.62884497807075
x =  0.012 log bayes =  1.554592159902699 p-value =  19.60482195393931
x =  0.013 log bayes =  1.655949547422388 p-value =  13.91970464846517
x =  0.014 log bayes =  1.758798138970574 p-value =  14.43709057971318
x =  0.015 log bayes =  1.862924552695767 p-value =  10.10370958869166
x =  0.016 log bayes =  1.968191499782834 p-value =  7.072008175623298
x =  0.017 log bayes =  2.074402188206613 p-value =  4.958953725054154
===========[ 95% threshold ]
===========[ bayes 2 threshold ]
x =  0.018 log bayes =  2.181432149711834 p-value =  3.48764883806858
x =  0.019 log bayes =  2.289117262338078 p-value =  3.636716683421755
x =  0.02 log bayes =  2.397472831657991 p-value =  2.513152474416863
x =  0.021 log bayes =  2.50623527497538 p-value =  1.740532329913697
x =  0.022 log bayes =  2.615377419133608 p-value =  1.2092064358047
x =  0.023 log bayes =  2.7248543753746 p-value =  0.8432694395557437
===========[ 99% threshold ]
===========[ bayes 2.7 threshold ]
x =  0.024 log bayes =  2.834507143043413 p-value =  0.8872943936829412
x =  0.025 log bayes =  2.944246534090083 p-value =  0.6068957711007117
x =  0.026 log bayes =  3.054000294021984 p-value =  0.4163837491960345
x =  0.027 log bayes =  3.163757417852231 p-value =  0.2867438640397117
x =  0.028 log bayes =  3.27332658065278 9 p-value =  0.1983032132119638
x =  0.029 log bayes =  3.382565458987208 p-value =  0.211444602142885
x =  0.03 log bayes =  3.491481064902819 p-value =  0.1432404301496832
x =  0.031 log bayes =  3.599998359823178 p-value =  0.09738081326308919
===========[ 99.9% threshold ]
x =  0.032 log bayes =  3.707753476978134 p-value =  0.06647576084940104
===========[ bayes 3.7 threshold ]
x =  0.033 log bayes =  3.815093707397006 p-value =  0.04558499816313139
x =  0.034 log bayes =  3.921336491134962 p-value =  0.03141064302827002
x =  0.035 log bayes =  4.02691403596671 p-value =  0.03316496316963895
```

- Maximum high-risk cohort mortality rate $p_2 = 0.10$

```
f(t) := lbayesmax(320,1, t, 10/100);
```

```
g(t) := pdistr(320,1,t);
xlist: makelist(t/1000,t,10,35,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.01 log bayes =  1.709610797227587 p-value =  38.84303075052667
x =  0.011 log bayes =  1.813317486577115 p-value =  27.62884497807075
x =  0.012 log bayes =  1.919285831353542 p-value =  19.60482195393931
x =  0.013 log bayes =  2.02726006704199 p-value =  13.91970464846517
===========[ bayes 2 threshold ]
x =  0.014 log bayes =  2.136984960974096 p-value =  14.43709057971318
x =  0.015 log bayes =  2.24826350046977 p-value =  10.10370958869166
x =  0.016 log bayes =  2.360976215289907 p-value =  7.072008175623298
x =  0.017 log bayes =  2.474945744574832 p-value =  4.958953725054154
===========[ 95% threshold ]
x =  0.018 log bayes =  2.590068848265894 p-value =  3.48764883806858
x =  0.019 log bayes =  2.706204638180443 p-value =  3.636716683421755
===========[ bayes 2.7 threshold ]
x =  0.02 log bayes =  2.823393895067389 p-value =  2.513152474416863
x =  0.021 log bayes =  2.941401019347554 p-value =  1.740532329913697
x =  0.022 log bayes =  3.0602296299133 p-value =  1.2092064358047
x =  0.023 log bayes =  3.179868778351299 p-value =  0.8432694395557437
===========[ 99% threshold ]
x =  0.024 log bayes =  3.300196934390387 p-value =  0.8872943936829412
x =  0.025 log bayes =  3.421166338431283 p-value =  0.6068957711007117
x =  0.026 log bayes =  3.542750600335664 p-value =  0.4163837491960345
x =  0.027 log bayes =  3.664989545759764 p-value =  0.2867438640397117
x =  0.028 log bayes =  3.78774823103065 p-value =  0.1983032132119638
===========[ bayes 3.7 threshold ]
x =  0.029 log bayes =  3.910946902110273 p-value =  0.211444602142885
x =  0.03 log bayes =  4.034662015460534 p-value =  0.1432404301496832
x =  0.031 log bayes =  4.158895579840856 p-value =  0.09738081326308919
===========[ 99.9% threshold ]
x =  0.032 log bayes =  4.283369133301711 p-value =  0.06647576084940104
x =  0.033 log bayes =  4.408524488026684 p-value =  0.04558499816313139
x =  0.034 log bayes =  4.533783452130874 p-value =  0.03141064302827002
x =  0.035 log bayes =  4.65969310559565 p-value =  0.03316496316963895
```

6.4. Bayesian factor analysis of efficacy thresholds for hospitalization rate reduction

Hospitalization rate reduction: From Procter study [13], 320 high-risk patients treated with 6 hospitalizations, against untreated mortality rates.

- Maximum high-risk cohort hospitalization rate $p_2 = 0.10$.

```
f(t) := lbayesmax(320,6, t, 10/100);
g(t) := pdistr(320,6,t);
xlist: makelist(t/1000,t,35,65,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.035 log bayes =  1.446753215102681 p-value =  12.7532931285363
x =  0.036 log bayes =  1.517289170918644 p-value =  12.99892776641984
x =  0.037 log bayes =  1.589340175843624 p-value =  10.06751552424303
x =  0.038 log bayes =  1.662852155923733 p-value =  7.77527411245212
x =  0.039 log bayes =  1.73776608026608 p-value =  5.995878931138274
x =  0.04 log bayes =  1.814017822096732 p-value =  6.122271737867003
x =  0.041 log bayes =  1.891537786017222 p-value =  4.66327408784768
===========[ 95% threshold ]
```

```
x =  0.042 log bayes =  1.970250296980515 p-value =  3.547947269443758
x =  0.043 log bayes =  2.050198204833941 p-value =  2.699178732939873
===========[ bayes 2 threshold ]
x =  0.044 log bayes =  2.13121898274089 p-value =  2.7625598984677
x =  0.045 log bayes =  2.213369496787871 p-value =  2.074170478424906
x =  0.046 log bayes =  2.296501491636956 p-value =  1.557453739783845
x =  0.047 log bayes =  2.380671292763019 p-value =  1.170607013495124
x =  0.048 log bayes =  2.46579439927524 p-value =  1.202390260363017
x =  0.049 log bayes =  2.551809590425132 p-value =  0.8911814107362057
===========[ 99% threshold ]
x =  0.05 log bayes =  2.638689167906482 p-value =  0.6611825051739697
x =  0.051 log bayes =  2.726404349797012 p-value =  0.4914151719906096
===========[ bayes 2.7 threshold ]
x =  0.052 log bayes =  2.814930310712895 p-value =  0.5073769120364107
x =  0.053 log bayes =  2.904239560701249 p-value =  0.3715760087288503
x =  0.054 log bayes =  2.994273497469943 p-value =  0.2725860651910377
x =  0.055 log bayes =  3.085006557966146 p-value =  0.2004487955212581
x =  0.056 log bayes =  3.176428255440152 p-value =  0.2084014375883334
x =  0.057 log bayes =  3.268487906360863 p-value =  0.150895999792609
x =  0.058 log bayes =  3.361147436312254 p-value =  0.1095045062408967
x =  0.059 log bayes =  3.454366845815508 p-value =  0.07969825867093394
===========[ 99.9% threshold ]
x =  0.06 log bayes =  3.548103963300445 p-value =  0.05820540819801348
x =  0.061 log bayes =  3.642314159405314 p-value =  0.05986208366501996
x =  0.062 log bayes =  3.737083569695446 p-value =  0.04298571825714922
===========[ bayes 3.7 threshold ]
x =  0.063 log bayes =  3.832290941945655 p-value =  0.03096977558525352
x =  0.064 log bayes =  3.927853961967385 p-value =  0.02239863415163661
x =  0.065 log bayes =  4.023785031723088 p-value =  0.02325623551427935
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.15$.

```
f(t) := lbayesmax(320,6, t, 15/100);
g(t) := pdistr(320,6,t);
xlist: makelist(t/1000,t,35,65,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.035 log bayes =  1.694537654762189 p-value =  12.7532931285363
x =  0.036 log bayes =  1.768013995640774 p-value =  12.99892776641984
x =  0.037 log bayes =  1.843078006757563 p-value =  10.06751552424303
x =  0.038 log bayes =  1.919678413132618 p-value =  7.77527411245212
x =  0.039 log bayes =  1.997759132299508 p-value =  5.995878931138274
x =  0.04 log bayes =  2.077259145701067 p-value =  6.122271737867003
===========[ bayes 2 threshold ]
x =  0.041 log bayes =  2.158112137168999 p-value =  4.66327408784768
===========[ 95% threshold ]
x =  0.042 log bayes =  2.240245894098762 p-value =  3.547947269443758
x =  0.043 log bayes =  2.323706925268556 p-value =  2.699178732939873
x =  0.044 log bayes =  2.408336573727605 p-value =  2.7625598984677
x =  0.045 log bayes =  2.494195802187452 p-value =  2.074170478424906
x =  0.046 log bayes =  2.581140695919159 p-value =  1.557453739783845
x =  0.047 log bayes =  2.669232183856161 p-value =  1.170607013495124
x =  0.048 log bayes =  2.758390652082855 p-value =  1.202390260363017
===========[ bayes 2.7 threshold ]
x =  0.049 log bayes =  2.848560073014853 p-value =  0.8911814107362057
```

```
===========[ 99% threshold ]
x =  0.05 log bayes =  2.93971827260551 p-value =  0.6611825051739697
x =  0.051 log bayes =  3.031842351687958 p-value =  0.4914151719906096
x =  0.052 log bayes =  3.124913756316431 p-value =  0.5073769120364107
x =  0.053 log bayes =  3.218911689963446 p-value =  0.3715760087288503
x =  0.054 log bayes =  3.313784702546772 p-value =  0.2725860651910377
x =  0.055 log bayes =  3.409514882722295 p-value =  0.2004487955212581
x =  0.056 log bayes =  3.506099940059745 p-value =  0.2084014375883334
x =  0.057 log bayes =  3.603497982012326 p-value =  0.150895999792609
x =  0.058 log bayes =  3.701680375425803 p-value =  0.1095045062408967
===========[ bayes 3.7 threshold ]
x =  0.059 log bayes =  3.800617274229498 p-value =  0.07969825867093394
===========[ 99.9% threshold ]
x =  0.06 log bayes =  3.900277441321558 p-value =  0.05820540819801348
x =  0.061 log bayes =  4.000628039717964 p-value =  0.05986208366501996
x =  0.062 log bayes =  4.10176794105927 p-value =  0.04298571825714922
x =  0.063 log bayes =  4.203589668747608 p-value =  0.03096977558525352
x =  0.064 log bayes =  4.306025830957871 p-value =  0.02239863415163661
x =  0.065 log bayes =  4.409105018673765 p-value =  0.02325623551427935
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.20$.

```
f(t) := lbayesmax(320,6, t, 20/100);
g(t) := pdistr(320,6,t);
xlist: makelist(t/1000,t,35,65,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.035 log bayes =  1.851323758622472 p-value =  12.7532931285363
x =  0.036 log bayes =  1.925952992351988 p-value =  12.99892776641984
x =  0.037 log bayes =  2.00218716767809 p-value =  10.06751552424303
===========[ bayes 2 threshold ]
x =  0.038 log bayes =  2.07997540500506 p-value =  7.77527411245212
x =  0.039 log bayes =  2.159262029544684 p-value =  5.995878931138274
x =  0.04 log bayes =  2.239986443198745 p-value =  6.122271737867003
x =  0.041 log bayes =  2.3220827635488 p-value =  4.66327408784768
===========[ 95% threshold ]
x =  0.042 log bayes =  2.405479225566203 p-value =  3.547947269443758
x =  0.043 log bayes =  2.49022279999255 p-value =  2.699178732939873
x =  0.044 log bayes =  2.576155306817253 p-value =  2.7625598984677
x =  0.045 log bayes =  2.663338201287756 p-value =  2.074170478424906
x =  0.046 log bayes =  2.751628077456785 p-value =  1.557453739783845
===========[ bayes 2.7 threshold ]
x =  0.047 log bayes =  2.841086389968512 p-value =  1.170607013495124
x =  0.048 log bayes =  2.931634068265618 p-value =  1.202390260363017
x =  0.049 log bayes =  3.023215646525257 p-value =  0.8911814107362057
===========[ 99% threshold ]
x =  0.05 log bayes =  3.115809531661047 p-value =  0.6611825051739697
x =  0.051 log bayes =  3.209393425502499 p-value =  0.4914151719906096
x =  0.052 log bayes =  3.303949396018667 p-value =  0.5073769120364107
x =  0.053 log bayes =  3.399457290445092 p-value =  0.3715760087288503
x =  0.054 log bayes =  3.495866325291286 p-value =  0.2725860651910377
x =  0.055 log bayes =  3.593159279667971 p-value =  0.2004487955212581
x =  0.056 log bayes =  3.691334578554732 p-value =  0.2084014375883334
x =  0.057 log bayes =  3.790351070922741 p-value =  0.150895999792609
===========[ bayes 3.7 threshold ]
```

