

Selected topics for revision

Applied Multivariate Statistics – Spring 2012



Review of

- Gaussian Mixture Models
- LDA
- Random Forest

Gaussian Mixture Models (GMMs)

Gaussian Mixture Models (GMM)

- Gaussian Mixture Model:

$$f(x; p, \theta) = \sum_{j=1}^K p_j g_j(x; \theta_j)$$

K populations with different probability distributions

- Find number of classes and parameters p_j and θ_j given data
- Assign observation x to cluster j , where estimated value of

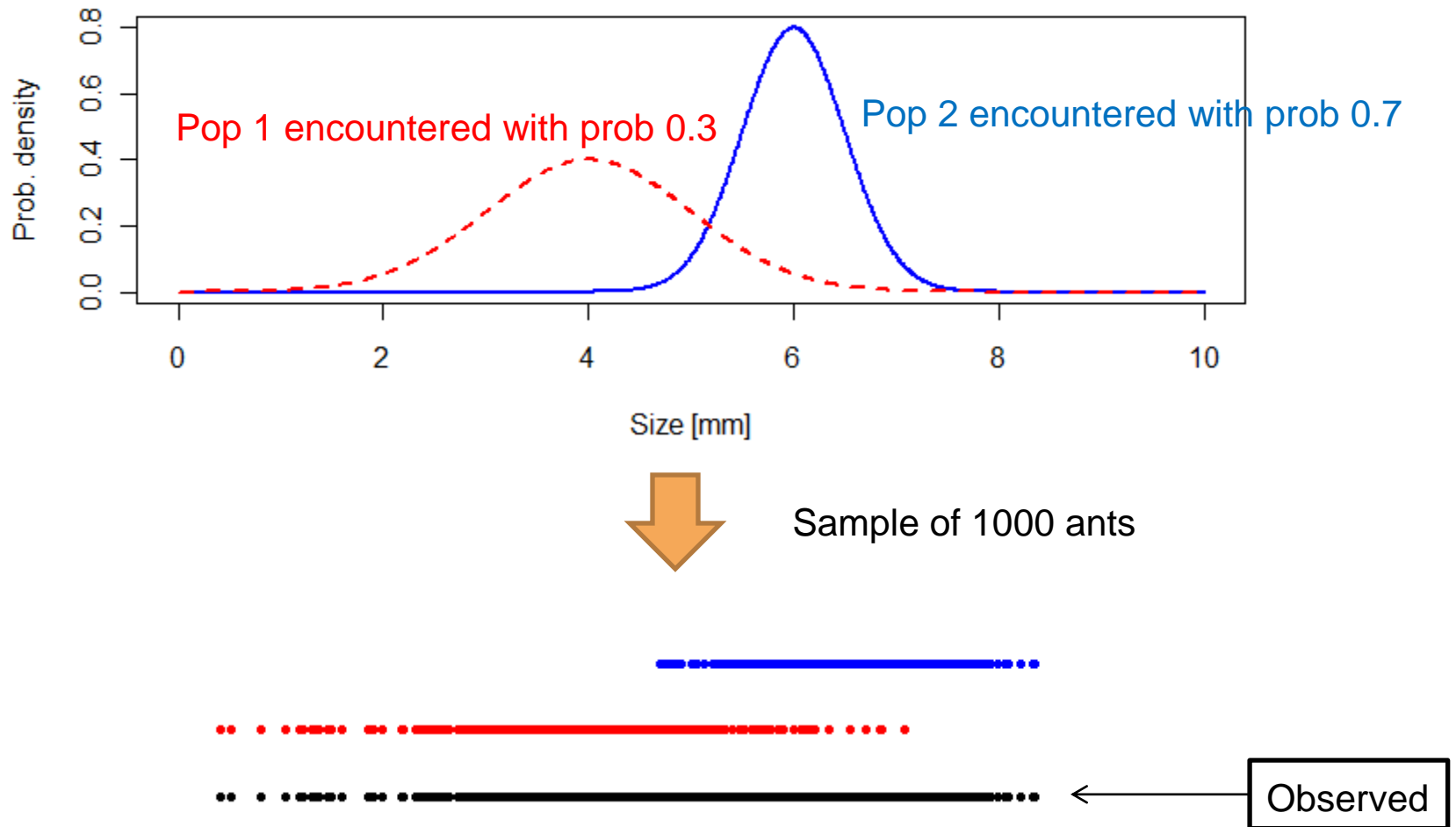
$$P(\text{cluster } j|x) = \frac{p_j g_j(x; \theta_j)}{f(x; p, \theta)}$$

