## Statistical Learning– MATH 6333 Set 7 (Ensemble Methods)

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\* Last updated November 10, 2021

# A preamble to Bootstrap

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#### Bootstrap

By Efron (1979, 1981), to estimate



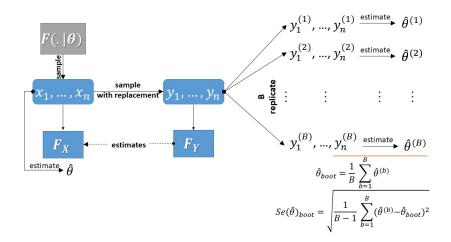
Standard error

- Confidence interval (5 different ways)
- correlation, regression parameters, prediction

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# Bootstrap

Estimation



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#### Bootstrap Estimation

- B = 50 is good enough.
- The probability that any item is selected in any one of the bootstrap samples is given by

$$1-(1-\frac{1}{n})^n \approx 1-e^{-1}=.632$$

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Expected number of distinct points in a sample is .632*n*.

#### Bootstrap

**Confidence Interval** 

100(1 –  $\alpha$ )% Bootstrap Confidence Intervals (BCI):

1. Standard Normal BCI

$$\hat{ heta}_{boot} \pm z_{lpha/2} se(\hat{ heta})_{boot}$$

2. Basic BCI

$$\left(2\hat{ heta}_{boot}-\hat{ heta}_{1-lpha/2},2\hat{ heta}_{boot}-\hat{ heta}_{lpha/2}
ight)$$

3. Percentile BCI

$$\left(\hat{\theta}_{\alpha/2},\hat{\theta}_{1-\alpha/2}\right)$$

4. t-type - BCI

$$\left(\hat{\theta}_{boot} - t^*_{1-\alpha/2} se(\hat{\theta}), \hat{\theta}_{boot} + t^*_{\alpha/2} se(\hat{\theta})\right)$$

#### Bootstrap Confidence Interval

with  $t_{\alpha}^*$  is the  $\alpha$  quantile of  $\{t^{(1)}, \ldots, t^{(B)}\}$  where

$$t^{(i)} = rac{\hat{ heta}^{(i)} - \hat{ heta}_{boot}}{oldsymbol{se}(\hat{ heta}^{(i)})}$$

and estimation of  $se(\hat{\theta}^{(i)})$  requires a further bootstrap from the bootstrapped sample  $y_1^{(i)}, \ldots, y_n^{(i)}$ 

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#### Bootstrap

**Confidence Interval** 

100(1 –  $\alpha$ )% Bootstrap Confidence Intervals (BCI):

1. Bias Corrected accelerated BCI or BCa - BCI

$$\left( \hat{\theta}_{lpha_{1}}^{*}, \hat{\theta}_{lpha_{2}}^{*} 
ight)$$

are the  $\alpha_1$  and  $\alpha_2$  quantiles of  $\{\hat{\theta}^{(1)}, \dots, \hat{\theta}^{(B)}\}$  and

$$\alpha_1 = \Phi(\hat{z}_0 + \frac{\hat{z}_0 + z_{\alpha/2}}{1 - \hat{a}(\hat{z}_0 + z_{\alpha/2})})$$

and

$$\alpha_2 = \Phi(\hat{z}_0 + \frac{\hat{z}_0 + z_{1-\alpha/2}}{1 - \hat{a}(\hat{z}_0 + z_{1-\alpha/2})})$$

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#### Bootstrap Confidence Interval

where  $\Phi$  is the cdf of the standard normal,  $z_{\alpha/2}$  is the standard normal quantile, and the bias corrector

$$\hat{z}_0 = \Phi^{-1} \left( rac{1}{B} \sum_{i=1}^B I(\hat{ heta}^{(i)} \leq \hat{ heta}) 
ight)$$

where I is the indicator function, and the acceleration factor

$$\hat{a} = \frac{\sum_{i=1}^{B} (\hat{\theta}^{(i)} - \hat{\theta})^3}{6 \left( \sum_{i=1}^{B} (\hat{\theta}^{(i)} - \hat{\theta})^2 \right)^{3/2}}$$

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which measures skewness.