```
x =  0.058 log bayes =  3.890180892462395 p-value =  0.1095045062408967
x =  0.059 log bayes =  3.99079499456264 p-value =  0.07969825867093394
===========[ 99.9% threshold ]
x =  0.06 log bayes =  4.092162967559015 p-value =  0.05820540819801348
x =  0.061 log bayes =  4.194252833325294 p-value =  0.05986208366501996
x =  0.062 log bayes =  4.297164355307967 p-value =  0.04298571825714922
x =  0.063 log bayes =  4.40079098328237 p-value =  0.03096977558525352
x =  0.064 log bayes =  4.505066288080642 p-value =  0.02239863415163661
x =  0.065 log bayes =  4.610019861449511 p-value =  0.02325623551427935
```

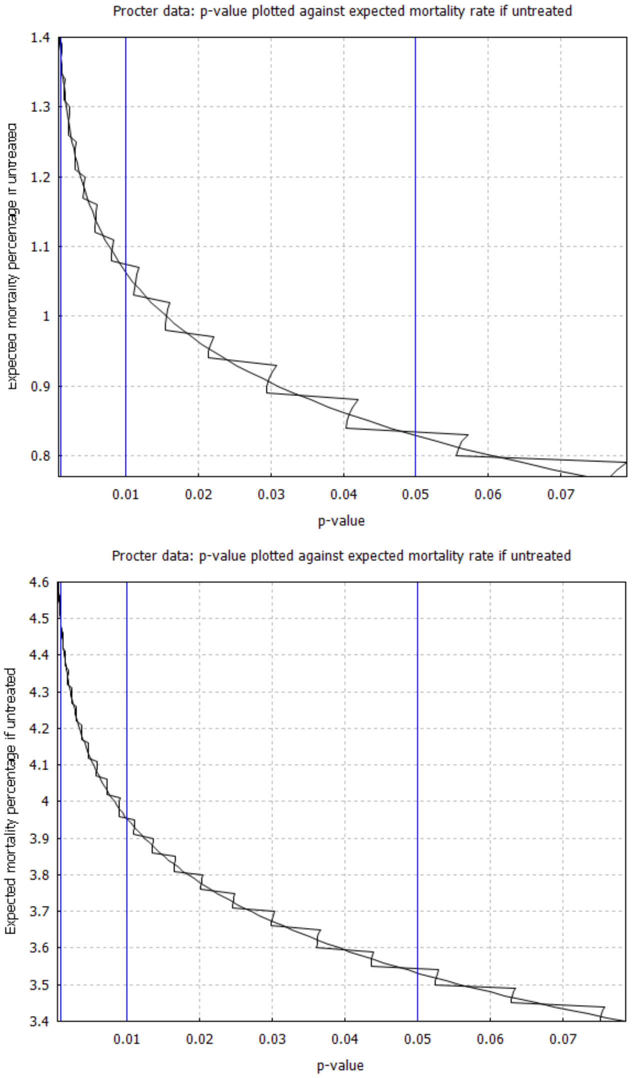

Figure 10: Relationship between *p*-value and expected mortality and hospitalization rate for high risk patients without early treatment, based on the case series data from Procter's dataset of 869 high-risk patients [14].

7. Analysis of Procter's data – 2nd study

7.1. Frequentist efficacy threshold calculation for mortality rate reduction

- Mortality rate reduction: From Procter study [14], 869 high-risk patients treated with 2 deaths, against untreated mortality rates.

```
g(t) := pdistr(869,2,t);
xlist: makelist(t/1000,t,1,14,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.001 p-value =  21.61722189137326
x =  0.002 p-value =  69.4254826802348
x =  0.003 p-value =  100.0
x =  0.004 p-value =  59.45897396666187
x =  0.005 p-value =  46.16271537375738
x =  0.006 p-value =  18.93782840635735
x =  0.007 p-value =  10.33088826739651
x =  0.008 p-value =  5.551268198499255
x =  0.009 p-value =  2.950659592148073
x =  0.01 p-value =  1.556795174687752
x =  0.011 p-value =  0.8177114621309273
x =  0.012 p-value =  0.4286400110426079
x =  0.013 p-value =  0.2246962171650994
x =  0.014 p-value =  0.07641209958529434
g(t) := pdistr(869,2,t);
xlist: makelist(t/10000,t,80,90,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.008 p-value =  5.551268198499255
x =  0.0081 p-value =  5.58313383491276
x =  0.0082 p-value =  5.641101943429484
x =  0.0083 p-value =  5.724967586575343
x =  0.0084 p-value =  4.04188577298651
===========[ 95% threshold ]
x =  0.0085 p-value =  4.051778918900128
x =  0.0086 p-value =  4.082004274776216
x =  0.0087 p-value =  4.132460285378906
x =  0.0088 p-value =  4.203067927435425
x =  0.0089 p-value =  2.93840741423051
x =  0.009 p-value =  2.950659592148073
g(t) := pdistr(869,2,t);
xlist: makelist(t/10000,t,100,110,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.01 p-value =  1.556795174687752
x =  0.0101 p-value =  1.578705509361261
x =  0.0102 p-value =  1.60963145090928
x =  0.0103 p-value =  1.111198479978945
x =  0.0104 p-value =  1.116606337744332
x =  0.0105 p-value =  1.12872352349069
x =  0.0106 p-value =  1.147595451645446
x =  0.0107 p-value =  1.173284441298622
x =  0.0108 p-value =  0.800886685780233
===========[ 99% threshold ]
x =  0.0109 p-value =  0.806788811398927
x =  0.011 p-value =  0.8177114621309273
g(t) := pdistr(869,2,t);
```

```
xlist: makelist(t/10000,t,130,140,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.013 p-value =  0.2246962171650994
x =  0.0131 p-value =  0.1507619659263774
x =  0.0132 p-value =  0.1521042826127172
x =  0.0133 p-value =  0.1545376827326893
x =  0.0134 p-value =  0.1580847220488376
x =  0.0135 p-value =  0.1072302618710838
x =  0.0136 p-value =  0.10777159838621
x =  0.0137 p-value =  0.109100110607515
x =  0.0138 p-value =  0.1112315576690632
x =  0.0139 p-value =  0.1141853911714461
x =  0.014 p-value =  0.07641209958529434
===========[ 99.9% threshold ]
```

- Selection bias threshold for 95% confidence (threshold 0.84%)

```
g(t) := pdistr(869, ceiling(869*0.0084), t);
xlist: makelist(t/1000, t, 15, 20);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.015 p-value =  20.62628762705687
x =  0.016 p-value =  13.45708016164396
x =  0.017 p-value =  8.60464441867564
x =  0.018 p-value =  5.404753923103907
x =  0.019 p-value =  3.341409111313987
x =  0.02 p-value =  2.036690776337255
g(t) := pdistr(869, ceiling(869*0.0084), t);
xlist: makelist(t/10000, t, 180, 190);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.018 p-value =  5.404753923103907
x =  0.0181 p-value =  5.443777175070581
x =  0.0182 p-value =  4.218795113566983
=========[ 95% selection bias threshold ]
x =  0.0183 p-value =  4.221858931648762
x =  0.0184 p-value =  4.234805690017189
x =  0.0185 p-value =  4.257609785818984
x =  0.0186 p-value =  4.290250805111322
x =  0.0187 p-value =  3.308833672516614
x =  0.0188 p-value =  3.311491030760805
x =  0.0189 p-value =  3.322353707945403
x =  0.019 p-value =  3.341409111313987
```

- Selection bias threshold for 99% confidence (threshold 1.08%)

```
g(t) := pdistr(869, ceiling(869*0.0108), t);
xlist: makelist(t/1000, t, 21, 27);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.021 p-value =  5.673717461614833
x =  0.022 p-value =  3.609993427057649
x =  0.023 p-value =  2.264571218478077
x =  0.024 p-value =  1.402357335947793
x =  0.025 p-value =  0.8582557356209384
x =  0.026 p-value =  0.5196414068347732
x =  0.027 p-value =  0.3115471338362369
```

```
g(t) := pdistr(869, ceiling(869*0.0108), t);
xlist: makelist(t/10000, t, 240, 250);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.024 p-value =  1.402357335947793
x =  0.0241 p-value =  1.077722387447588
x =  0.0242 p-value =  1.078627941092553
x =  0.0243 p-value =  1.082407859940978
x =  0.0244 p-value =  1.089069060559432
x =  0.0245 p-value =  1.098621984285136
x =  0.0246 p-value =  0.8407733242827532
=========[ 99% selection bias threshold ]
x =  0.0247 p-value =  0.8416354997054275
x =  0.0248 p-value =  0.8448310763541865
x =  0.0249 p-value =  0.8503675890332216
x =  0.025 p-value =  0.8582557356209384
```

- Selection bias threshold for 99.9% confidence (threshold 1.40%)

```
g(t) := pdistr(869, ceiling(869*0.0140), t);
xlist: makelist(t/1000, t, 30, 35);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.03 p-value =  0.6918289299195072
x =  0.031 p-value =  0.4288036381800545
x =  0.032 p-value =  0.2631529630611572
x =  0.033 p-value =  0.1600029117188593
x =  0.034 p-value =  0.09644472965245574
x =  0.035 p-value =  0.05766407013695021
g(t) := pdistr(869, ceiling(869*0.0140), t);
xlist: makelist(t/10000, t, 330, 340);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.033 p-value =  0.1600029117188593
x =  0.0331 p-value =  0.1615723913771697
x =  0.0332 p-value =  0.1227559260153859
x =  0.0333 p-value =  0.1229163868583616
x =  0.0334 p-value =  0.1234480779493917
x =  0.0335 p-value =  0.1243536812831283
x =  0.0336 p-value =  0.1256366074706261
x =  0.0337 p-value =  0.09509652511164528
=========[ 99.9% selection bias threshold ]
x =  0.0338 p-value =  0.09524957096862513
x =  0.0339 p-value =  0.09569819161281824
x =  0.034 p-value =  0.09644472965245574
```

- Plot code for Fig. 10

```
f(t) := pdistr(869, 2, t/100)/100;
g(t) := pdistrcp(869, 2, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 77, 140, 1);
dat2: makelist([g(t/100), float(t/100)], t, 77, 140, 1);
draw2d(
grid=true,
title="Procter data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
ylabel="Expected mortality percentage if untreated",
color=black,
```

```
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 0.77, 1.4),
parametric(0.01, x, x, 0.77, 1.4),
parametric(0.001, x, x, 0.77, 1.4)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(869,2,t);
xlist: makelist(t/1000,t,1,14,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.001 p-value =  188.447935848015
x =  0.002 p-value =  149.4459612717086
x =  0.003 p-value =  103.289029557523
x =  0.004 p-value =  64.95126866766935
x =  0.005 p-value =  38.21166275073203
x =  0.006 p-value =  21.40664281521124
x =  0.007 p-value =  11.5526439122813
x =  0.008 p-value =  6.053982096589138
x =  0.009 p-value =  3.097966354356327
x =  0.01 p-value =  1.554478258656832
x =  0.011 p-value =  0.7672189569130647
x =  0.012 p-value =  0.3733580787163425
x =  0.013 p-value =  0.1794839196587316
x =  0.014 p-value =  0.0853645370810961
g(t) := pdistrcp(869,2,t);
xlist: makelist(t/10000,t,80,90,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.008 p-value =  6.053982096589138
x =  0.0081 p-value =  5.667289188506781
x =  0.0082 p-value =  5.304066071701827
x =  0.0083 p-value =  4.962994018256992
===========[ 95% threshold ]
x =  0.0084 p-value =  4.642819087819651
x =  0.0085 p-value =  4.342349803066838
x =  0.0086 p-value =  4.060454820947502
x =  0.0087 p-value =  3.796060611620774
x =  0.0088 p-value =  3.5481491554659
x =  0.0089 p-value =  3.315755667136201
x =  0.009 p-value =  3.097966354356327
g(t) := pdistrcp(869,2,t);
xlist: makelist(t/10000,t,100,110,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.01 p-value =  1.554478258656832
x =  0.0101 p-value =  1.449511265282969
x =  0.0102 p-value =  1.351413378300286
x =  0.0103 p-value =  1.259753688140494
x =  0.0104 p-value =  1.17412671535934
```

```
x =  0.0105 p-value =  1.094151050524112
x =  0.0106 p-value =  1.019468054035388
x =  0.0107 p-value =  0.9497406144961659
===========[ 99% threshold ]
x =  0.0108 p-value =  0.8846519641281237
x =  0.0109 p-value =  0.8239045496438593
x =  0.011 p-value =  0.7672189569130647
g(t) := pdistrcp(869,2,t);
xlist: makelist(t/10000,t,130,140,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.013 p-value =  0.1794839196587316
x =  0.0131 p-value =  0.16670561231941
x =  0.0132 p-value =  0.1548207257503181
x =  0.0133 p-value =  0.1437681715134229
x =  0.0134 p-value =  0.1334909214220025
x =  0.0135 p-value =  0.1239357476502213
x =  0.0136 p-value =  0.1150529786149242
x =  0.0137 p-value =  0.1067962697486219
x =  0.0138 p-value =  0.09912238832490272
===========[ 99.9% threshold ]
x =  0.0139 p-value =  0.09199101153841559
x =  0.014 p-value =  0.0853645370810961
```

7.2. Frequentist efficacy threshold calculation for hospitalization rate reduction

- Hospitalization rate reduction: From Procter study [14], 869 high-risk patients treated with 20 hospitalizations, against untreated mortality rates.

```
g(t) := pdistr(869,20,t);
xlist: makelist(t/1000,t,32,47,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.032 p-value =  14.76067947088058
x =  0.033 p-value =  10.6053717284124
x =  0.034 p-value =  7.51074269978017
x =  0.035 p-value =  5.247206263128196
x =  0.036 p-value =  3.618902272038815
===========[ 95% threshold ]
x =  0.037 p-value =  3.0301984188679
x =  0.038 p-value =  2.050135348603014
x =  0.039 p-value =  1.37133903170457
x =  0.04 p-value =  0.9074205909202083
===========[ 99% threshold ]
x =  0.041 p-value =  0.5942972625875153
x =  0.042 p-value =  0.3854266686405413
x =  0.043 p-value =  0.2476386841591093
x =  0.044 p-value =  0.1576942467149889
x =  0.045 p-value =  0.09956431823974554
===========[ 99.9% threshold ]
x =  0.046 p-value =  0.06235071652209687
x =  0.047 p-value =  0.03874173879622215
```

- Selection bias threshold for 95% confidence (threshold 3.6%)

```
g(t) := pdistr(869, ceiling(869*0.036), t);
xlist: makelist(t/1000, t, 50, 55);
```

```
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.05 p-value =  8.605284449933507
x =  0.051 p-value =  6.356837657800075
x =  0.052 p-value =  4.644272908649455
=========[ 95% selection bias threshold ]
x =  0.053 p-value =  3.357264463790124
x =  0.054 p-value =  2.402271925520261
x =  0.055 p-value =  1.702130066747377
```

- Selection bias threshold for 99% confidence (threshold 4.0%)

```
g(t) := pdistr(869, ceiling(869*0.040), t);
xlist: makelist(t/1000, t, 55, 65);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.055 p-value =  6.227069314626104
x =  0.056 p-value =  4.589360625498874
x =  0.057 p-value =  3.348173733493748
x =  0.058 p-value =  2.418860606926613
x =  0.059 p-value =  1.731051610096626
x =  0.06 p-value =  1.22756561126695
x =  0.061 p-value =  0.8628685099287247
=========[ 99% selection bias threshold ]
x =  0.062 p-value =  0.6013544143049383
x =  0.063 p-value =  0.4156376208438818
x =  0.064 p-value =  0.3485431891390163
x =  0.065 p-value =  0.2375673387751247
```

- Selection bias threshold for 99.9% confidence (threshold 4.5%)