is largest

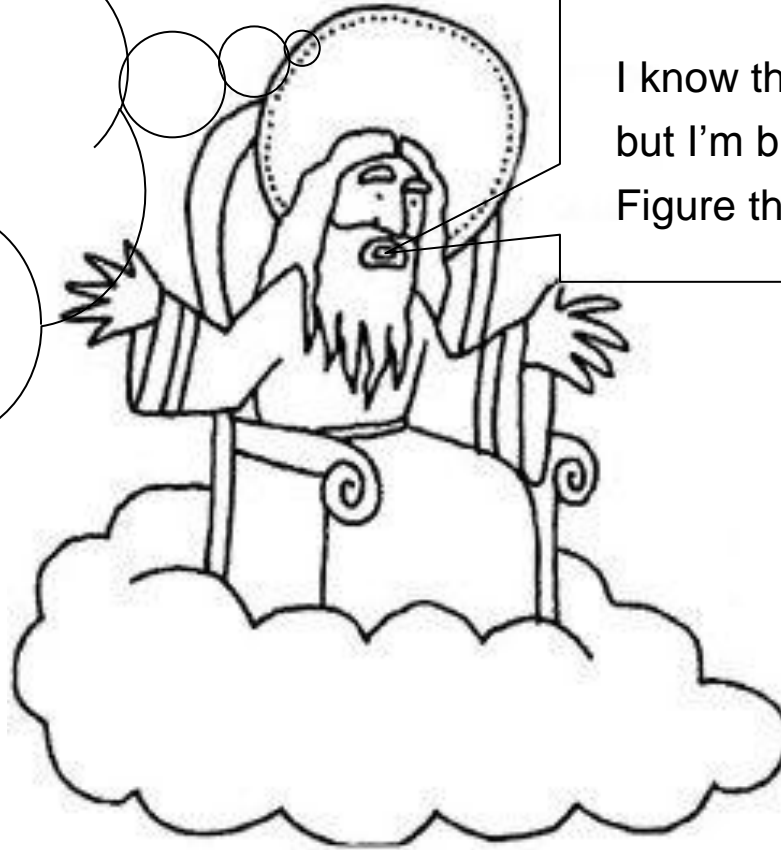
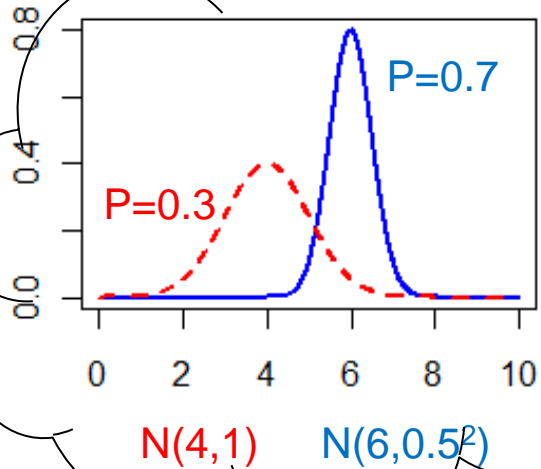
Example (1/6): Size of ants in two populations

Suppose ants *look the same apart from size*:

How can we learn about the two populations, if we can only observe a mixture of them ?



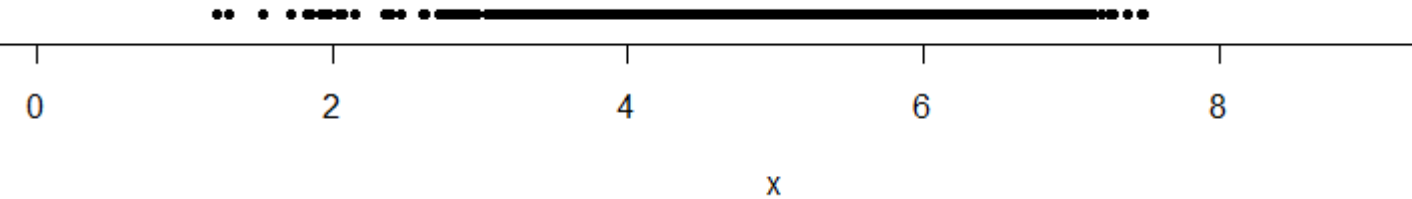
Example (2/6): Someone might know, but...