## Bootstrap

Prediction

For each b (b = 1, 2, ..., B), bootstrap sample  $y_1^{(b)}, ..., y_n^{(b)}$  could be use to make a prediction function  $\hat{f}^{(b)}(x)$  and the prediction error for that bootstrap training is

$$\widehat{Err}^{(b)} = \frac{1}{n} \sum_{i=1}^{n} L(y_i, \hat{f}^{(b)}(x_i))$$

and then the bootstrap error is estimated by

$$\widehat{Err}_{boot} = \frac{1}{B} \sum_{i=1}^{B} \widehat{Err}^{(b)}$$

but it can be far below the correct error.



So another suggested error is the Leave-one-out bootstrap estimate of prediction error is

$$\widehat{Err}_{boot}^{(1)} = \frac{1}{n} \sum_{i=1}^{n} \frac{1}{|C_{-i}|} \sum_{b \in C_{-i}} L(y_i, \hat{f}^{(b)}(x_i))$$

where  $C_{-i}$  is the set of all indices of bootstrap samples that don't contain observation *i*. (Only if they they are non-empty.)

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But it is upwardly biased.

#### Bootstrap Prediction

It is suggested to use the ".632 estimator" that corrects for that bias

$$\widehat{\textit{Err}}_{\textit{boot}}^{(632)} = .368 \overline{\textit{err}} + .632 \widehat{\textit{Err}}_{\textit{boot}}^{(1)}$$

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where *err* is the training error rate.

Still not the best. Look for  $\widehat{Err}_{boot}^{(632+)}$ .

# A preamble to Jackknife

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#### Jackknife

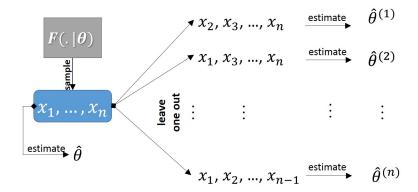
By Quenouille and Tukey, to estimate



Standard error

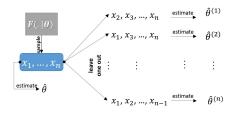
The estimate  $\hat{\theta}$  must be a smooth plug-in estimator: small changes in the data results in small changes in the value of the estimate. The sample mean is a smooth plug-in for the population mean while the sample median is not.

#### Jackknife



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#### Jackknife



Let  $\hat{\hat{\theta}}_J = \frac{1}{n} \sum_{i=1}^n \hat{\theta}^{(i)}$ 

•  $\hat{Bias} = (n-1)(\hat{\bar{\theta}}_J - \hat{\theta})$  where  $\hat{\theta}$  is the estimate of  $\theta$  using the original sample  $x_1, \ldots, x_n$ 

Standard error se(θ̂<sub>J</sub>) is √n−1 times the standard deviation of the jackknife estimates θ̂<sup>(1)</sup>,..., θ̂<sup>(n)</sup>

The idea is to combine predictions from many "building blocks." They are usually weak learners that wouldn't stand on their own. It is usually based on weighted output of their predictions and performance-based evaluation.

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- Bayesian model averaging
- Bagging (Bootstrap aggregating)
- Stacking
- Boosting
- Random forests

# Bayesian Model Averaging

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Bayesian model averaging

 Recall that in Bayesian inference, the posterior distribution is given by

$$P(\theta|X) = \frac{P(X|\theta) P(\theta)}{\int_{\Theta} P(X|\theta') P(\theta') d\theta'}$$

- The maximum posterior distribution (MAP) is commonly used as a point estimate.
- To make predictions we use the predictive posterior distribution

$$P(x_*|X) = \int_{\Theta} P(x_*| heta') P( heta'|X) d heta'$$

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#### Bayesian model averaging Similarly, for *L* number of models $\mathcal{M}_k$ , k = 1, 2, ..., L