```
g(t) := pdistr(869, ceiling(869*0.045), t);
xlist: makelist(t/1000, t, 70, 80);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.07 p-value =  0.4190559576457418
x =  0.071 p-value =  0.2913942330617219
x =  0.072 p-value =  0.2011147707539199
x =  0.073 p-value =  0.16840930984415
x =  0.074 p-value =  0.1147235654108616
x =  0.075 p-value =  0.07759685897298356
=========[ 99.9% selection bias threshold ]
x =  0.076 p-value =  0.05212168298374127
x =  0.077 p-value =  0.03477354006233704
x =  0.078 p-value =  0.02304649432419963
x =  0.079 p-value =  0.01517580848776772
x =  0.08 p-value =  0.0099300580224234
```

- Plot code for Fig. 10

```
f(t) := pdistr(869, 20, t/100)/100;
g(t) := pdistrcp(869, 20, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 340, 460, 1);
dat2: makelist([g(t/100), float(t/100)], t, 340, 460, 1);
draw2d(
grid=true,
title="Procter data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
```

```
ylabel="Expected mortality percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 3.4, 4.6),
parametric(0.01, x, x,  3.4, 4.6),
parametric(0.001, x, x,  3.4, 4.6)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(869,20,t);
xlist: makelist(t/1000,t,32,47,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.032 p-value =  14.87107145080219
x =  0.033 p-value =  10.89823177670925
x =  0.034 p-value =  7.866513427131406
x =  0.035 p-value =  5.5959196738498
x =  0.036 p-value =  3.925238193150566
===========[ 95% threshold ]
x =  0.037 p-value =  2.716434802443442
x =  0.038 p-value =  1.855645464560918
x =  0.039 p-value =  1.25189235823688
x =  0.04 p-value =  0.8344861167945341
===========[ 99% threshold ]
x =  0.041 p-value =  0.549851553443764
x =  0.042 p-value =  0.3582865587461026
x =  0.043 p-value =  0.2309667990121553
x =  0.044 p-value =  0.1473563859378623
x =  0.045 p-value =  0.09307791384459997
===========[ 99.9% threshold ]
x =  0.046 p-value =  0.05822807488227708
x =  0.047 p-value =  0.03608847381922844
```

7.3. Bayesian factor analysis of efficacy thresholds for mortality rate reduction

Mortality rate reduction: From Procter study [14], 869 high-risk patients treated with 2 deaths, against untreated mortality rates. Integrals were calculated symbolically with exact arithmetic.

- Maximum high-risk cohort mortality rate $p_2 = 0.02$

```
f(t) := lbayesmax(869, 2, t, 2/100);
g(t) := pdistr(869, 2,t);
xlist: makelist(t/1000,t,4,14,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.004 log bayes =  0.9216741436832364 p-value =  59.45897396666187
x =  0.005 log bayes =  1.124432714437732 p-value =  46.16271537375738
x =  0.006 log bayes =  1.346528399688844 p-value =  18.93782840635735
x =  0.007 log bayes =  1.582623609519089 p-value =  10.33088826739651
x =  0.008 log bayes =  1.82894890423076 p-value =  5.551268198499255
```

```
x =  0.009 log bayes =  2.08261119506154 p-value =  2.950659592148073
x =  0.01 log bayes =  2.341260162761791 p-value =  1.556795174687752
x =  0.011 log bayes =  2.60280116275791 p-value =  0.8177114621309273
x =  0.012 log bayes =  2.865350304509806 p-value =  0.4286400110426079
x =  0.013 log bayes =  3.126989311361998 p-value =  0.2246962171650994
x =  0.014 log bayes =  3.385441669583598 p-value =  0.07641209958529434
f(t) := lbayesmax(869, 2, t, 2/100);
g(t) := pdistr(869, 2,t);
xlist: makelist(t/10000,t,80,160,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.008 log bayes =  1.82894890423076 p-value =  5.551268198499255
x =  0.0081 log bayes =  1.854042236395875 p-value =  5.58313383491276
x =  0.0082 log bayes =  1.879162122212257 p-value =  5.641101943429484
x =  0.0083 log bayes =  1.9044046817336 p-value =  5.724967586575343
x =  0.0084 log bayes =  1.929672545808192 p-value =  4.04188577298651
===========[ 95% threshold ]
x =  0.0085 log bayes =  1.955025580107435 p-value =  4.051778918900128
x =  0.0086 log bayes =  1.980428162440138 p-value =  4.082004274776216
x =  0.0087 log bayes =  2.005890356422563 p-value =  4.132460285378906
===========[ bayes 2 threshold ]
x =  0.0088 log bayes =  2.031413369114568 p-value =  4.203067927435425
x =  0.0089 log bayes =  2.056983139495119 p-value =  2.93840741423051
x =  0.009 log bayes =  2.08261119506154 p-value =  2.950659592148073
x =  0.0091 log bayes =  2.10828672489498 p-value =  2.978484070991474
x =  0.0092 log bayes =  2.134003246008104 p-value =  3.0218579743419
x =  0.0093 log bayes =  2.159782513875695 p-value =  3.080780956701758
x =  0.0094 log bayes =  2.185569623419358 p-value =  2.131712027055285
x =  0.0095 log bayes =  2.211450427967347 p-value =  2.144828521990627
x =  0.0096 log bayes =  2.23730372061648 p-value =  2.169792399960326
x =  0.0097 log bayes =  2.263268798250611 p-value =  2.206628155294791
x =  0.0098 log bayes =  2.289219734062781 p-value =  1.539839279375531
x =  0.0099 log bayes =  2.315214227749695 p-value =  1.54384997187088
x =  0.01 log bayes =  2.341260162761791 p-value =  1.556795174687752
x =  0.0101 log bayes =  2.367275213997604 p-value =  1.578705509361261
x =  0.0102 log bayes =  2.393399591893812 p-value =  1.60963145090928
x =  0.0103 log bayes =  2.419504983165912 p-value =  1.111198479978945
x =  0.0104 log bayes =  2.445610522917661 p-value =  1.116606337744332
x =  0.0105 log bayes =  2.471803244991397 p-value =  1.12872352349069
x =  0.0106 log bayes =  2.497960797309141 p-value =  1.147595451645446
x =  0.0107 log bayes =  2.52414007710879 p-value =  1.173284441298622
x =  0.0108 log bayes =  2.550379620346845 p-value =  0.800886685780233
===========[ 99% threshold ]
x =  0.0109 log bayes =  2.576581272609192 p-value =  0.806788811398927
x =  0.011 log bayes =  2.60280116275791 p-value =  0.8177114621309273
x =  0.0111 log bayes =  2.629079039587379 p-value =  0.8337057598856714
x =  0.0112 log bayes =  2.655315980663836 p-value =  0.5745904620471886
x =  0.0113 log bayes =  2.681540441613401 p-value =  0.5767075682376291
x =  0.0114 log bayes =  2.707847417735584 p-value =  0.5825316117984622
===========[ bayes 2.7 threshold ]
x =  0.0115 log bayes =  2.734110089447495 p-value =  0.5921018423765262
x =  0.0116 log bayes =  2.760327681210285 p-value =  0.605469446058129
x =  0.0117 log bayes =  2.786625882522511 p-value =  0.4123667483791651
x =  0.0118 log bayes =  2.812903971725551 p-value =  0.4150277047170398
x =  0.0119 log bayes =  2.839133161854902 p-value =  0.4204393251124112
```

```
x =  0.012 log bayes =  2.865350304509806 p-value =  0.4286400110426079
x =  0.0121 log bayes =  2.891632726096154 p-value =  0.2950037916186713
x =  0.0122 log bayes =  2.917862092471496 p-value =  0.2957858809120028
x =  0.0123 log bayes =  2.944037336904451 p-value =  0.298577662369295
x =  0.0124 log bayes =  2.970225604785544 p-value =  0.3034068468271118
x =  0.0125 log bayes =  2.996442919473866 p-value =  0.3103089169772158
x =  0.0126 log bayes =  3.022601479502367 p-value =  0.2109127674023332
x =  0.0127 log bayes =  3.048700043624835 p-value =  0.2121092802247944
x =  0.0128 log bayes =  3.074797537853958 p-value =  0.2147873677424833
x =  0.0129 log bayes =  3.100925987160084 p-value =  0.218972495076487
x =  0.013 log bayes =  3.126989311361998 p-value =  0.2246962171650994
x =  0.0131 log bayes =  3.152986087890309 p-value =  0.1507619659263774
x =  0.0132 log bayes =  3.178924531079312 p-value =  0.1521042826127172
x =  0.0133 log bayes =  3.204937929246509 p-value =  0.1545376827326893
x =  0.0134 log bayes =  3.230879133368 p-value =  0.1580847220488376
x =  0.0135 log bayes =  3.256746532910163 p-value =  0.1072302618710838
x =  0.0136 log bayes =  3.282538469219808 p-value =  0.10777159838621
x =  0.0137 log bayes =  3.308319976580868 p-value =  0.109100110607515
x =  0.0138 log bayes =  3.334109616007613 p-value =  0.1112315576690632
x =  0.0139 log bayes =  3.359817464698002 p-value =  0.1141853911714461
x =  0.014 log bayes =  3.385441669583598 p-value =  0.07641209958529434
===========[ 99.9% threshold ]
x =  0.0141 log bayes =  3.410980328318138 p-value =  0.07706238518708941
x =  0.0142 log bayes =  3.436503218972758 p-value =  0.07828970292828503
x =  0.0143 log bayes =  3.462018680534907 p-value =  0.08010765336234357
x =  0.0144 log bayes =  3.487441570071898 p-value =  0.05422070073615025
x =  0.0145 log bayes =  3.512769788754855 p-value =  0.05446933612430254
x =  0.0146 log bayes =  3.538001188781477 p-value =  0.05513153158908501
x =  0.0147 log bayes =  3.563152344860148 p-value =  0.05621662019693911
x =  0.0148 log bayes =  3.588337641648244 p-value =  0.0577360969797817
x =  0.0149 log bayes =  3.613418400307944 p-value =  0.03853068077356633
x =  0.015 log bayes =  3.638392281925555 p-value =  0.0388491352475015З
x =  0.0151 log bayes =  3.663256901209138 p-value =  0.03946960638922417
x =  0.0152 log bayes =  3.688009827352069 p-value =  0.04040000811374433
x =  0.0153 log bayes =  3.712704128581882 p-value =  0.02728014404142987
===========[ bayes 3.7 threshold ]
x =  0.0154 log bayes =  3.737380166344664 p-value =  0.02739702595088803
x =  0.0155 log bayes =  3.761936007846519 p-value =  0.0277291410680588
x =  0.0156 log bayes =  3.786369052446516 p-value =  0.02828185106262401
x =  0.0157 log bayes =  3.81067666054744 p-value =  0.02906174997736768
x =  0.0158 log bayes =  3.83485615538582 p-value =  0.01933792226828514
x =  0.0159 log bayes =  3.85892440033177 p-value =  0.01949587216301078
x =  0.016 log bayes =  3.882993708881782 p-value =  0.01981051454672118
```

- Maximum high-risk cohort mortality rate $p_2 = 0.05$

```
f(t) := lbayesmax(869, 2, t, 5/100);
g(t) := pdistr(869, 2,t);
xlist: makelist(t/1000,t,4,14,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.004 log bayes =  1.380306498422318 p-value =  59.45897396666187
x =  0.005 log bayes =  1.601544621659313 p-value =  46.16271537375738
x =  0.006 log bayes =  1.843836339183742 p-value =  18.93782840635735
x =  0.007 log bayes =  2.102117735896064 p-value =  10.33088826739651
```

```
x =  0.008 log bayes =  2.372957777269133 p-value =  5.551268198499255
x =  0.009 log bayes =  2.653886614977321 p-value =  2.950659592148073
x =  0.01 log bayes =  2.943089211894467 p-value =  1.556795174687752
x =  0.011 log bayes =  3.23915475302657 p-value =  0.8177114621309273
x =  0.012 log bayes =  3.54107966562481 p-value =  0.4286400110426079
x =  0.013 log bayes =  3.848082771778691 p-value =  0.2246962171650994
x =  0.014 log bayes =  4.159351210055678 p-value =  0.07641209958529434
f(t) := lbayesmax(869, 2, t, 5/100);
g(t) := pdistr(869, 2,t);
xlist: makelist(t/10000,t,60,140,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.006 log bayes =  1.843836339183742 p-value =  18.93782840635735
x =  0.0061 log bayes =  1.86901116980743 p-value =  18.96634106244928
x =  0.0062 log bayes =  1.894341372235579 p-value =  19.05771346664879
x =  0.0063 log bayes =  1.919823572392048 p-value =  19.21034380642506
x =  0.0064 log bayes =  1.945454061243872 p-value =  19.42258007785663
x =  0.0065 log bayes =  1.971228788460035 p-value =  14.01787655031823
x =  0.0066 log bayes =  1.997143352839095 p-value =  14.0482159330508
x =  0.0067 log bayes =  2.023192989445783 p-value =  14.13052721190162
===========[ bayes 2 threshold ]
x =  0.0068 log bayes =  2.049372553358202 p-value =  14.26373961570385
x =  0.0069 log bayes =  2.075676499887541 p-value =  14.44675962981091
x =  0.007 log bayes =  2.102117735896064 p-value =  10.33088826739651
x =  0.0071 log bayes =  2.128696636067565 p-value =  10.36279012338161
x =  0.0072 log bayes =  2.15538830575764 p-value =  10.43667412185116
x =  0.0073 log bayes =  2.182185838782917 p-value =  10.55186348044637
x =  0.0074 log bayes =  2.209101824949341 p-value =  10.70767845991108
x =  0.0075 log bayes =  2.236156615047448 p-value =  7.585104013205156
x =  0.0076 log bayes =  2.26330260195981 p-value =  7.617574209564607
x =  0.0077 log bayes =  2.290541338090859 p-value =  7.683370686014498
x =  0.0078 log bayes =  2.317930010043384 p-value =  7.782096816022395
x =  0.0079 log bayes =  2.345392862448122 p-value =  7.913365707007443
x =  0.008 log bayes =  2.372957777269133 p-value =  5.551268198499255
x =  0.0081 log bayes =  2.400646082825713 p-value =  5.58313383491276
x =  0.0082 log bayes =  2.428388845656341 p-value =  5.641101943429484
x =  0.0083 log bayes =  2.456282674216843 p-value =  5.724967586575343
x =  0.0084 log bayes =  2.484230699449026 p-value =  4.04188577298651
===========[ 95% threshold ]
x =  0.0085 log bayes =  2.512293299143956 p-value =  4.051778918900128
x =  0.0086 log bayes =  2.540435375601026 p-value =  4.082004274776216
x =  0.0087 log bayes =  2.568667529652982 p-value =  4.132460285378906
x =  0.0088 log bayes =  2.596991518667676 p-value =  4.203067927435425
x =  0.0089 log bayes =  2.625393845399807 p-value =  2.93840741423051
x =  0.009 log bayes =  2.653886614977321 p-value =  2.950659592148073
x =  0.0091 log bayes =  2.68245960836548 p-value =  2.978484070991474
x =  0.0092 log bayes =  2.711106949124312 p-value =  3.0218579743419
===========[ bayes 2.7 threshold ]
x =  0.0093 log bayes =  2.739851014360817 p-value =  3.080780956701758
x =  0.0094 log bayes =  2.7686375361471 p-value =  2.131712027055285
x =  0.0095 log bayes =  2.79755302092569 p-value =  2.144828521990627
x =  0.0096 log bayes =  2.826476931329351 p-value =  2.169792399960326
x =  0.0097 log bayes =  2.85554925066962 p-value =  2.206628155294791
x =  0.0098 log bayes =  2.884644755942042 p-value =  1.539839279375531
x =  0.0099 log bayes =  2.913821868516217 p-value =  1.54384997187088
```