I know the true parameters –
but I'm busy;
Figure them out from the data !



Example (3/6): We just see this



and we guess that there are two Normal populations involved



Example (4/6): How likely is the observation?

- Likelihood function for one observation x :

$$f(x; p, \theta) = p \cdot \frac{1}{\sqrt{2\pi\sigma_1^2}} \exp(-(x - \mu_1)^2 / 2\sigma_1^2) + \\ + (1 - p) \cdot \frac{1}{\sqrt{2\pi\sigma_2^2}} \exp(-(x - \mu_2)^2 / 2\sigma_2^2)$$

Parameters to estimate: $p, \mu_1, \mu_2, \sigma_1, \sigma_2$

- Likelihood function for n (independent) observations x_1, \dots, x_n :

$$\tilde{f}(x_1, \dots, x_n; p, \theta) = \prod_{i=1}^n f(x_i; p; \theta)$$

- For numerical reasons, compute log-Likelihood function:

$$l(x_1, \dots, x_n; p, \theta) = \log(\tilde{f}(x_1, \dots, x_n; p, \theta))$$

Example (5/6): Find the set of parameters under which the observation is most likely

Guessing the parameters:

p	μ_1	μ_2	σ_1	σ_2	Log-Likelihood
0.5	3	5	2	1	-1891
0.4	3.5	5.5	1	0.5	-1723
0.7	5	7	1	1	-1678
Etc.					

Using some numerical optimization technique:

p	μ_1	μ_2	σ_1	σ_2	Log-Likelihood
0.35	4.18	6.03	1.05	0.47	-1365

True parameters:

p	μ_1	μ_2	σ_1	σ_2	Log-Likelihood
0.3	4	6	1	0.5	-1366

Example (6/6): Doing it with R

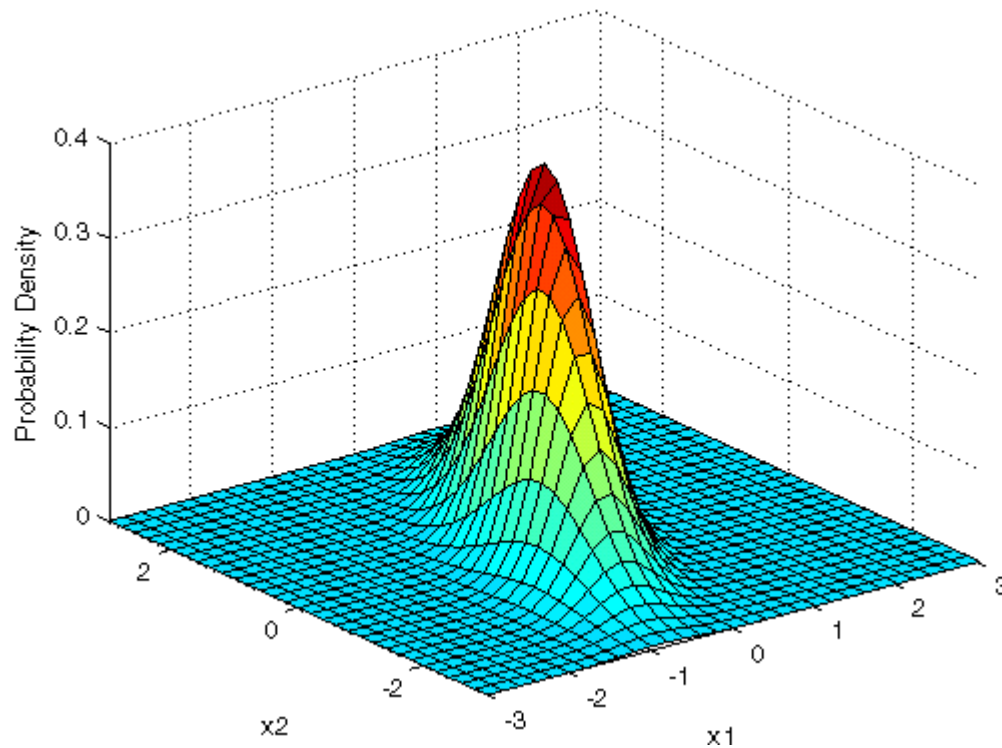
```
> res <- Mclust(xobs)
> str(res)
List of 11
 $ modelName      : chr "v"
 $ n              : int 1000
 $ d              : num 1
 $ G              : int 2
 $ BIC            : num [1:9, 1:2] -3120 -2826 -2840 -2854 -2812 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : chr [1:9] "1" "2" "3" "4" ...
 .. ..$ : chr [1:2] "E" "V"
 ..- attr(*, "G")= num [1:9] 1 2 3 4 5 6 7 8 9
 ..- attr(*, "modelName")= chr [1:2] "E" "V"
 ..- attr(*, "oneD")= logi TRUE
 $ bic           : num -2765
 $ loglik       : num -1365
 $ parameters   :List of 4
 ..$ vinv       : NULL
 ..$ pro        : num [1:2] 0.347 0.653
 ..$ mean       : Named num [1:2] 4.18 6.03
 .. ..- attr(*, "names")= chr [1:2] "1" "2"
 ..$ variance:List of 5
 .. ..$ modelName: chr "v"
 .. ..$ d         : num 1
 .. ..$ G         : int 2
 .. ..$ sigmasq   : num [1:2] 1.113 0.223
 .. ..$ scale     : num [1:2] 1.113 0.223
 $ classification: num [1:1000] 1 1 1 1 1 1 1 1 1 1 ...
 $ uncertainty   : num [1:1000] 2.06e-01 6.30e-09 7.56e-02 1.57e-02 1.15e-02 ...
 $ z            : num [1:1000, 1:2] 0.794 1 0.924 0.984 0.988 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : NULL
 .. ..$ : NULL
 - attr(*, "class")= chr "Mclust"
```