 $\blacktriangleright P(X|\mathcal{M}_k) = \int P(X|\theta_k, \mathcal{M}_k) P(\theta_k|\mathcal{M}_k) d\theta_k$ 

$$\blacktriangleright P(\mathcal{M}_k|X) = \frac{P(X|\mathcal{M}_k) P(\mathcal{M}_k)}{\sum_{\ell=1}^{L} P(X|\mathcal{M}_\ell) P(\mathcal{M}_\ell)}$$

and so the posterior distribution of prediction f(x\*) is given by

$$P(f(x_*)|X) = \sum_{\ell=1}^{L} P(f(x_*)|\mathcal{M}_{\ell}, X) P(\mathcal{M}_{\ell}|X)$$

and the mean (as a weighted average) is

$$E(f(x_*)|X) = \sum_{\ell=1}^{L} E(f(x_*)|\mathcal{M}_{\ell}, X) P(\mathcal{M}_{\ell}|X)$$

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Bayesian model averaging

Other types...

Committee method that the prediction is a simple average

$$\frac{1}{L}\sum_{\ell=1}^{L}E(f(x_*)|\mathcal{M}_{\ell},X)$$

 Using the Bayesian Information Criterion (BIC) for the same model type with the same number of parameters

$$\sum_{\ell=1}^{L} E(f(x_*)|\mathcal{M}_{\ell}, X) \frac{e^{-BIC_{\ell}}}{\sum_{k=1}^{L} e^{-BIC_{\ell}}}$$

Bayesian model averaging

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# Bagging (Bootstrap aggregating)

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Bagging

 Helps to reduce high variance learning methods (especially decision trees)

► Recall that, if { $X_i$ ; i = 1, ..., n} are independent with mean  $\mu$  and variance  $\sigma^2$ , then  $V(\bar{X}) = V(\frac{1}{n}\sum_{i=1}^n X_i) = \frac{\sigma^2}{n} < \sigma^2$  (decreased), while  $E(\bar{X}) = \mu$  (remains)

► If they were only identical with correlation  $\rho$  then  $V(\bar{X}) = V(\frac{1}{n}\sum_{i=1}^{n}X_i) = \frac{\sigma^2}{n}(1 + (n-1)\rho) \le \sigma^2$ 

which could be done for prediction over *n* training data sets, but we can not have that many training data sets...

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Bagging

Use bootstraping to produce *B* bootstrap samples, train the statistical learning method (like trees) on each one of them and make a prediction f<sup>(b)</sup>(x) for regression or a class C<sup>(b)</sup>(x) for classification

from which we get the bagging prediction

$$\hat{f}_{bag}(x) = rac{1}{B} \sum_{b=1}^{B} \hat{f}^{(b)}(x)$$
 for regression

and

 $\hat{C}_{bag}(x) =$  majority vote  $\{\hat{C}^{(1)}(x), \hat{C}^{(2)}(x), \dots, \hat{C}^{(B)}(x)\}$ 

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for classification.

Bagging

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$$\hat{C}_{bag}(x) =$$
 majority vote  $\{\hat{C}^{(1)}(x), \hat{C}^{(2)}(x), \dots, \hat{C}^{(B)}(x)\}$ 

for classification.

Bagging

 Out-of-Bag (OOB) error estimation: OOB are the approximately .386*n* points not selected on a bootstrap sample and can be used for estimating testing error

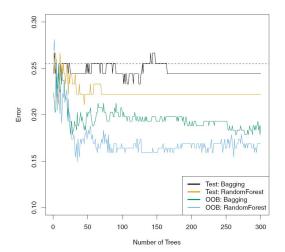
$$\widehat{Err}_{boot}^{(1)} = \frac{1}{n} \sum_{i=1}^{n} \frac{1}{|C_{-i}|} \sum_{b \in C_{-i}} L(y_i, \hat{f}^{(b)}(x_i))$$

where  $C_{-i}$  is the set of all indices of bootstrap samples that don't contain observation *i*.