```
x =  0.01 log bayes =  2.943089211894467 p-value =  1.556795174687752
x =  0.0101 log bayes =  2.972365219927849 p-value =  1.578705509361261
x =  0.0102 log bayes =  3.001790881440859 p-value =  1.60963145090928
x =  0.0103 log bayes =  3.03123868152001 p-value =  1.111198479978945
x =  0.0104 log bayes =  3.060728574184431 p-value =  1.116606337744332
x =  0.0105 log bayes =  3.090348433310358 p-value =  1.12872352349069
x =  0.0106 log bayes =  3.11997676855977 p-value =  1.147595451645446
x =  0.0107 log bayes =  3.149671361216961 p-value =  1.173284441298622
x =  0.0108 log bayes =  3.179471654204773 p-value =  0.800886685780233
===========[ 99% threshold ]
x =  0.0109 log bayes =  3.209280423621518 p-value =  0.806788811398927
x =  0.011 log bayes =  3.23915475302657 p-value =  0.8177114621309273
x =  0.0111 log bayes =  3.269135370747314 p-value =  0.8337057598856714
x =  0.0112 log bayes =  3.299124359381592 p-value =  0.5745904620471886
x =  0.0113 log bayes =  3.329151205759957 p-value =  0.5767075682376291
x =  0.0114 log bayes =  3.35931196324438 p-value =  0.5825316117984622
x =  0.0115 log bayes =  3.389480897868048 p-value =  0.5921018423765262
x =  0.0116 log bayes =  3.419658347967055 p-value =  0.605469446058129
x =  0.0117 log bayes =  3.449971145887905 p-value =  0.4123667483791651
x =  0.0118 log bayes =  3.480319742515163 p-value =  0.4150277047170398
x =  0.0119 log bayes =  3.510676553851935 p-value =  0.4204393251124112
x =  0.012 log bayes =  3.54107966562481 p-value =  0.4286400110426079
x =  0.0121 log bayes =  3.571607670266646 p-value =  0.2950037916186713
x =  0.0122 log bayes =  3.602143532304917 p-value =  0.2957858809120028
x =  0.0123 log bayes =  3.632687517066231 p-value =  0.298577662369295
x =  0.0124 log bayes =  3.66330813613271 p-value =  0.303406846827118
x =  0.0125 log bayes =  3.694022813932266 p-value =  0.3103089169772158
x =  0.0126 log bayes =  3.724745185684166 p-value =  0.2109127674023332
===========[ bayes 3.7 threshold ]
x =  0.0127 log bayes =  3.755475483180455 p-value =  0.2121092802247944
x =  0.0128 log bayes =  3.78627414255031 p-value =  0.2147873677424833
x =  0.0129 log bayes =  3.817174736674563 p-value =  0.218972495076487
x =  0.013 log bayes =  3.848082771778691 p-value =  0.2246962171650994
x =  0.0131 log bayes =  3.878998450882225 p-value =  0.1507619659263774
x =  0.0132 log bayes =  3.909931653756917 p-value =  0.1521042826127172
x =  0.0133 log bayes =  3.941017374649799 p-value =  0.1545376827326893
x =  0.0134 log bayes =  3.972110211575215 p-value =  0.1580847220488376
x =  0.0135 log bayes =  4.003210342733108 p-value =  0.1072302618710838
x =  0.0136 log bayes =  4.034317940450495 p-value =  0.10777159838621
x =  0.0137 log bayes =  4.065499912751127 p-value =  0.109100110607515
x =  0.0138 log bayes =  4.096776737617468 p-value =  0.1112315576690632
x =  0.0139 log bayes =  4.128060452864347 p-value =  0.1141853911714461
x =  0.014 log bayes =  4.159351210055678 p-value =  0.07641209958529434
===========[ 99.9% threshold ]
```

- Maximum high-risk cohort mortality rate $p_2 = 0.10$

```
f(t) := lbayesmax(869, 2, t, 10/100);
g(t) := pdistr(869, 2,t);
xlist: makelist(t/1000, t,4,14,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.004 log bayes =  1.699819899780317 p-value =  59.45897396666187
x =  0.005 log bayes =  1.926055713172816 p-value =  46.16271537375738
x =  0.006 log bayes =  2.173511516297252 p-value =  18.93782840635735
```

```
x =  0.007 log bayes =  2.437132228870415 p-value =  10.33088826739651
x =  0.008 log bayes =  2.713496314216795 p-value =  5.551268198499255
x =  0.009 log bayes =  3.000144150578681 p-value =  2.950659592148073
x =  0.01 log bayes =  3.295271730005841 p-value =  1.556795174687752
x =  0.011 log bayes =  3.597480152644981 p-value =  0.8177114621309273
x =  0.012 log bayes =  3.905778741158155 p-value =  0.4286400110426079
x =  0.013 log bayes =  4.219400300330294 p-value =  0.2246962171650994
x =  0.014 log bayes =  4.537547160531914 p-value =  0.07641209958529434
x =  0.015 log bayes =  4.859778832748123 p-value =  0.03884913524750153
x =  0.016 log bayes =  5.185557694824984 p-value =  0.01981051454672118
x =  0.017 log bayes =  5.514681596888656 p-value =  0.01014611030933425
x =  0.018 log bayes =  5.846609523293752 p-value =  0.003384544088298451
x =  0.019 log bayes =  6.181215054548065 p-value =  0.001682707856920103
f(t) := lbayesmax(869, 2, t, 10/100);
g(t) := pdistr(869, 2,t);
xlist: makelist(t/10000,t,50,140,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.005 log bayes =  1.926055713172816 p-value =  46.16271537375738
x =  0.0051 log bayes =  1.949942310823714 p-value =  34.04807252473163
x =  0.0052 log bayes =  1.974040060403106 p-value =  34.16113514882318
x =  0.0053 log bayes =  1.998324076735364 p-value =  34.35341363268383
x =  0.0054 log bayes =  2.022820003334021 p-value =  34.62172359367307
===========[ bayes 2 threshold ]
x =  0.0055 log bayes =  2.047490567818293 p-value =  34.96278564273948
x =  0.0056 log bayes =  2.072335601624028 p-value =  25.48351389231885
x =  0.0057 log bayes =  2.097380804221261 p-value =  25.58505602958749
x =  0.0058 log bayes =  2.122593263884354 p-value =  25.75794221228247
x =  0.0059 log bayes =  2.147970956575641 p-value =  25.99981021443051
x =  0.006 log bayes =  2.173511516297252 p-value =  18.93782840635735
x =  0.0061 log bayes =  2.19921224183143 p-value =  18.96634106244928
x =  0.0062 log bayes =  2.225070100110548 p-value =  19.05771346664879
x =  0.0063 log bayes =  2.251081726309397 p-value =  19.21034380642506
x =  0.0064 log bayes =  2.27724342071339 p-value =  19.42258007785663
x =  0.0065 log bayes =  2.30355114237793 p-value =  14.01787655031823
x =  0.0066 log bayes =  2.330000499556679 p-value =  14.0482159330508
x =  0.0067 log bayes =  2.35658673683891 p-value =  14.13052721190162
x =  0.0068 log bayes =  2.38330471889728 p-value =  14.26373961570385
x =  0.0069 log bayes =  2.410148910708147 p-value =  14.44675962981091
x =  0.007 log bayes =  2.437132228870415 p-value =  10.33088826739651
x =  0.0071 log bayes =  2.464255057876476 p-value =  10.36279012338161
x =  0.0072 log bayes =  2.49149251296333 p-value =  10.43667412185116
x =  0.0073 log bayes =  2.518837697902391 p-value =  10.55186348044637
x =  0.0074 log bayes =  2.546303212528549 p-value =  10.70767845991108
x =  0.0075 log bayes =  2.573909417736177 p-value =  7.585104013205156
x =  0.0076 log bayes =  2.601608716587184 p-value =  7.617574209564607
x =  0.0077 log bayes =  2.629402671741714 p-value =  7.683370686014498
x =  0.0078 log bayes =  2.65734848013534 p-value =  7.782096816022395
x =  0.0079 log bayes =  2.685370396809304 p-value =  7.913365707007443
x =  0.008 log bayes =  2.713496314216795 p-value =  5.551268198499255
===========[ bayes 2.7 threshold ]
x =  0.0081 log bayes =  2.741747571245524 p-value =  5.58313383491276
x =  0.0082 log bayes =  2.770055245082544 p-value =  5.641101943429484
x =  0.0083 log bayes =  2.798515954913118 p-value =  5.724967586575343
x =  0.0084 log bayes =  2.827032842490157 p-value =  4.04188577298651
```

```
===========[ 95% threshold ]
x =  0.0085 log bayes =  2.855666296498323 p-value =  4.051778918900128
x =  0.0086 log bayes =  2.884381230213951 p-value =  4.082004274776216
x =  0.0087 log bayes =  2.913188255530871 p-value =  4.132460285378906
x =  0.0088 log bayes =  2.94208914096296 p-value =  4.203067927435425
x =  0.0089 log bayes =  2.971070400496719 p-value =  2.93840741423051
x =  0.009 log bayes =  3.000144150578681 p-value =  2.950659592148073
x =  0.0091 log bayes =  3.029300183580096 p-value =  2.978484070991474
x =  0.0092 log bayes =  3.058532634555513 p-value =  3.0218579743419
x =  0.0093 log bayes =  3.087863892195683 p-value =  3.080780956701758
x =  0.0094 log bayes =  3.11723970024672 p-value =  2.131712027055285
x =  0.0095 log bayes =  3.146746576916221 p-value =  2.144828521990627
x =  0.0096 log bayes =  3.176263996694112 p-value =  2.169792399960326
x =  0.0097 log bayes =  3.205931954842025 p-value =  2.206628155294791
x =  0.0098 log bayes =  3.235625240399513 p-value =  1.539839279375531
x =  0.0099 log bayes =  3.265402286875096 p-value =  1.54384997187088
x =  0.01 log bayes =  3.295271730005841 p-value =  1.556795174687752
x =  0.0101 log bayes =  3.325152015974318 p-value =  1.578705509361261
x =  0.0102 log bayes =  3.355184146034462 p-value =  1.60963145090928
x =  0.0103 log bayes =  3.385240617800984 p-value =  1.111198479978945
x =  0.0104 log bayes =  3.415341397921042 p-value =  1.116606337744332
x =  0.0105 log bayes =  3.445574372999817 p-value =  1.12872352349069
x =  0.0106 log bayes =  3.475818065530107 p-value =  1.147595451645446
x =  0.0107 log bayes =  3.506130269730081 p-value =  1.173284441298622
x =  0.0108 log bayes =  3.536550441560425 p-value =  0.800886685780233
===========[ 99% threshold ]
x =  0.0109 log bayes =  3.566981370262515 p-value =  0.806788811398927
x =  0.011 log bayes =  3.597480152644981 p-value =  0.8177114621309273
x =  0.0111 log bayes =  3.628087530391825 p-value =  0.8337057598856714
x =  0.0112 log bayes =  3.658705599565978 p-value =  0.5745904620471886
x =  0.0113 log bayes =  3.689363860572756 p-value =  0.5767075682376291
x =  0.0114 log bayes =  3.72015838045967 p-value =  0.5825316117984622
===========[ bayes 3.7 threshold ]
x =  0.0115 log bayes =  3.750963439057356 p-value =  0.5921018423765262
x =  0.0116 log bayes =  3.781779388612585 p-value =  0.605469446058129
x =  0.0117 log bayes =  3.81273307549685 p-value =  0.4123667483791651
x =  0.0118 log bayes =  3.84372496473525 p-value =  0.4150277047170398
x =  0.0119 log bayes =  3.874727486588352 p-value =  0.4204393251124112
x =  0.012 log bayes =  3.905778741158155 p-value =  0.4286400110426079
x =  0.0121 log bayes =  3.936957335372348 p-value =  0.2950037916186713
x =  0.0122 log bayes =  3.968146248373771 p-value =  0.2957858809120028
x =  0.0123 log bayes =  3.999345760226463 p-value =  0.298577662369295
x =  0.0124 log bayes =  4.030624397373122 p-value =  0.3034068468271118
x =  0.0125 log bayes =  4.061999599226847 p-value =  0.3103089169772158
x =  0.0126 log bayes =  4.093385016118079 p-value =  0.2109127674023332
x =  0.0127 log bayes =  4.124780895077316 p-value =  0.2121092802247944
x =  0.0128 log bayes =  4.156247687600958 p-value =  0.2147873677424833
x =  0.0129 log bayes =  4.187818982067146 p-value =  0.218972495076487
x =  0.013 log bayes =  4.219400300330294 p-value =  0.2246962171650994
x =  0.0131 log bayes =  4.250991861171807 p-value =  0.1507619659263774
x =  0.0132 log bayes =  4.282603560259875 p-value =  0.1521042826127172
x =  0.0133 log bayes =  4.314370407873882 p-value =  0.1545376827326893
x =  0.0134 log bayes =  4.346147018198137 p-value =  0.1580847220488376
x =  0.0135 log bayes =  4.377933585741403 p-value =  0.1072302618710838
```

```
x =  0.0136 log bayes =  4.409730299280312 p-value =  0.10777159838621
x =  0.0137 log bayes =  4.4416040834302 p-value =  0.109100110607515
x =  0.0138 log bayes =  4.473575432908977 p-value =  0.1112315576690632
x =  0.0139 log bayes =  4.505556402412298 p-value =  0.1141853911714461
x =  0.014 log bayes =  4.537547160531914 p-value =  0.07641209958529434
===========[ 99.9% threshold ]
```

7.4. Bayesian factor analysis of efficacy thresholds for hospitalization rate reduction

Hospitalization rate reduction: From Procter study [14], 869 high-risk patients treated with 20 hospitalizations, against untreated mortality rates.

- Maximum high-risk cohort hospitalization rate $p_2 = 0.10$.