Annotations:

- Vector with observations (points to `xobs`)
- Two groups were found (points to `$ G`)
- Optimized log-likelihood (points to `$ loglik`)
- Probability of group 1 (points to `..$ pro`)
- Probability of group 2 (points to `..$ pro`)
- Mean of group 1 (points to `..$ mean`)
- Mean of group 2 (points to `..$ mean`)
- Variance of group 2 (points to `..$ sigmasq`)
- Variance of group 1 (points to `..$ sigmasq`)

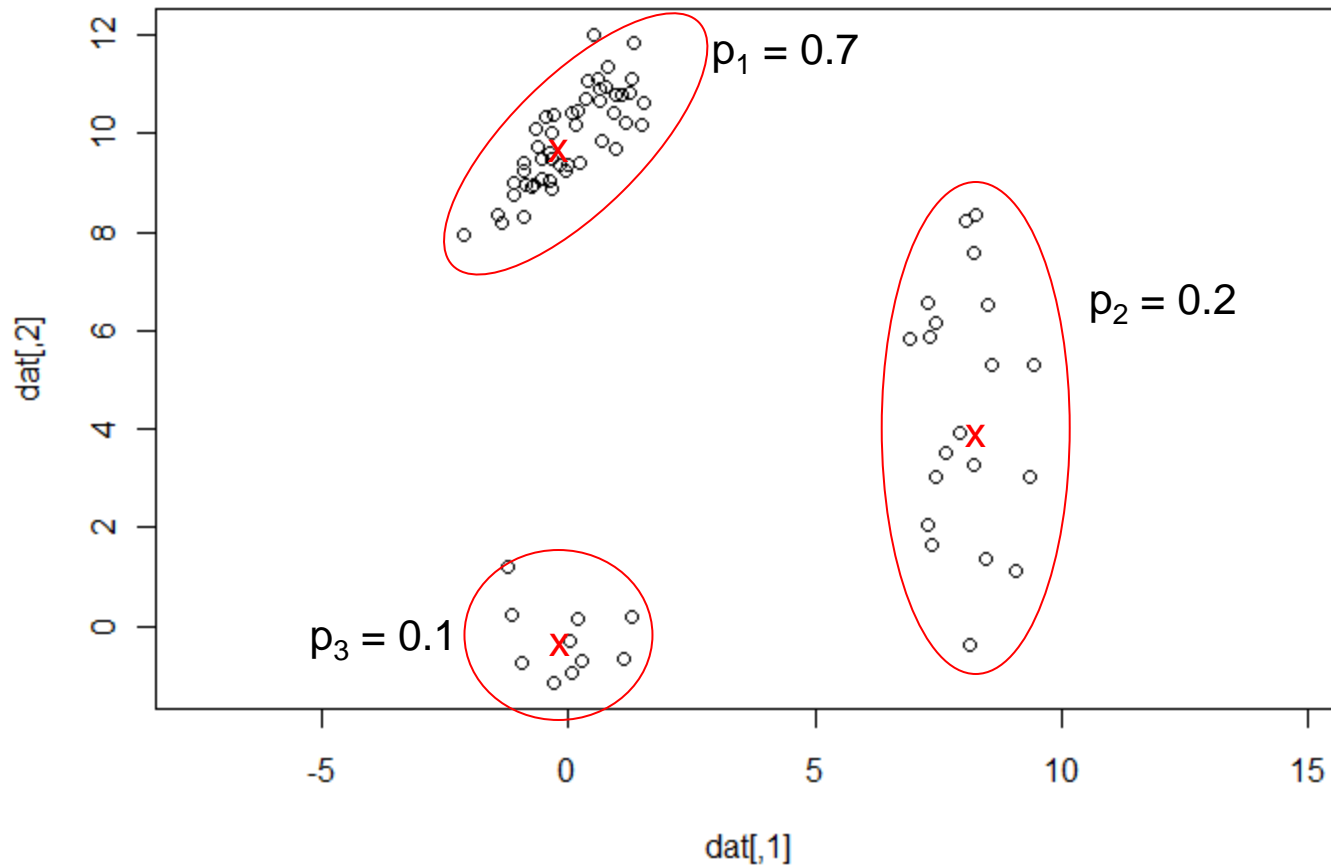
Revision: Multivariate Normal Distribution