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#### Example (Another Heart data) Test error vs OOB



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Stacking

- Uses LOOCV for model averaging with normalized weights ŵ<sub>k</sub> that are relatively lower for complex model and not best-fit models
- ▶ If there are *K* number of models  $M_k$  with vector parameter  $\theta_k$ , k = 1, 2, ..., K, which is to be estimated using the training data then

$$\hat{f}_{stack}(x) = \sum_{k=1}^{K} \hat{w}_k f_k(x|\hat{\theta}_k)$$

► Where

$$(\hat{w}_1, \hat{w}_2, \dots, \hat{w}_K) = \operatorname{argmin}_w \sum_{i=1}^n \left( y_i - \sum_{k=1}^K w_k f_k^{(-i)}(x_i | \hat{\theta}_k) \right)^2$$

► LOOCV selection of the best model happens if we require one  $w_k = 1$  and the rest are zeros.

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Where

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LOOCV selection of the best model happens if we require one w<sub>k</sub> = 1 and the rest are zeros.

Stacking

What can go wrong if we rather do find

$$(\hat{w}_1, \hat{w}_2, \dots, \hat{w}_K) = \operatorname{argmin}_w \sum_{i=1}^n \left( y_i - \sum_{k=1}^K w_k f_k(x_i | \hat{\theta}_k) \right)^2$$

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▶ If it is a linear regression problem with subsets as the the *K* models then the full model with the full model will have the weight = 1 and the rest  $w_k = 0$  since

Stacking

What can go wrong if we rather do find

$$(\hat{w}_1, \hat{w}_2, \dots, \hat{w}_K) = argmin_w \sum_{i=1}^n \left( y_i - \sum_{k=1}^K w_k f_k(x_i | \hat{\theta}_k) \right)^2$$

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▶ If it is a linear regression problem with subsets as the the *K* models then the full model with the full model will have the weight = 1 and the rest  $w_k = 0$  since





Boosting

 Used mostly for classification problems and could be extended for regression

▶ It is a committee of weak learners whose error rate are a little bit better than random guessing  $(\bar{err} = \frac{1}{n} \sum_{i=1}^{n} I(y_i \neq G(x_i)) < .5)$ 

There are several boosting algorithms, like the Adaptive Boosting algorithm Adaboost.M1, which are very powerful than other classification methods

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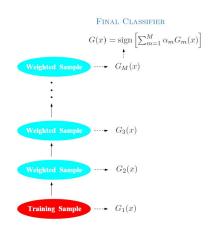
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Boosting - AdaBoost.M1 Algorithm aka Discrete AdaBoost

Consider a two class classification problem  $Y \in \{-1, 1\}$ 

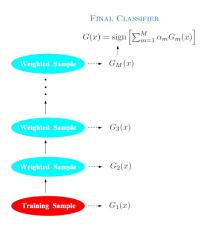
- Give weights to each item  $(x_i, y_i)$ of  $w_i^m$  such that  $w_i^1 = \frac{1}{n}$
- The algorithm keep modifying the data through re-weighting and train the learning method on the new weighted data to produce weak learners that form a committee at the end
- ► The sequence of weights {*a<sub>m</sub>*; *m* = 1, 2, ..., *M*} are produced by the algorithm



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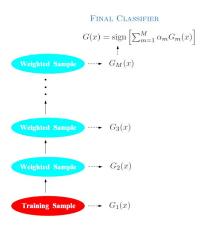
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Boosting - AdaBoost.M1 Algorithm aka Discrete AdaBoost

Algorithm 10.1 AdaBoost.M1.

- 1. Initialize the observation weights  $w_i = 1/N, i = 1, 2, ..., N$ .
- 2. For m = 1 to M:
  - (a) Fit a classifier  $G_m(x)$  to the training data using weights  $w_i$ .
  - (b) Compute

$$\operatorname{err}_{m} = \frac{\sum_{i=1}^{N} w_{i} I(y_{i} \neq G_{m}(x_{i}))}{\sum_{i=1}^{N} w_{i}}.$$

(c) Compute  $\alpha_m = \log((1 - \operatorname{err}_m)/\operatorname{err}_m)$ .