```
f(t) := lbayesmax(869, 20, t, 10/100);
g(t) := pdistr(869, 20, t);
xlist: makelist(t/1000,t,32,47,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.032 log bayes =  1.429441310453267 p-value =  14.76067947088058
x =  0.033 log bayes =  1.558403135868002 p-value =  10.6053717284124
x =  0.034 log bayes =  1.693871446871974 p-value =  7.51074269978017
x =  0.035 log bayes =  1.83554597260723 p-value =  5.247206263128196
x =  0.036 log bayes =  1.983248007196173 p-value =  3.618902272038815
===========[ 95% threshold ]
x =  0.037 log bayes =  2.136651620896273 p-value =  3.0301984188679
===========[ bayes 2 threshold ]
x =  0.038 log bayes =  2.295649751453722 p-value =  2.050135348603014
x =  0.039 log bayes =  2.459952015817668 p-value =  1.37133903170457
x =  0.04 log bayes =  2.629345629312588 p-value =  0.9074205909202083
===========[ 99% threshold ]
x =  0.041 log bayes =  2.803628394148187 p-value =  0.5942972625875153
===========[ bayes 2.7 threshold ]
x =  0.042 log bayes =  2.982645039005348 p-value =  0.3854266686405413
x =  0.043 log bayes =  3.166249780945224 p-value =  0.2476386841591093
x =  0.044 log bayes =  3.354165110314228 p-value =  0.1576942467149889
x =  0.045 log bayes =  3.546286566798949 p-value =  0.09956431823974554
===========[ 99.9% threshold ]
x =  0.046 log bayes =  3.742490888524176 p-value =  0.06235071652209687
===========[ bayes 3.7 threshold ]
x =  0.047 log bayes =  3.942570203712613 p-value =  0.03874173879622215
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.15$.

```
f(t) := lbayesmax(869, 20, t, 15/100);
g(t) := pdistr(869, 20, t);
xlist: makelist(t/1000,t,32,47,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.032 log bayes =  1.668814405053147 p-value =  14.76067947088058
x =  0.033 log bayes =  1.800514194913344 p-value =  10.6053717284124
x =  0.034 log bayes =  1.938785500557017 p-value =  7.51074269978017
x =  0.035 log bayes =  2.083330456317985 p-value =  5.247206263128196
===========[ bayes 2 threshold ]
x =  0.036 log bayes =  2.23397288454876 p-value =  3.618902272038815
===========[ 95% threshold ]
x =  0.037 log bayes =  2.390389514926119 p-value =  3.0301984188679
```

```
x =  0.038 log bayes =  2.552476084625646 p-value =  2.050135348603014
x =  0.039 log bayes =  2.719945159593566 p-value =  1.37133903170457
===========[ bayes 2.7 threshold ]
x =  0.04 log bayes =  2.892587064087186 p-value =  0.9074205909202083
===========[ 99% threshold ]
x =  0.041 log bayes =  3.070202880446664 p-value =  0.5942972625875153
x =  0.042 log bayes =  3.25264080092936 p-value =  0.3854266686405413
x =  0.043 log bayes =  3.43975870295793 p-value =  0.2476386841591093
x =  0.044 log bayes =  3.631282948572813 p-value =  0.1576942467149889
x =  0.045 log bayes =  3.827113176374636 p-value =  0.09956431823974554
===========[ bayes 3.7 threshold ]
===========[ 99.9% threshold ]
x =  0.046 log bayes =  4.027130467999983 p-value =  0.06235071652209687
x =  0.047 log bayes =  4.231131558816991 p-value =  0.03874173879622215
```

- Maximum high-risk cohort hospitalization rate $p_2 = 0.20$.

```
f(t) := lbayesmax(869, 20, t, 20/100);
g(t) := pdistr(869, 20, t);
xlist: makelist(t/1000,t,32,47,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.032 log bayes =  1.822241679472883 p-value =  14.76067947088058
x =  0.033 log bayes =  1.955044804314761 p-value =  10.6053717284124
x =  0.034 log bayes =  2.094435599370164 p-value =  7.51074269978017
===========[ bayes 2 threshold ]
x =  0.035 log bayes =  2.240116560178275 p-value =  5.247206263128196
x =  0.036 log bayes =  2.391911881259976 p-value =  3.618902272038815
===========[ 95% threshold ]
x =  0.037 log bayes =  2.549498675846653 p-value =  3.0301984188679
x =  0.038 log bayes =  2.712773076498105 p-value =  2.050135348603014
===========[ bayes 2.7 threshold ]
x =  0.039 log bayes =  2.88144805683875 p-value =  1.37133903170457
x =  0.04 log bayes =  3.055314361584868 p-value =  0.9074205909202083
===========[ 99% threshold ]
x =  0.041 log bayes =  3.234173506826493 p-value =  0.5942972625875153
x =  0.042 log bayes =  3.417874132396836 p-value =  0.3854266686405413
x =  0.043 log bayes =  3.60627457768197 p-value =  0.2476386841591093
x =  0.044 log bayes =  3.799101681662496 p-value =  0.1576942467149889
===========[ bayes 3.7 threshold ]
x =  0.045 log bayes =  3.996255575474981 p-value =  0.09956431823974554
===========[ 99.9% threshold ]
x =  0.046 log bayes =  4.197617849537667 p-value =  0.06235071652209687
x =  0.047 log bayes =  4.402985764929424 p-value =  0.03874173879622215
```

8. Analysis of Raoult's data

8.1. Frequentist efficacy threshold calculation for mortality rate reduction

- Mortality rate reduction: High risk group older than 60 (1495 patients with 5 deaths) [15] against untreated mortality rates.

```
g(t) := pdistr(1495,5,t);
xlist: makelist(t/1000,t,1,14,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
```

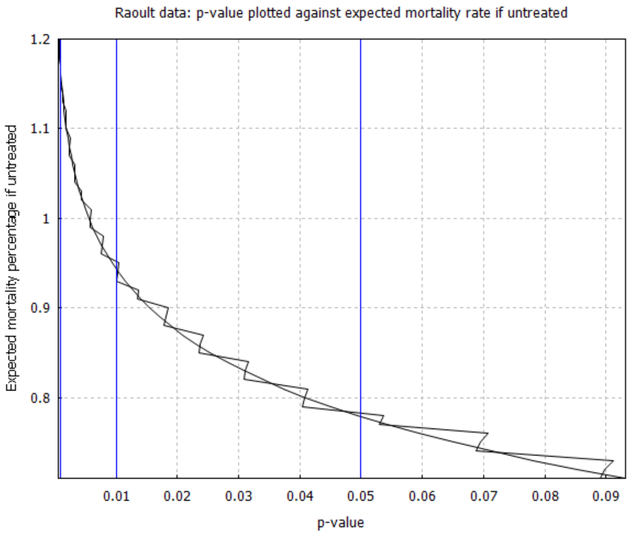

Figure 11: Relationship between *p*-value and expected mortality rate for high risk patients without early treatment, based on the case series data from Didier Raoult's dataset of 1495 high-risk patients older than 60 [15]

```
x =  0.001 p-value =  1.828312187061036
x =  0.002 p-value =  23.30269007228956
x =  0.003 p-value =  80.9640199558048
x =  0.004 p-value =  100.0
x =  0.005 p-value =  46.38008666190668
x =  0.006 p-value =  23.81878512791918
x =  0.007 p-value =  11.69725918696211
x =  0.008 p-value =  4.069315238885027
x =  0.009 p-value =  1.848779903956496
x =  0.01 p-value =  0.581195295706084
x =  0.011 p-value =  0.1774930322185887
x =  0.012 p-value =  0.07476443540285577
x =  0.013 p-value =  0.02142831131494066
x =  0.014 p-value =  0.006050082056618004
g(t) := pdistr(1495,5,t);
xlist: makelist(t/10000,t,70,120,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.007 p-value =  11.69725918696211
x =  0.0071 p-value =  8.898849247581843
x =  0.0072 p-value =  8.974139079362958
x =  0.0073 p-value =  9.115647447712988
x =  0.0074 p-value =  6.88183766887816
x =  0.0075 p-value =  6.951473422073926
x =  0.0076 p-value =  7.076417986779846
x =  0.0077 p-value =  5.301247177455311
x =  0.0078 p-value =  5.365038626194091
x =  0.0079 p-value =  4.049022709179763
===========[ 95% threshold ]
x =  0.008 p-value =  4.069315238885027
x =  0.0081 p-value =  4.127139411901921
x =  0.0082 p-value =  3.092304773912224
```

```
x =  0.0083 p-value =  3.113804524966511
x =  0.0084 p-value =  3.165651507160916
x =  0.0085 p-value =  2.354322749345709
x =  0.0086 p-value =  2.375946556820785
x =  0.0087 p-value =  2.421933861259354
x =  0.0088 p-value =  1.787489145781218
x =  0.0089 p-value =  1.808415161524708
x =  0.009 p-value =  1.848779903956496
x =  0.0091 p-value =  1.353787284586766
x =  0.0092 p-value =  1.373439084371367
x =  0.0093 p-value =  1.017140589806407
x =  0.0094 p-value =  1.02309774749169
x =  0.0095 p-value =  1.041111584570076
x =  0.0096 p-value =  0.7649978626812526
===========[ 99% threshold ]
x =  0.0097 p-value =  0.7717346518594089
x =  0.0098 p-value =  0.7879198056784475
x =  0.0099 p-value =  0.57427374829861
x =  0.01 p-value =  0.581195295706084
x =  0.0101 p-value =  0.5954940386953036
x =  0.0102 p-value =  0.4304030357540509
x =  0.0103 p-value =  0.4371122962179401
x =  0.0104 p-value =  0.320257363252172
x =  0.0105 p-value =  0.3221387095806921
x =  0.0106 p-value =  0.3283892785598433
x =  0.0107 p-value =  0.238554477874591
x =  0.0108 p-value =  0.2408411854459276
x =  0.0109 p-value =  0.2464975049812564
x =  0.011 p-value =  0.1774930322185887
x =  0.0111 p-value =  0.1799049654466882
x =  0.0112 p-value =  0.1849100700914028
x =  0.0113 p-value =  0.1319428887020915
x =  0.0114 p-value =  0.1343010669822639
x =  0.0115 p-value =  0.09730459634041816
x =  0.0116 p-value =  0.09801739522275196
x =  0.0117 p-value =  0.1002152627548012
x =  0.0118 p-value =  0.07193429381107941
===========[ 99.9% threshold ]
x =  0.0119 p-value =  0.07278300386057966
x =  0.012 p-value =  0.07476443540285577
```

- Selection bias threshold for 95% confidence (threshold 0.79%)

```
g(t) := pdistr(1495, ceiling(1495*0.0079), t);
xlist: makelist(t/1000, t, 10, 15);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.01 p-value =  51.65827641899256
x =  0.011 p-value =  32.07302407369374
x =  0.012 p-value =  18.97467043237389
x =  0.013 p-value =  10.79986049457359
x =  0.014 p-value =  4.705206422867697
x =  0.015 p-value =  2.466345312560823
g(t) := pdistr(1495, ceiling(1495*0.0079), t);
xlist: makelist(t/10000, t, 130, 145);
```

```
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.013 p-value =  10.79986049457359
x =  0.0131 p-value =  8.755350709269992
x =  0.0132 p-value =  8.788148644233624
x =  0.0133 p-value =  8.857138845641636
x =  0.0134 p-value =  7.145396400089252
x =  0.0135 p-value =  7.174586705571698
x =  0.0136 p-value =  7.235458356834578
x =  0.0137 p-value =  5.809032303301375
x =  0.0138 p-value =  5.835113140406241
x =  0.0139 p-value =  5.88868549127431
x =  0.014 p-value =  4.705206422867697
=========[ 95% selection bias threshold ]
x =  0.0141 p-value =  4.728574839413165
x =  0.0142 p-value =  4.77560951061743
x =  0.0143 p-value =  3.797700375461193
x =  0.0144 p-value =  3.818670750499596
x =  0.0145 p-value =  3.85986585004481
```

- Selection bias threshold for 99% confidence (threshold 0.96%)

```
g(t) := pdistr(1495, ceiling(1495*0.0096), t);
xlist: makelist(t/1000, t, 15, 20);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.015 p-value =  13.47825695884342
x =  0.016 p-value =  7.822498469123147
x =  0.017 p-value =  3.507823811488124
x =  0.018 p-value =  1.892959688940663
x =  0.019 p-value =  0.780690197275418
x =  0.02 p-value =  0.3975496198656012
g(t) := pdistr(1495, ceiling(1495*0.0096), t);
xlist: makelist(t/10000, t, 180, 190);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.018 p-value =  1.892959688940663
x =  0.0181 p-value =  1.510647788150163
x =  0.0182 p-value =  1.515667493985482
x =  0.0183 p-value =  1.529145466824243
x =  0.0184 p-value =  1.215500950685904
x =  0.0185 p-value =  1.22019752262221
x =  0.0186 p-value =  1.231988643675574
x =  0.0187 p-value =  0.9753931235874168
=========[ 99% selection bias threshold ]
x =  0.0188 p-value =  0.9797636301670337
x =  0.0189 p-value =  0.9900584992648864
x =  0.019 p-value =  0.780690197275418
```

- Selection bias threshold for 99.9% confidence (threshold 1.18%)

```
g(t) := pdistr(1495, ceiling(1495*0.0118), t);
xlist: makelist(t/1000, t, 20, 27);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.02 p-value =  2.608139828496721
x =  0.021 p-value =  1.438218422591191
x =  0.022 p-value =  0.6096557546415
```

```
x =  0.023 p-value =  0.3185349886735838
x =  0.024 p-value =  0.1268313086395425
x =  0.025 p-value =  0.06336992860729752
x =  0.026 p-value =  0.02391202049109388
x =  0.027 p-value =  0.01151880053852555
g(t) := pdistr(1495, ceiling(1495*0.0118), t);
xlist: makelist(t/10000, t, 240, 250);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.024 p-value =  0.1268313086395425
x =  0.0241 p-value =  0.1275390306355952
x =  0.0242 p-value =  0.1291565166814991
x =  0.0243 p-value =  0.1005350426952762
x =  0.0244 p-value =  0.1011927202653624
x =  0.0245 p-value =  0.1025917593539209
x =  0.0246 p-value =  0.079543936566475
=========[ 99.9% selection bias threshold ]
x =  0.0247 p-value =  0.08014684801876852
x =  0.0248 p-value =  0.08135237308972108
x =  0.0249 p-value =  0.06282370994800104
x =  0.025 p-value =  0.06336992860729752
```