$$f(x; \mu, \Sigma) = \frac{1}{\sqrt{2\pi|\Sigma|}} \exp\left(-\frac{1}{2} \cdot (x - \mu)^T \Sigma^{-1} (x - \mu)\right)$$



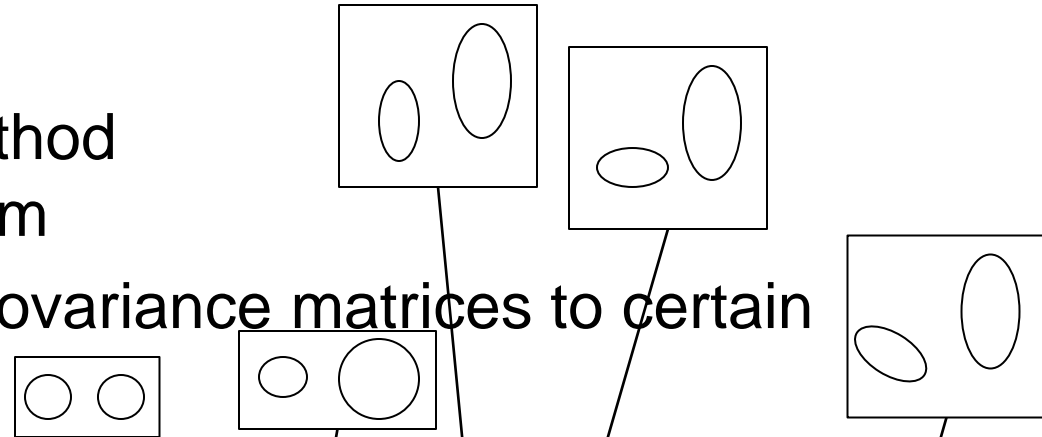
GMM: Example estimated manually

- 3 clusters
- $p_1 = 0.7$, $p_2 = 0.2$, $p_3 = 0.1$
- Mean vector and cov. Matrix per cluster