- (d) Set  $w_i \leftarrow w_i \cdot \exp[\alpha_m \cdot I(y_i \neq G_m(x_i))], i = 1, 2, \dots, N.$
- 3. Output  $G(x) = \operatorname{sign} \left[ \sum_{m=1}^{M} \alpha_m G_m(x) \right].$

## **Random Forests**

**Random Forests** 

- It is bagging of a decision tree. It decreases variance and keep the low bias.
- Again, bagging does use V(X) = V(<sup>1</sup>/<sub>n</sub> Σ<sup>n</sup><sub>i=1</sub> X<sub>i</sub>) = <sup>σ<sup>2</sup></sup>/<sub>n</sub>(1 + (n − 1)ρ) = ρσ<sup>2</sup> + <sup>1−ρ</sup>/<sub>n</sub>σ<sup>2</sup> ≤ σ<sup>2</sup>, while random forest tries to diminish the second term by using many bootstrap samples (large *B*) and break down the correlation (making ρ ~ 0) to decrease the first term and still not upsetting σ<sup>2</sup>.
- The latter is achieved by random selection and usage of m bootstrap sample.

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- The latter is achieved by random selection and usage of m bootstrap sample.

#### **Random Forests**

Algorithm 15.1 Random Forest for Regression or Classification.

- 1. For b = 1 to B:
  - (a) Draw a bootstrap sample  $\mathbf{Z}^*$  of size N from the training data.
  - (b) Grow a random-forest tree  $T_b$  to the bootstrapped data, by recursively repeating the following steps for each terminal node of the tree, until the minimum node size  $n_{min}$  is reached.
    - i. Select m variables at random from the p variables.
    - ii. Pick the best variable/split-point among the m.
    - iii. Split the node into two daughter nodes.
- 2. Output the ensemble of trees  $\{T_b\}_1^B$ .

To make a prediction at a new point x:

Regression: 
$$\hat{f}_{rf}^B(x) = \frac{1}{B} \sum_{b=1}^B T_b(x).$$

Classification: Let  $\hat{C}_b(x)$  be the class prediction of the *b*th random-forest tree. Then  $\hat{C}^B_{\mathrm{rf}}(x) = majority \ vote \ \{\hat{C}_b(x)\}_1^B$ .

**Random Forests** 

#### Tuning parameters:

For regression problems:  $m = \lfloor \frac{p}{3} \rfloor$  and  $n_{min} = 5$ 

For classification problems:  $m = \lfloor \sqrt{p} \rfloor$  and  $n_{min} = 1$ 

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**Random Forests** 

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**Random Forests** 

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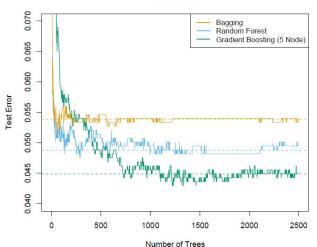
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**Random Forests** 

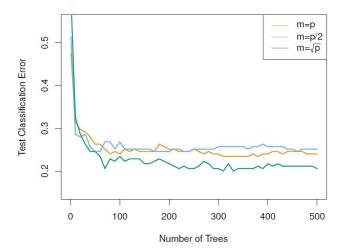
#### Example (Spam data)



Spam Data

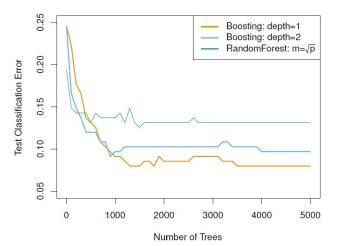
**Random Forests** 

#### Example (Gene data)



**Random Forests** 

#### Example (Gene data)



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#### **DIY** in R

- 1. Carry out a boosting regression tree for the prostate cancer data using library(gbm)
- 2. Carry out a random forest for the SA hearth disease data using library(randomForest)

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## End of Set 7

# EM algorithm

- EM is used for incomplete data, e.g. missing data, censored data or latent variables.
- ▶ If the complete data X = (O, M) where *O* is the observed data and *M* is the missing data.
- Note that

$$f(X|\theta) = f(M|\theta, O) \cdot f(O|\theta)$$

That is

$$L(\theta|X) = f(M|\theta, O) \cdot L(\theta|O)$$

► L(θ|X) is the complete likelihood function and L(θ|O) is the incomplete likelihood function

and

$$logL(\theta|O) = logL(\theta|X) - log(f(M|\theta, O))$$

so

or

$$\int log L(\theta|O) f(M|\theta', O) dM = \int log L(\theta|X) f(M|\theta', O) dM$$
$$-\int log (f(M|\theta, O)) f(M|\theta', O) dM$$