- Plot code for Fig. 11

```
f(t) := pdistr(1495, 5, t/100)/100;
g(t) := pdistrcp(1495, 5, t/100)/100;
dat1: makelist([f(t/100), float(t/100)], t, 71, 120, 1);
dat2: makelist([g(t/100), float(t/100)], t, 71, 120, 1);
draw2d(
grid=true,
title="Raoult data: p-value plotted against expected mortality rate if untreated",
xlabel="p-value",
ylabel="Expected mortality percentage if untreated",
color=black,
nticks=200,
xtics=0.01,
ytics=0.1,
point_type=dot,
points_joined=true,
points(dat1),
points(dat2),
color=blue,
parametric(0.05, x, x, 0.71, 1.2),
parametric(0.01, x, x, 0.71, 1.2),
parametric(0.001, x, x, 0.71, 1.2)
);
```

- Clopper-Pearson interval:

```
g(t) := pdistrcp(1495,5,t);
xlist: makelist(t/10000,t,70,120,1);
for t in xlist do print("x = ", float(t), "p-value = ", g(t));
x =  0.007 p-value =  10.16889867037196
x =  0.0071 p-value =  9.315322560455328
x =  0.0072 p-value =  8.527004609083553
x =  0.0073 p-value =  7.79967853572757
x =  0.0074 p-value =  7.129273741703857
```

```
x =  0.0075 p-value =  6.511916641022937
x =  0.0076 p-value =  5.943930307389322
x =  0.0077 p-value =  5.42183267439964
x =  0.0078 p-value =  4.942333506590362
===========[ 95% threshold ]
x =  0.0079 p-value =  4.502330339913705
x =  0.008 p-value =  4.09890357169207
x =  0.0081 p-value =  3.729310862290104
x =  0.0082 p-value =  3.390980993778831
x =  0.0083 p-value =  3.08150731484089
x =  0.0084 p-value =  2.798640886141164
x =  0.0085 p-value =  2.540283426397698
x =  0.0086 p-value =  2.304480146446682
x =  0.0087 p-value =  2.089412546697286
x =  0.0088 p-value =  1.893391242497484
x =  0.0089 p-value =  1.714848872049531
x =  0.009 p-value =  1.552333132583608
x =  0.0091 p-value =  1.404499982473598
x =  0.0092 p-value =  1.270107039809207
x =  0.0093 p-value =  1.148007201569506
x =  0.0094 p-value =  1.037142501919049
x =  0.0095 p-value =  0.9365382232130232
===========[ 99% threshold ]
x =  0.0096 p-value =  0.845297268996994
x =  0.0097 p-value =  0.7625948045655151
x =  0.0098 p-value =  0.6876731674497716
x =  0.0099 p-value =  0.6198370474874091
x =  0.01 p-value =  0.5584489338400964
x =  0.0101 p-value =  0.5029248244213961
x =  0.0102 p-value =  0.4527301916371936
x =  0.0103 p-value =  0.4073761970842912
x =  0.0104 p-value =  0.3664161468637607
x =  0.0105 p-value =  0.3294421784111653
x =  0.0106 p-value =  0.2960821691955231
x =  0.0107 p-value =  0.2659968572653524
x =  0.0108 p-value =  0.2388771633983895
x =  0.0109 p-value =  0.2144417045191306
x =  0.011 p-value =  0.1924344880650957
x =  0.0111 p-value =  0.1726227770906633
x =  0.0112 p-value =  0.1547951160805288
x =  0.0113 p-value =  0.1387595076891858
x =  0.0114 p-value =  0.1243417309159321
x =  0.0115 p-value =  0.1113837915559022
x =  0.0116 p-value =  0.09974249612711407
===========[ 99.9% threshold ]
x =  0.0117 p-value =  0.08928814085333807
x =  0.0118 p-value =  0.0799033076757547
x =  0.0119 p-value =  0.07148175966691836
x =  0.012 p-value =  0.06392742862344496
```

8.2. Bayesian factor analysis of efficacy thresholds for mortality rate reduction

Mortality rate reduction: High risk group older than 60 (1495 patients with 5 deaths) [15] against untreated mortality rates. Integrals were calculated numerically.

- Maximum high-risk cohort mortality rate $p_2 = 0.02$

```
f(t) := lbayesmax(1495,5, t, 2/100);
g(t) := pdistr(1495,5,t);
xlist: makelist(t/10000,t,70,130,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.007 log bayes =  1.590243787263156 p-value =  11.69725918696211
x =  0.0071 log bayes =  1.625004633759666 p-value =  8.898849247581843
x =  0.0072 log bayes =  1.660066344171671 p-value =  8.974139079362958
x =  0.0073 log bayes =  1.695421784953936 p-value =  9.115647447712988
x =  0.0074 log bayes =  1.731063494819919 p-value =  6.88183766887816
x =  0.0075 log bayes =  1.766983675281301 p-value =  6.951473422073926
x =  0.0076 log bayes =  1.803174177396208 p-value =  7.076417986779846
x =  0.0077 log bayes =  1.83962648467389 p-value =  5.301247177455311
x =  0.0078 log bayes =  1.876331692045667 p-value =  5.365038626194091
x =  0.0079 log bayes =  1.913280480776554 p-value =  4.049022709179763
===========[ 95% threshold ]
x =  0.008 log bayes =  1.950476922725589 p-value =  4.069315238885027
x =  0.0081 log bayes =  1.987943360123626 p-value =  4.127139411901921
x =  0.0082 log bayes =  2.025632380831605 p-value =  3.092304773912224
===========[ bayes 2 threshold ]
x =  0.0083 log bayes =  2.063533301577686 p-value =  3.113804524966511
x =  0.0084 log bayes =  2.101634890569997 p-value =  3.165651507160916
x =  0.0085 log bayes =  2.14000698247772 p-value =  2.354322749345709
x =  0.0086 log bayes =  2.17857493564457 p-value =  2.375946556820785
x =  0.0087 log bayes =  2.217318518848302 p-value =  2.421933861259354
x =  0.0088 log bayes =  2.256287403997312 p-value =  1.787489145781218
x =  0.0089 log bayes =  2.295466693226178 p-value =  1.808415161524708
x =  0.009 log bayes =  2.334794130664931 p-value =  1.848779903956496
x =  0.0091 log bayes =  2.374346823847259 p-value =  1.353787284586766
x =  0.0092 log bayes =  2.414076816396918 p-value =  1.373439084371367
x =  0.0093 log bayes =  2.45393472132213 p-value =  1.017140589806407
x =  0.0094 log bayes =  2.494047796529968 p-value =  1.02309774749169
x =  0.0095 log bayes =  2.53426207843015 p-value =  1.041111584570076
x =  0.0096 log bayes =  2.574681035463586 p-value =  0.7649978626812526
===========[ 99% threshold ]
x =  0.0097 log bayes =  2.615240799123143 p-value =  0.7717346518594089
x =  0.0098 log bayes =  2.65594939029272 p-value =  0.7879198056784475
x =  0.0099 log bayes =  2.696832710692876 p-value =  0.57427374829861
x =  0.01 log bayes =  2.737824599678029 p-value =  0.581195295706084
===========[ bayes 2.7 threshold ]
x =  0.0101 log bayes =  2.779008588617419 p-value =  0.5954940386953036
x =  0.0102 log bayes =  2.820277243611168 p-value =  0.4304030357540509
x =  0.0103 log bayes =  2.861737947545418 p-value =  0.4371122962179401
x =  0.0104 log bayes =  2.903276674647444 p-value =  0.320257363252172
x =  0.0105 log bayes =  2.944988951116496 p-value =  0.3221387095806921
x =  0.0106 log bayes =  2.98679092061447 p-value =  0.3283892785598433
x =  0.0107 log bayes =  3.028728292093368 p-value =  0.238554477874591
x =  0.0108 log bayes =  3.07078655825374 p-value =  0.2408411854459276
x =  0.0109 log bayes =  3.112921041847679 p-value =  0.2464975049812564
```

```
x =  0.011 log bayes =  3.155228556705267 p-value =  0.1774930322185887
x =  0.0111 log bayes =  3.197543150504225 p-value =  0.1799049654466882
x =  0.0112 log bayes =  3.240080089183124 p-value =  0.1849100700914028
x =  0.0113 log bayes =  3.282632384394694 p-value =  0.1319428887020915
x =  0.0114 log bayes =  3.325302310606427 p-value =  0.1343010669822639
x =  0.0115 log bayes =  3.36808485766263 p-value =  0.09730459634041816
x =  0.0116 log bayes =  3.410864949697741 p-value =  0.09801739522275196
x =  0.0117 log bayes =  3.453859349993975 p-value =  0.1002152627548012
x =  0.0118 log bayes =  3.496857154276509 p-value =  0.07193429381107941
===========[ 99.9% threshold ]
x =  0.0119 log bayes =  3.539912053579815 p-value =  0.07278300386057966
x =  0.012 log bayes =  3.583119684093875 p-value =  0.07476443540285577
x =  0.0121 log bayes =  3.626313746162385 p-value =  0.05315318346878455
x =  0.0122 log bayes =  3.66960566033073 p-value =  0.05403297595362255
x =  0.0123 log bayes =  3.712995900715565 p-value =  0.05577581361154507
===========[ bayes 3.7 threshold ]
x =  0.0124 log bayes =  3.756365793937757 p-value =  0.03926529748610354
x =  0.0125 log bayes =  3.79984282281448 p-value =  0.04011227106732372
x =  0.0126 log bayes =  3.843394388860504 p-value =  0.02870782976285236
x =  0.0127 log bayes =  3.886918120434884 p-value =  0.02900455545026168
x =  0.0128 log bayes =  3.930524552472023 p-value =  0.02978289728820217
x =  0.0129 log bayes =  3.97421447620592 p-value =  0.02110018935250118
x =  0.013 log bayes =  4.017868303053985 p-value =  0.02142831131494066
```

- Maximum high-risk cohort mortality rate $p_2 = 0.05$

```
f(t) := lbayesmax(1495,5, t, 5/100);
g(t) := pdistr(1495,5,t);
xlist: makelist(t/10000,t,60,120,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.006 log bayes =  1.758193146943509 p-value =  23.81878512791918
x =  0.0061 log bayes =  1.791621533344085 p-value =  24.03270681971289
x =  0.0062 log bayes =  1.825469072321574 p-value =  18.71543856864613
x =  0.0063 log bayes =  1.85971717796978 p-value =  18.80730896513931
x =  0.0064 log bayes =  1.894336933392722 p-value =  19.00306714547602
x =  0.0065 log bayes =  1.929335019881668 p-value =  14.68180083739779
x =  0.0066 log bayes =  1.964725264283162 p-value =  14.76801010034541
x =  0.0067 log bayes =  2.000469069432828 p-value =  14.94523938594154
===========[ bayes 2 threshold ]
x =  0.0068 log bayes =  2.036561286578106 p-value =  11.45747359056833
x =  0.0069 log bayes =  2.072996437159218 p-value =  11.53824336819699
x =  0.007 log bayes =  2.109768723064743 p-value =  11.69725918696211
x =  0.0071 log bayes =  2.146872032811149 p-value =  8.898849247581843
x =  0.0072 log bayes =  2.184299943781251 p-value =  8.974139079362958
x =  0.0073 log bayes =  2.222045720619301 p-value =  9.115647447712988
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x =  0.0075 log bayes =  2.298462330679909 p-value =  6.951473422073926
x =  0.0076 log bayes =  2.337118062153857 p-value =  7.076417986779846
x =  0.0077 log bayes =  2.376061426301485 p-value =  5.301247177455311
x =  0.0078 log bayes =  2.415283967497839 p-value =  5.365038626194091
x =  0.0079 log bayes =  2.454776827724949 p-value =  4.049022709179763
===========[ 95% threshold ]
x =  0.008 log bayes =  2.494544551205089 p-value =  4.069315238885027
x =  0.0081 log bayes =  2.534609964568008 p-value =  4.127139411901921
```

```
x =  0.0082 log bayes =  2.574926152513506 p-value =  3.092304773912224
x =  0.0083 log bayes =  2.615482941470509 p-value =  3.113804524966511
x =  0.0084 log bayes =  2.656269622649316 p-value =  3.165651507160916
x =  0.0085 log bayes =  2.697356567480481 p-value =  2.354322749345709
x =  0.0086 log bayes =  2.73866968530613 p-value =  2.375946556820785
===========[ bayes 2.7 threshold ]
x =  0.0087 log bayes =  2.780189310637094 p-value =  2.421933861259354
x =  0.0088 log bayes =  2.821965696369218 p-value =  1.787489145781218
x =  0.0089 log bayes =  2.863984541420942 p-value =  1.808415161524708
x =  0.009 log bayes =  2.906184203068331 p-value =  1.848779903956496
x =  0.0091 log bayes =  2.948642418943908 p-value =  1.353787284586766
x =  0.0092 log bayes =  2.991311880340297 p-value =  1.373439084371367
x =  0.0093 log bayes =  3.034143866148718 p-value =  1.017140589806407
x =  0.0094 log bayes =  3.077266319047157 p-value =  1.02309774749169
x =  0.0095 log bayes =  3.120525979807935 p-value =  1.041111584570076
x =  0.0096 log bayes =  3.164027041562517 p-value =  0.7649978626812526
===========[ 99% threshold ]
x =  0.0097 log bayes =  3.207706381591641 p-value =  0.7717346518594089
x =  0.0098 log bayes =  3.251572788470163 p-value =  0.7879198056784475
x =  0.0099 log bayes =  3.295652954354955 p-value =  0.57427374829861
x =  0.01 log bayes =  3.33988153266443 p-value =  0.581195295706084
x =  0.0101 log bayes =  3.384342893382804 p-value =  0.5954940386953036
x =  0.0102 log bayes =  3.428930466743257 p-value =  0.4304030357540509
x =  0.0103 log bayes =  3.473752526296482 p-value =  0.4371122962179401
x =  0.0104 log bayes =  3.518695964526822 p-value =  0.320257363252172
x =  0.0105 log bayes =  3.563857254596042 p-value =  0.3221387095806921
x =  0.0106 log bayes =  3.609153517000048 p-value =  0.3283892785598433
x =  0.0107 log bayes =  3.654631468619256 p-value =  0.238554477874591
x =  0.0108 log bayes =  3.700277642459555 p-value =  0.2408411854459276
===========[ bayes 3.7 threshold ]
x =  0.0109 log bayes =  3.746048435300598 p-value =  0.2464975049812564
x =  0.011 log bayes =  3.792041770133871 p-value =  0.1774930322185887
x =  0.0111 log bayes =  3.838092840413482 p-value =  0.1799049654466882
x =  0.0112 log bayes =  3.88441809602416 p-value =  0.1849100700914028
x =  0.0113 log bayes =  3.930811772366738 p-value =  0.1319428887020915
x =  0.0114 log bayes =  3.977377409172089 p-value =  0.1343010669822639
x =  0.0115 log bayes =  4.024111304862666 p-value =  0.09730459634041816
x =  0.0116 log bayes =  4.07089973735535 p-value =  0.09801739522275196
x =  0.0117 log bayes =  4.117960870903818 p-value =  0.1002152627548012
x =  0.0118 log bayes =  4.165085251478104 p-value =  0.07193429381107941
===========[ 99.9% threshold ]
x =  0.0119 log bayes =  4.212328071820549 p-value =  0.07278300386057966
x =  0.012 log bayes =  4.259786523592357 p-value =  0.07476443540285577
```