Fitting GMMs 1/2

- Maximum Likelihood Method
Hard optimization problem
- Simplification: Restrict Covariance matrices to certain patterns (e.g. diagonal)



identifier	Model	HC	EM	Distribution	Volume	Shape	Orientation
E		•	•	(univariate)	equal		
V		•	•	(univariate)	variable		
EII	λI	•	•	Spherical	equal	equal	NA
VII	$\lambda_k I$	•	•	Spherical	variable	equal	NA
EEI	λA		•	Diagonal	equal	equal	coordinate axes
VEI	$\lambda_k A$		•	Diagonal	variable	equal	coordinate axes
EVI	λA_k		•	Diagonal	equal	variable	coordinate axes
VVI	$\lambda_k A_k$		•	Diagonal	variable	variable	coordinate axes
EEE	$\lambda D A D^T$	•	•	Ellipsoidal	equal	equal	equal
EEV	$\lambda D_k A D_k^T$		•	Ellipsoidal	equal	equal	variable
VEV	$\lambda_k D_k A D_k^T$		•	Ellipsoidal	variable	equal	variable
VVV	$\lambda_k D_k A_k D_k^T$	•	•	Ellipsoidal	variable	variable	variable

Fitting GMMs 2/2

- Problem: Fit will never get worse if you use more cluster or allow more complex covariance matrices
→ How to choose optimal model ?
- Solution: Trade-off between model fit and model complexity

$BIC = \log\text{-likelihood} - \log(n)/2 * (\text{number of parameters})$

Find solution with maximal BIC

GMMs in R

- Function “Mclust” in package “mclust”

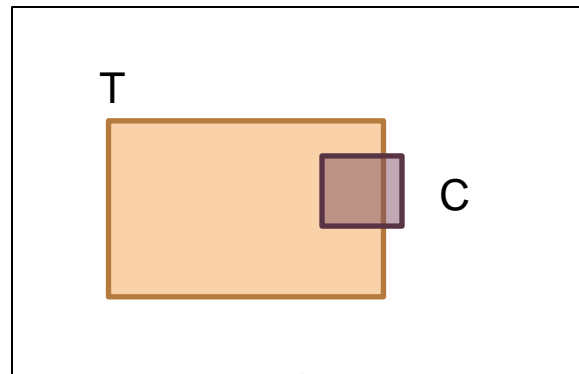
Linear Discriminant Analysis (LDA)

Conditional Probability

T: Med. Test positive

C: Patient has cancer

Sample space



(Marginal) Probability:
 $P(T), P(C)$

New sample space:
People with cancer

$P(T|C)$
large



Conditional Probability:
 $P(T|C), P(C|T)$

New sample space:
People with pos. test

$P(C|T)$
small



Bayes Theorem:

$$\text{posterior} \rightarrow P(C|T) = \frac{P(T|C)P(C)}{P(T)} \leftarrow \text{prior}$$

Class conditional probability

One approach to supervised learning

$$P(C|X) = \frac{P(C)P(X|C)}{P(X)} \sim P(C)P(X|C)$$

Find some estimate \nearrow Prior / prevalence: Fraction of samples in that class \nearrow Assume: $X|C \sim N(\mu_c, \Sigma_c)$

Bayes rule:

Choose class where $P(C|X)$ is maximal
(rule is “optimal” if all types of error are equally costly)

Special case: Two classes (0/1)

- choose $c=1$ if $P(C=1|X) > 0.5$ or
- choose $c=1$ if posterior odds $P(C=1|X)/P(C=0|X) > 1$

In Practice: Estimate $P(C), \mu_c, \Sigma_c$

QDA: Doing the math... $\frac{1}{\sqrt{(2\pi)^d |\Sigma_C|}} \exp\left(-\frac{1}{2}(x - \mu_c)^T \Sigma_C^{-1} (x - \mu_c)\right)$

- $P(C|X) \sim P(C)P(X|C)$
- Use the fact: $\max P(C|X) \Leftrightarrow \max(\log(P(C|X)))$
- $\delta_c(x) = \log(P(C|X)) = \log(P(C)) + \log(P(X|C)) =$
 $= \underbrace{\log(P(C))}_{\text{Prior}} - \frac{1}{2} \underbrace{\log(|\Sigma_C|)}_{\text{Additional term}} - \frac{1}{2} \underbrace{(x - \mu_c)^T \Sigma_C^{-1} (x - \mu_c)}_{\text{Sq. Mahalanobis distance}} + c$

- Choose class where $\delta_c(x)$ is maximal
- Special case: Two classes
 Decision boundary: Values of x where $\delta_0(x) = \delta_1(x)$ is quadratic in x

▪ Quadratic Discriminant Analysis (QDA)