 $logL(\theta|O) = \mathsf{E}_{M|\theta',O}(logL(\theta|X)) - \mathsf{E}_{M|\theta',O}(log(f(M|\theta,O)))$ 

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#### EM Algorithm:

1. Start from initial point  $\theta^{(0)}$ , then for each  $k \ge 1$ 

2. **E** step: Find 
$$Q_k(\theta|\theta^{(k)}) := \mathbf{E}_{M|\theta^{(k)},O}(logL(\theta|X))$$

3. **M** step: Find 
$$\theta^{(k+1)} = \operatorname{argmax}_{\theta \in \Theta} Q_k(\theta | \theta^{(k)})$$

4. Stop when  $|\theta^{(k+1)} - \theta^{(k)}| / \theta^{(k)} < TOL$ Remark: Convergence is theoretically guaranteed.

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Example: Let  $x_1, x_2, ..., x_n$  be an observed data of completion time at checking out at a grocery store with two cashiers and no waiting lines. They are modeled by a mixture of two exponential distributions with rates  $\lambda_1$  and  $\lambda_2$  with probability of selection (mixture weights) p and 1 - p.

The parameter vector is  $\theta = (p, \lambda_1, \lambda_2)$  and  $f(x_i|\lambda) = \lambda e^{-\lambda x_i}$ . The incomplete likelihood function

$$L(\theta|\mathbf{x}) = \prod_{i=1}^{n} \left( p \cdot f(\mathbf{x}_i|\lambda_1) + (1-p) \cdot f(\mathbf{x}_i|\lambda_2) \right)$$

But what we didn't observe is from where each data point is coming from. That corresponds to latent variable  $z_1, \ldots, z_n$  for which cashier was selected, encoded as  $z_i = 1$  if cashier 1 is selected and  $z_i = 0$  if cashier 2 is selected.

By Bayes' theorem

$$p_i := P(Z_i = 1 | X = x_i, \theta) = \frac{p \cdot f(x_i | \lambda_1)}{p \cdot f(x_i | \lambda_1) + (1 - p) \cdot f(x_i | \lambda_2)}$$

and the complete likelihood function

$$L(\theta|\mathbf{x},\mathbf{z}) = \prod_{i=1}^{n} \left( z_i p \cdot f(x_i|\lambda_1) + (1-z_i)(1-p) \cdot f(x_i|\lambda_2) \right)$$

and

$$\mathsf{E}_{Z|X,\theta}(logL(\theta|X,Z)) = \sum_{j=0}^{1} \sum_{i=1}^{n} \log (z_i p \cdot f(x_i|\lambda_1) + (1-z_i)(1-p))$$

$$f(x_i|\lambda_2)) \cdot P(Z_i = j|X = x_i, \theta)$$

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#### Expectation – Maximization (EM) algorithm Thus, E step:

$$Q_k( heta| heta^{(k)}) = \mathsf{E}_{\mathcal{Z}|\mathcal{X}, heta^{(k)}}(\mathit{logL}( heta|x,z)) =$$

 $\sum_{i=1}^{n} p_i^{(k)}(\log(p) + \log(f(x_i|\lambda_1))) + (1 - p_i^{(k)})(\log(1 - p) + \log(f(x_i|\lambda_2))) =$ 

$$\sum_{i=1}^{n} \left( p_i^{(k)} \log(p) + (1 - p_i^{(k)}) \log(1 - p) \right) + \sum_{i=1}^{n} \left( p_i^{(k)} \log(f(x_i|\lambda_1)) + (1 - p_i^{(k)}) \log(f(x_i|\lambda_2)) \right)$$

where

n

$$p_{i}^{(k)} := P(Z_{i} = 1 | X = x_{i}, \theta^{(k)}) = \frac{p^{(k)} \cdot f(x_{i} | \lambda_{1}^{(k)})}{p^{(k)} \cdot f(x_{i} | \lambda_{1}^{(k)}) + (1 - p^{(k)}) \cdot f(x_{i} | \lambda_{2}^{(k)})}$$