- Maximum high-risk cohort mortality rate $p_2 = 0.10$

```
f(t) := lbayesmax(1495,5, t, 10/100);
g(t) := pdistr(1495,5,t);
xlist: makelist(t/10000,t,50,120,1);
for t in xlist do print("x = ", float(t), "log bayes = ", f(t), "p-value = ", g(t));
x =  0.005 log bayes =  1.772368401169081 p-value =  46.38008666190668
x =  0.0051 log bayes =  1.80218833619137 p-value =  46.49979726909253
x =  0.0052 log bayes =  1.832085669189462 p-value =  46.74821236561556
x =  0.0053 log bayes =  1.862398913043684 p-value =  37.36691920214581
```

```
x =  0.0054 log bayes =  1.893216215827102 p-value =  37.47971048074269
x =  0.0055 log bayes =  1.924522944330381 p-value =  37.72298830876053
x =  0.0056 log bayes =  1.956291001129976 p-value =  29.87547892680247
x =  0.0057 log bayes =  1.988512523513351 p-value =  29.98061572242807
x =  0.0058 log bayes =  2.021204226162635 p-value =  30.21111086353742
===========[ bayes 2 threshold ]
x =  0.0059 log bayes =  2.054304722185877 p-value =  23.72069023596992
x =  0.006 log bayes =  2.087868324057019 p-value =  23.81878512791918
x =  0.0061 log bayes =  2.121822605368093 p-value =  24.03270681971289
x =  0.0062 log bayes =  2.15619780019655 p-value =  18.71543856864613
x =  0.0063 log bayes =  2.190975331887125 p-value =  18.80730896513931
x =  0.0064 log bayes =  2.226126292862237 p-value =  19.00306714547602
x =  0.0065 log bayes =  2.261657373799574 p-value =  14.68180083739779
x =  0.0066 log bayes =  2.297582411000751 p-value =  14.76801010034541
x =  0.0067 log bayes =  2.333862816825945 p-value =  14.94523938594154
x =  0.0068 log bayes =  2.370493452117196 p-value =  11.45747359056833
x =  0.0069 log bayes =  2.407468847979816 p-value =  11.53824336819699
x =  0.007 log bayes =  2.444783216039097 p-value =  11.69725918696211
x =  0.0071 log bayes =  2.482430454620052 p-value =  8.898849247581843
x =  0.0072 log bayes =  2.520404150986928 p-value =  8.974139079362958
x =  0.0073 log bayes =  2.558697579738764 p-value =  9.115647447712988
x =  0.0074 log bayes =  2.597303697420241 p-value =  6.88183766887816
x =  0.0075 log bayes =  2.636215133368631 p-value =  6.951473422073926
x =  0.0076 log bayes =  2.675424176781232 p-value =  7.076417986779846
x =  0.0077 log bayes =  2.714922759952337 p-value =  5.301247177455311
===========[ bayes 2.7 threshold ]
x =  0.0078 log bayes =  2.75470243758981 p-value =  5.365038626194091
x =  0.0079 log bayes =  2.794754362086098 p-value =  4.049022709179763
===========[ 95% threshold ]
x =  0.008 log bayes =  2.835083088152752 p-value =  4.069315238885027
x =  0.0081 log bayes =  2.875711452987822 p-value =  4.127139411901921
x =  0.0082 log bayes =  2.916592551939728 p-value =  3.092304773912224
x =  0.0083 log bayes =  2.957716222166767 p-value =  3.113804524966511
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x =  0.0085 log bayes =  3.040729564834834 p-value =  2.354322749345709
x =  0.0086 log bayes =  3.082615539919071 p-value =  2.375946556820785
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x =  0.0089 log bayes =  3.209661096517897 p-value =  1.808415161524708
x =  0.009 log bayes =  3.252441738669705 p-value =  1.848779903956496
x =  0.0091 log bayes =  3.295482994158551 p-value =  1.353787284586766
x =  0.0092 log bayes =  3.338737565771501 p-value =  1.373439084371367
x =  0.0093 log bayes =  3.382156743983596 p-value =  1.017140589806407
x =  0.0094 log bayes =  3.425868483146774 p-value =  1.02309774749169
x =  0.0095 log bayes =  3.469719535798476 p-value =  1.041111584570076
x =  0.0096 log bayes =  3.51381410692726l p-value =  0.7649978626812526
===========[ 99% threshold ]
x =  0.0097 log bayes =  3.558089085764057 p-value =  0.7717346518594089
x =  0.0098 log bayes =  3.602553272927618 p-value =  0.7879198056784475
x =  0.0099 log bayes =  3.647233372713844 p-value =  0.57427374829861
x =  0.01 log bayes =  3.692064050775798 p-value =  0.581195295706084
x =  0.0101 log bayes =  3.737129689429265 p-value =  0.5954940386953036
===========[ bayes 3.7 threshold ]
x =  0.0102 log bayes =  3.782323731336887 p-value =  0.4304030357540509
```

```
x =  0.0103 log bayes =  3.827754462577463 p-value =  0.4371122962179401
x =  0.0104 log bayes =  3.873308788263448 p-value =  0.320257363252172
x =  0.0105 log bayes =  3.919083194285498 p-value =  0.3221387095806921
x =  0.0106 log bayes =  3.964994813970391 p-value =  0.3283892785598433
x =  0.0107 log bayes =  4.011090377132373 p-value =  0.238554477874591
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x =  0.0118 log bayes =  4.52849047369819 p-value =  0.07193429381107941
===========[ 99.9% threshold ]
x =  0.0119 log bayes =  4.576379004556999 p-value =  0.07278300386057966
x =  0.012 log bayes =  4.624485599125723 p-value =  0.07476443540285577
```

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A. Zelenko’s March 2020 letter

Dr. Vladimir (Zev) Zelenko
Board Certified Family Practitioner
501 Rt 208, Monroe, NY 10950
845-238-0000

March 23, 2020

To all medical professionals around the world:

My name is Dr. Zev Zelenko and I practice medicine in Monroe, NY. For the last 16 years, I have cared for approximately 75% of the adult population of Kiryas Joel, which is a very close knit community of approximately 35,000 people in which the infection spread rapidly and unchecked prior to the imposition of social distancing.

As of today my team has tested approximately 200 people from this community for Covid-19, and 65% of the results have been positive. If extrapolated to the entire community, that means more than 20,000 people are infected at the present time. Of this group, I estimate that there are 1500 patients who are in the high-risk category (i.e. >60, immunocompromised, comorbidities, etc).

Given the urgency of the situation, I developed the following treatment protocol in the pre-hospital setting and have seen only positive results:

1. Any patient with shortness of breath regardless of age is treated.

2. Any patient in the high-risk category even with just mild symptoms is treated.

3. Young, healthy and low risk patients even with symptoms are not treated (unless their circumstances change and they fall into category 1 or 2).

My out-patient treatment regimen is as follows:

1. Hydroxychloroquine 200mg twice a day for 5 days

2. Azithromycin 500mg once a day for 5 days

3. Zinc sulfate 220mg once a day for 5 days

The rationale for my treatment plan is as follows. I combined the data available from China and South Korea with the recent study published from France (sites available on request). We know that hydroxychloroquine helps Zinc enter the cell. We know that Zinc slows viral replication within the cell. Regarding the use of azithromycin, I postulate it prevents secondary bacterial infections. These three drugs are well known and usually well tolerated, hence the risk to the patient is low.

Since last Thursday, my team has treated approximately 350 patients in Kiryas Joel and another 150 patients in other areas of New York with the above regimen.

Of this group and the information provided to me by affiliated medical teams, we have had ZERO deaths, ZERO hospitalizations, and ZERO intubations. In addition, I have not heard of any negative side effects other than approximately 10% of patients with temporary nausea and diarrhea.

In sum, my urgent recommendation is to initiate treatment in the outpatient setting as soon as possible in accordance with the above. Based on my direct experience, it prevents acute respiratory distress syndrome (ARDS), prevents the need for hospitalization and saves lives.

With much respect,

Dr. Zev Zelenko

cc: President Donald J. Trump; Mr. Mark Meadows, Chief of Staff

B. Zelenko's April 2020 letter

Dr. Vladimir (Zev) Zelenko M.D.
Board Certified Family Practitioner
501 Rt 208, Monroe, NY 10950
845-782-0000

April 28, 2020

To all medical professionals around the world:

The current sensitivity and specificity of the RT-PCR nasal swab test for Covid-19 is 99% and 66%, respectively.[1] In simple terms, when the test is positive, it is very accurate to diagnose patients with Covid-19. However, when the test is negative it is wrong 33% of the time.

In most outpatient situations, the RT-PCR Covid-19 test takes two to three days to get the results. This is unacceptable since it is imperative to initiate treatment for viral infections as soon as possible.[2] This clinical principle is derived from the recommendations of treatment for other viral infections (i.e. influenza, herpes zoster, HIV, etc).

According to the CDC, symptoms of Covid-19 may appear 2-14 days after exposure to the virus. The clinical symptoms of Covid-19 are:[3]

- Cough and/or shortness of breath
- Fever or chills (with or without rigors)
- New loss of taste or smell
- Myalgia
- Headache and/or sore throat
- Diarrhea

Given the urgency of the situation, I recommend initiating treatment based on clinical suspicion as soon as possible, even without confirmatory testing.

I developed the following treatment protocol for the prehospital setting and have seen very positive results:

1. Any patient with shortness of breath is treated.
2. Any patient in a high-risk category with mild symptoms is treated.

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[1] medrxiv.org/content/10.1101/2020.04.05.20053355v2.full.pdf+html
[2] cdc.gov/flu/professionals/antivirals
[3] cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html

3. Young, healthy and low risk patients even with symptoms are not treated (unless their circumstances change and they fall into category 1 or 2); as is well known, these patients likely self resolve.

My outpatient treatment regimen is as follows:

1. Hydroxychloroquine 200 mg twice a day for 5 days
2. Azithromycin 500 mg once a day for 5 days
3. Zinc sulfate 220 mg once a day for 5 days

The rationale for my treatment plan is as follows. I combined the data available from China and South Korea with the recent study published from France (cites available on request). We know that hydroxychloroquine helps Zinc enter the cell. We know that Zinc slows viral replication within the cell. The use of azithromycin prevents secondary bacterial infections and has antiviral effects.[4] These three drugs are well known and usually well tolerated, hence the risk to the patient is low.

Since 3/15/20, my team has seen approximately 1450 patients in Monroe, New York with either test proven or clinically suspected coronavirus infection. The majority of the patients were treated with only supportive care. The patients with shortness of breath or who are in the high risk category were treated with the above regimen (approximately 405 patients at this point).

Of this group and the information provided to me by affiliated medical teams, we have had two deaths, six hospitalizations for pneumonia, and four intubations (all extubated now). In addition, to my knowledge there have not been any negative side effects other than approximately 10% of patients with temporary nausea and diarrhea.

In sum, **my urgent recommendation is to initiate treatment in the outpatient setting as soon as possible** in accordance with the above. Based on my direct experience, it prevents acute respiratory distress syndrome (ARDS), prevents the need for hospitalization and saves lives.

With much respect,

Dr. Vladimir (Zev) Zelenko M.D.

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[4] pubmed.ncbi.nlm.nih.gov/32302411/

C. Zelenko’s June 2020 letter

Dr. Vladimir (Zev) Zelenko M.D.
Board Certified Family Practitioner
845-782-0000

6/14/20

Dear Dr. Moshe Bar Siman Tov:

My name is Dr. Vladimir (Zev) Zelenko and I have been a board certified family practitioner in Monroe, NY for the last 16 years. The community consists of 35,000 people living within a square mile. Please allow me to present to you the following outcome data since mid-March.

1- Approximately 2200 patients seen with the Covid-19 infection. Diagnosis is based on pcr testing, clinical criteria and IgG antibody testing. The positive rate of testing is over 50%.

2- Approximately 1400 patients were only treated with supportive care (i.e. fluids, tylenol, and follow up). These patients were all under the age of 60, healthy, and with no shortness of breath.

3- Approximately 800 patients treated **in the outpatient setting** with the "Zelenko Protocol." These patients were considered high risk (over 60 years, chronic medical problems, or short of breath on presentation).

Zelenko Protocol:

1. Stratify patients into high and low risk. Treat only high risk.
2. Treat within the first 5 days of symptoms, even before results of pcr test.
3. Use three drug regimen:

A. hydroxychloroquine 200 bid x 5 days
B. azithromycin 500 qd x 5 days.
C. zinc sulfate 220 qd x 5 days

Outcomes: NO serious side effects. No cardiac arrhythmias.

2 deaths, 12 people hospitalized: 8 for iv antibiotics for bacterial pneumonia, 4 intubated for ARDS.

All are now extubated and discharged, all patients with pneumonia are discharged home.

I am in direct contact with the white house via Mr. Mark Meadows (the president's chief of staff), Senator Ron Johnson (WI), Mayor Rudy Guliani (the president's private legal counsel).

I have been contacted by several governments and have provided counsel to Ukraine, Brazil, Honduras, Peru, and Chile.

On a side note, I am in contact with Dr. Alan Moses, infectious disease from Hadassah hospital, and helped fund his clinical trial for prophylaxis of nursing home residents. It should be published next month.

My protocol has been endorsed by

Dr. Robert Susskind, Dean and founder of University of California School of Medicine.

Dr. William Grace, Oncology Lenox Hill Hospital, NY.

Dr. Rosy Joseph, Nephrology and Internal Medicine, Hackensack University Medical Center, Hackensack, NJ.

In summary, it is imperative to **initiate aggressive and early treatment of Covid-19 in the primary care setting,** before the patient develops pulmonary complications. According to my data, prompt treatment will reduce hospitalizations, intubations, and death. My data will be published in a peer review journal within the next few weeks.