Simplification

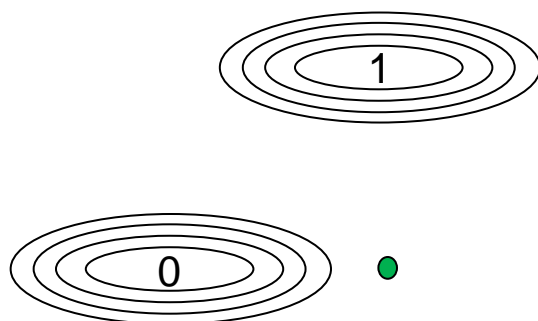
- Assume same covariance matrix in all classes, i.e.

$$X|C \sim N(\mu_c, \Sigma) \leftarrow \text{Fix for all classes}$$

$$\begin{aligned} \delta_c(x) &= \log(P(C)) - \frac{1}{2} \log(|\Sigma|) - \frac{1}{2} (x - \mu_c)^T \Sigma^{-1} (x - \mu_c) + c = \\ &\stackrel{\text{Prior}}{=} \log(P(C)) - \frac{1}{2} (x - \mu_c)^T \Sigma^{-1} (x - \mu_c) + d = \text{Sq. Mahalanobis distance} \\ &= \log(P(C)) + x^T \Sigma^{-1} \mu_c - \frac{1}{2} \mu_c^T \Sigma^{-1} \mu_c \end{aligned}$$

Decision boundary is linear in x

- Linear Discriminant Analysis (LDA)**



Classify to which class (assume equal prior)?

- Physical distance in space is equal
- Classify to class 0, since Mahal. Dist. is smaller

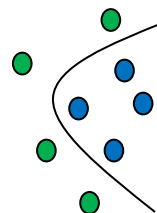
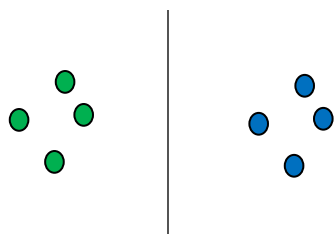
LDA

vs.

QDA

- + Only few parameters to estimate; accurate estimates
- Inflexible
(linear decision boundary)

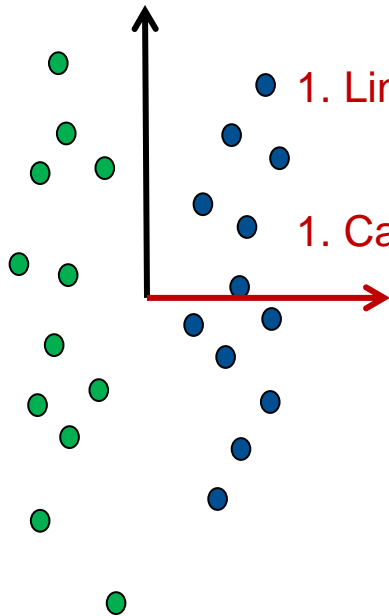
- Many parameters to estimate; less accurate
- + More flexible
(quadratic decision boundary)



Fisher's Discriminant Analysis: Idea

Find direction(s) in which groups are separated best

1. Principal Component



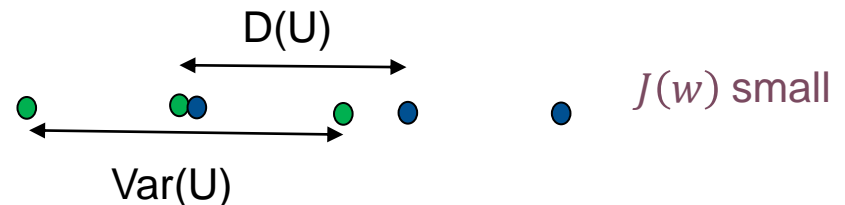
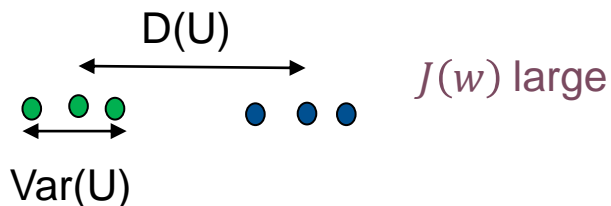
1. Linear Discriminant
=
1. Canonical Variable