And, M step can be split into M sub-step 1: Find

$$p^{(k+1)} = \operatorname{argmax}_{p \in (0,1)} \sum_{i=1}^{n} \left( p_i^{(k)} \log(p) + (1 - p_i^{(k)}) \log(1 - p) \right)$$

M sub-step 2: Find

$$\lambda_1^{(k+1)} = \operatorname{argmax}_{\lambda_1 \in (0,\infty)} \sum_{i=1}^n \left( p_i^{(k)} \log(f(x_i|\lambda_1)) \right)$$

M sub-step 3: Find

$$\lambda_{2}^{(k+1)} = \operatorname{argmax}_{\lambda_{2} \in (0,\infty)} \sum_{i=1}^{n} \left( (1 - p_{i}^{(k)}) \log(f(x_{i}|\lambda_{2})) \right)$$

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The last two are weighted MLE's.

#### Expectation – Maximization (EM) algorithm M sub-step 1: Gives

$$p^{(k+1)} = \frac{\sum_{i=1}^{n} p_i^{(k)}}{n}$$

M sub-step 2: Gives

$$\lambda_{1}^{(k+1)} = \frac{\sum_{i=1}^{n} p_{i}^{(k)}}{\sum_{i=1}^{n} p_{i}^{(k)} x_{i}}$$

M sub-step 3: Gives

$$\lambda_2^{(k+1)} = \frac{\sum_{i=1}^n (1 - p_i^{(k)})}{\sum_{i=1}^n (1 - p_i^{(k)}) x_i}$$

where

$$p_i^{(k)} := P(Z_i = 1 | X = x_i, \theta^{(k)}) = \frac{p^{(k)} \cdot f(x_i | \lambda_1^{(k)})}{p^{(k)} \cdot f(x_i | \lambda_1^{(k)}) + (1 - p^{(k)}) \cdot f(x_i | \lambda_2^{(k)})}$$

Example: Use a sample of n = 1000 generated from a mixture of  $exp(\lambda_1 = .3)$  and  $exp(\lambda_2 = .5)$  with probabilities p = .2 and 1 - p = .8, respectively, to estimate p,  $\lambda_1$  and  $\lambda_2$ . You consider them as 1000 finishing time of 1000 transactions through two different cashiers that you have collected. First, generate the 1000 points

```
n<-1000;p<-.2;lambda1<-.3;lambda2<-.5
lambda<-c(lambda1,lambda2)
K<-sample(1:2,n,prob=c(p,1-p),rep=T)
x<-rexp(n,rate=lambda[K])</pre>
```

```
TOL<-1e-8; j<-0
pold<-0.9;lambda1old<-0.1;lambda2old<-0.9
pnew<-.1;lambda1new<-1;lambda2new<-.1</pre>
vpnew<-pnew*dexp(x,lambda1new)/</pre>
(pnew*dexp(x,lambda1new)+(1-pnew)*dexp(x,lambda2new
while (max (abs (pnew-pold) /pold,
abs(lambda1new-lambda1old)/lambda1old,
abs(lambda2new-lambda2old)/lambda2old)>TOL) {
 i<-i+1
 pold<-pnew
 lambda1old<-lambda1new
 lambda2old<-lambda2new
 vpold<-vpnew
 pnew<-mean(vpold)
 lambdalnew<-1/weighted.mean(x, vpold)</pre>
 lambda2new<-1/weighted.mean(x, 1-vpold)</pre>
```

```
vpnew<-(pnew*dexp(x,lambda1new))/</pre>
(pnew*dexp(x,lambda1new)+(1-pnew)*dexp(x,lambda2new
}
i
[1] 6074
pnew
[1] 0.8089904
lambda1new
[1] 0.512815
lambda2new
[1] 0.2730581
```

```
Why the switch? Look at the initial values of the parameters.
Practical advice: Use different initial values of parameters \lambda_1
and \lambda_2 or p will not get updated (p^{(k)} = p^{(0)} for all k).
```