I humbly and respectfully request that you consider this outpatient treatment against Covid-19.

Sincerely,

Dr. Vladimir (Zev) Zelenko

D. Estimated COVID-19 Burden by the CDC

Centers for Disease
Control and Prevention

COVID-19

Estimated COVID-19 Burden

Updated Nov. 16, 2021

- Estimated COVID-19 Infections, Symptomatic Illnesses, Hospitalizations, and Deaths in the United States
- What Can Be Learned from Estimates of COVID-19 Infections, Illnesses, Hospitalizations, and Deaths in the United States
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To better reflect the full burden of COVID-19, CDC provides estimates of COVID-19 infections, symptomatic illnesses, hospitalizations, and deaths using statistical models to adjust for cases that national surveillance networks do not capture for a number of reasons. These estimates and the methodologies used to calculate them are published in *Clinical Infectious Diseases* and *The Lancet Regional Health – Americas* . These estimates will be updated periodically.

Estimated COVID-19 Infections, Symptomatic Illnesses, Hospitalizations, and Deaths in the United States

CDC estimates that from February 2020–September 2021:

1 in 4.0 (95% UI* 3.4 – 4.7) COVID–19 infections were reported.

1 in 3.4 (95% UI* 3.0 – 3.8) COVID–19 symptomatic illnesses were reported.

1 in 1.9 (95% UI* 1.7 – 2.1) COVID–19 hospitalizations were reported.

1 in 1.32 (95% UI* 1.29 – 1.34) COVID-19 deaths were reported.

These estimates suggest that during this period, there were approximately:

146.6 Million	124.0 Million	7.5 Million	921,000
Estimated Total Infections	Estimated Symptomatic Illnesses	Estimated Hospitalizations	Estimated Total Deaths

Last Updated: October 2, 2021

Table 1: Preliminary estimated COVID-19 cumulative incidence, by age group — United States, February 2020-September 2021[†]

	Infections		Symptomatic Illness		Hospitalizations		Deaths	
Age group	**Estimate**	**95% UI***	**Estimate**	**95% UI***	**Estimate**	**95% UI***	**Estimate**	**95% UI***
0-17 years	25,844,005	21,361,986 – 31,614,224	22,030,307	19,108,000 – 25,701,942	266,597	224,715 – 315,966	645	501 – 1,141
18-49 years	75,179,070	62,681,393 – 90,520,720	64,029,542	56,477,718 – 73,348,809	1,996,830	1,719,541 – 2,334,921	60,355	56,641 – 64,388
50-64 years	27,407,088	22,869,356 – 32,921,158	23,378,591	20,628,625 – 26,697,449	2,009,141	1,771,585 – 2,304,508	159,489	154,920 – 164,453
65+ years	18,012,882	14,527,427 – 22,761,991	14,626,141	12,913,173 – 16,745,092	3,232,213	2,864,006 – 3,683,201	700,882	688,959 – 713,090
All ages	146,585,169	125,980,377 – 171,574,943	123,979,337	111,032,406 – 139,954,539	7,506,029	6,715,747 – 8,465,642	921,371	902,527 – 941,172

* Adjusted estimates are presented in two parts: an uncertainty interval [UI] and a point estimate. The uncertainty interval provides a range in which the true number or rate of COVID-19 infections, symptomatic illnesses, hospitalizations, or deaths would be expected to fall if the same study was repeated many times, and it gives an idea of the precision of the point estimate. A 95% uncertainty interval means that if the study were repeated 100 times, then 95 out of 100 times the uncertainty interval would contain the true point estimate. Conversely, in only 5 times out of a 100 would the uncertainty interval not contain the true point estimate.

[†] These are preliminary estimates that may fluctuate up or down as more data become available and as we improve our understanding of the detection and reporting of COVID-19. CDC will continue to update these estimates periodically.

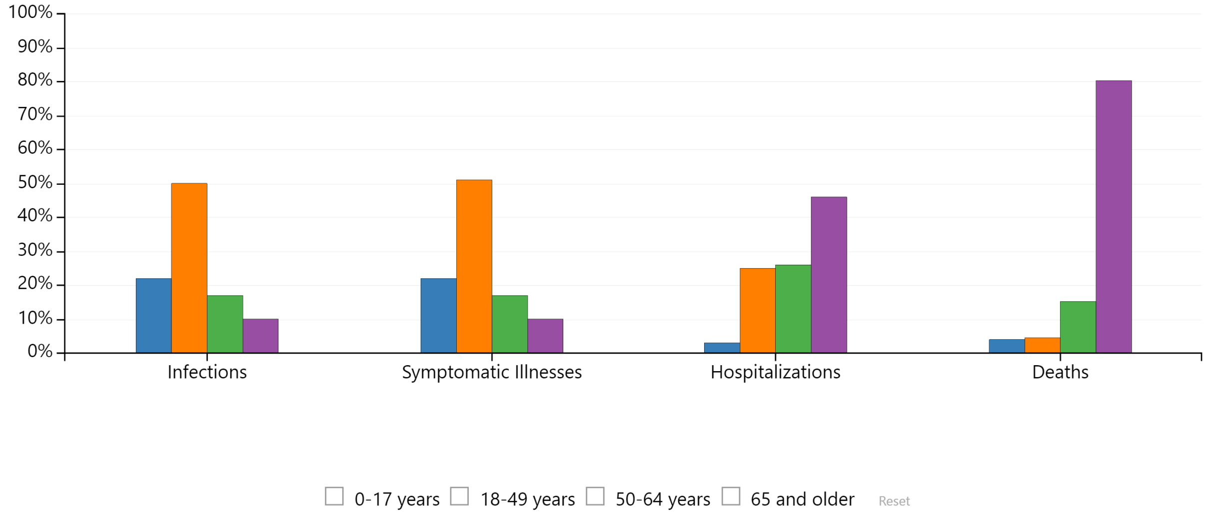
Table 2: Estimated rates of COVID-19 disease outcomes per 100,000, by age group — United States, February 2020-September 2021

	Infection rate per 100,000		Symptomatic Illness rate per 100,000		Hospitalization rate per 100,000		Death rate per 100,000	
Age group	**Estimate**	**95% UI***	**Estimate**	**95% UI***	**Estimate**	**95% UI***	**Estimate**	**95% UI***
0-17 years	35,490	29,335 – 43,414	30,253	26,240 – 35,295	366	309 – 434	0.9	0.7-1.6
18-49 years	54,860	45,740 – 66,055	46,724	41,213 – 53,525	1,457	1,255 – 1,704	43.7	41.0 – 46.6
50-64 years	43,656	36,428 – 52,439	37,239	32,859 – 42,526	3,200	2,822 – 3,671	253.5	246.2 – 261.3

	Infection rate per 100,000		Symptomatic Illness rate per 100,000		Hospitalization rate per 100,000		Death rate per 100,000	
Age group	Estimate	95% UI*	Estimate	95% UI*	Estimate	95% UI*	Estimate	95% UI*
65+ years	32,363	26,101 – 40,895	26,278	23,200 – 30,085	5,807	5,146 – 6,617	1296.5	1274.5 – 1319.1
All ages	44,650	38,374 – 52,262	37,764	33,821 – 42,630	2,286	2,046 – 2,579	280.7	275.0 – 286.7

* Adjusted rates are presented in two parts: an uncertainty interval [UI] and a point estimate. The uncertainty interval provides a range in which the true number or rate of COVID-19 infections, symptomatic illnesses, hospitalizations, or deaths would be expected to fall if the same study was repeated many times, and it gives an idea of the precision of the point estimate. A 95% uncertainty interval means that if the study were repeated 100 times, then 95 out of 100 times the uncertainty interval would contain the true point estimate. Conversely, in only 5 times out of a 100 would the uncertainty interval not contain the true point estimate.

Percentage of COVID-19 infections, symptomatic illness, and hospitalizations, and deaths, by age group—United States, February 2020-September 2021



Data Table −

	Infections	Symptomatic Illnesses	Hospitalizations	Deaths
0-17 years	22%	22%	3%	4%
18-49 years	50%	51%	25%	5%
50-64 years	17%	17%	26%	15%
65 and older	10%	10%	46%	80%

Download Table Data (csv)

What Can Be Learned fromEstimates of COVID-19 Infections, Illnesses, Hospitalizations, and Deaths in the United States

Estimating unreported cases, hospitalizations, and deaths helps to quantify the impact and severity of the COVID-19 pandemic on the healthcare system and society. Additionally, these estimates can inform how to direct and allocate healthcare resources; assist in planning for prevention and control measures, including vaccination; predict the future burden of COVID-19; and evaluate the potential impact of interventions.

Why CDC Estimates COVID-19 Infections, Illnesses, Hospitalizations, and Deaths

The cumulative burden of COVID-19 is an estimate of the number of people who may have been infected, sick, hospitalized, or died as a result of a COVID-19 infection in the United States. Confirmed COVID-19 cases and deaths are nationally reported, but these cases and deaths likely represent only a fraction of the true number that have occurred in the population. COVID-19 infections, symptomatic illnesses, hospitalizations, and deaths might be underdetected and go unreported for a variety of reasons. For example:

- Some people infected with SARS-CoV-2 never show symptoms (asymptomatic infection), so their infection will likely go undetected.
- Case reports sent to CDC are often missing patient information, like age or hospitalization status, or are delayed.
- Not everyone who is sick will seek medical care and/or be tested; and patients may not be tested for COVID-19 while hospitalized or if they die.
- Even if a sick outpatient or hospitalized patient is tested, an infection with COVID-19 may not be accurately captured if, for example:
  - the test was not completed correctly or within the appropriate timeframe for capturing infection;
  - the test result was falsely negative for a COVID-19 infection due to the sensitivity of the test;
  - the test result was falsely negative for a COVID-19 infection due to the quality or quantity of the specimen collected; or
  - the confirmed COVID-19 case was never reported to the local and state public health agency and then to CDC.
- For patients with COVID-19, death can occur several days or weeks after being tested and reported, and the death might be incorrectly attributed to a cause other than COVID-19 because of the time between testing positive and death.
- COVID-19 may result in non-respiratory complications or it might increase the severity of chronic conditions, which can lead to death (e.g., sepsis, circulatory diseases, respiratory diseases, diabetes, or renal failure), and COVID-19 might be incorrectly omitted as a contributing cause of death on the death certificate.

Because current surveillance systems do not capture all cases or deaths of COVID-19 occurring in the United States, CDC provides these estimates to better reflect the larger burden of COVID-19. CDC uses these types of estimates to inform policy decisions and public messages.

How CDC Estimates COVID-19 Infections, Symptomatic Illnesses and Hospitalizations

To estimate COVID-19 infections, symptomatic illnesses, and hospitalizations, CDC uses a statistical model applied to confirmed cases of COVID-19, adjusted for missing age and hospitalization status. Several data sources and surveillance systems are used to identify and characterize potential sources of underdetection, which include:

- **SARS-CoV-2 test sensitivity is lower**. People tested for SARS-CoV-2, the virus that causes COVID-19 disease, may not test positive even if infected with the virus due to the lower sensitivity of the test used. SARS-CoV-2 test sensitivity has been reported in the literature; a range of 79%-98% sensitivity for RT-PCR tests is used to account for false negative test results.
- **SARS-CoV-2 test is not ordered or not completed in a timely manner**. Not all outpatients who seek care for acute respiratory illness (ARI) or inpatients hospitalized with ARI are tested for COVID-19, and not all ordered tests are correctly completed in a timely manner. CDC uses two data sources to approximate how many outpatients with ARI are not tested for COVID-19:

  - IBM Watson Explorys Electronic Health Record database, a data repository of electronic health records from more than 39 health partners, 400 acute care facilities, and 400,000 unique providers; and
  - COVID Near You (CNY), a website application launched by Harvard University in March 2020 where participants can submit information on self-reported symptoms, efforts to obtain health care, and COVID-19 testing.
- **Not all patients with symptoms seek care or testing services**. Not all sick patients seek care or are tested for COVID-19, and therefore they are not included in national case reports. To approximate the number of symptomatic people who never sought medical care, researchers use data from COVID Near You (CNY) and Flu Near You (FNY) sites on health care seeking behaviors. While COVID Near You launched in March 2020, FNY has been collecting self-reported influenza participatory data since 2011.
- **Patients do not have symptoms**. Some people infected with SARS-CoV-2 never show symptoms (they have asymptomatic infection). People with asymptomatic infection are very likely to go undetected. The percentage of asymptomatic infections is reported in the literature and varies by age group. In people 0-64 years old, a range of 5%-24% is used to estimate asymptomatic infections, and for people 65 years and older, a range of 5%-32% is used.

The statistical model used to adjust hospitalized and non-hospitalized case counts for the above sources of underdetection is based on methods that have been previously used to estimate the disease burden of influenza, detailed elsewhere. These methods are peer-reviewed and published in *Clinical Infectious Diseases*.

How CDC Estimates COVID-19 Deaths

COVID-19 deaths are estimated using a statistical model to calculate the number of COVID-19 deaths that were unrecognized and those that were not recorded on death certificates and, as a result, were never reported as a death related to COVID-19.

To estimate these unrecognized COVID-19 deaths, all-cause deaths are obtained from the National Center of Health Statistics. Before applying the statistical model, reported COVID-19 deaths are subtracted by age, state, and week from all-cause deaths, so that these reported COVID-19 deaths are not included in the calculation of the expected deaths for the statistical model.

Then, to understand how many deaths may have not been recognized as being related to COVID-19, CDC uses a statistical model to estimate the number of expected deaths from all causes assuming that there was no circulation of COVID-19 (that is, those deaths expected in the absence of any COVID-19 illnesses). Researchers then use the model to predict the number of all-cause deaths that would have occurred taking into account information on COVID-19 circulation,. To obtain the number of unrecognized COVID-19 deaths, the number of expected all-cause deaths (without COVID-19 circulation) are subtracted from the number of predicted all-cause deaths (with COVID-19 circulation). The model is used to calculate estimates by state and age (for six age groups: 0-17, 18-49, 50-64, 65-74, 75-84, and ≥85 years).

Once investigators estimate unrecognized COVID-19 deaths, they add documented COVID-19 deaths to the unrecognized deaths to obtain an estimate of the total number of COVID-19-attributable deaths. These methods are peer-reviewed and published in *The Lancet Regional Health – Americas* .

Limitations

These estimates of COVID-19 infections, symptomatic illnesses, hospitalizations and deaths are subject to several limitations, either from the data inputs used or some statistical assumptions made in the methods. A detailed discussion of these limitations can be found in *Clinical Infectious Diseases* and *The Lancet Regional Health – Americas* . CDC continues to explore data sources and statistical methodologies for estimating COVID-19 disease burden and will refine estimates over time.

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