- Class Y , predictors $X = (X_1, \dots, X_d)$
 $\rightarrow U = w^T X$
- Find w so that groups are separated along U best
- Measure of separation: Rayleigh coefficient

$$J(w) = \frac{D(U)}{\text{Var}(U)}$$

where $D(U) = (E(U|Y = 0) - E(U|Y = 1))^2$

- $E[X|Y = j] = \mu_j, \text{Var}(X|Y = j) = \Sigma$
 $\Rightarrow E[U|Y = j] = w^T \mu_j, \text{Var}(U) = w^T \Sigma w$
- Concept extendable to many groups



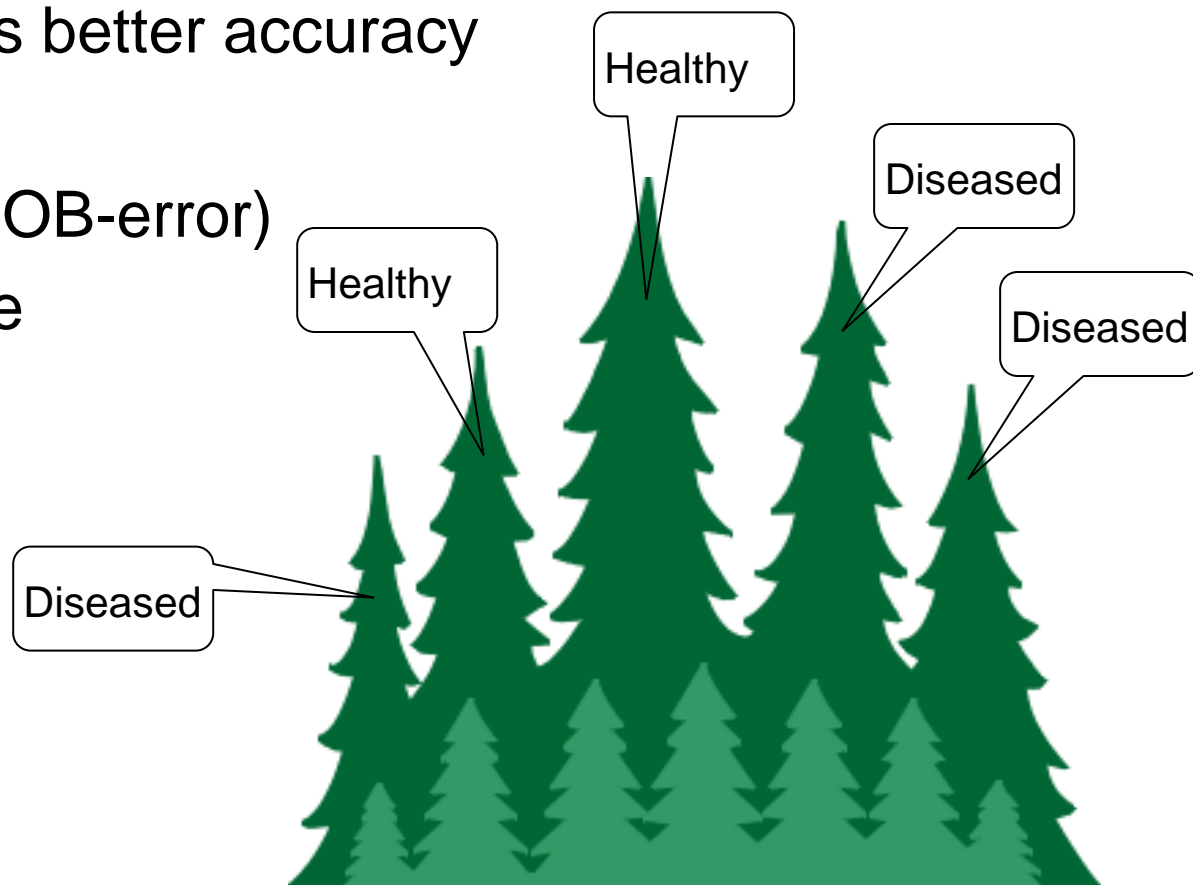
LDA and Linear Discriminants

- - Direction with largest $J(w)$: 1. Linear Discriminant (LD 1)
 - orthogonal to LD1, again largest $J(w)$: LD 2
 - etc.
- At most: $\min(\text{Nmb. dimensions}, \text{Nmb. Groups} - 1)$ LD's
e.g.: 3 groups in 10 dimensions – need 2 LD's
- R: Function «lda» in package MASS does LDA and computes linear discriminants (also «qda» available)

Random Forest

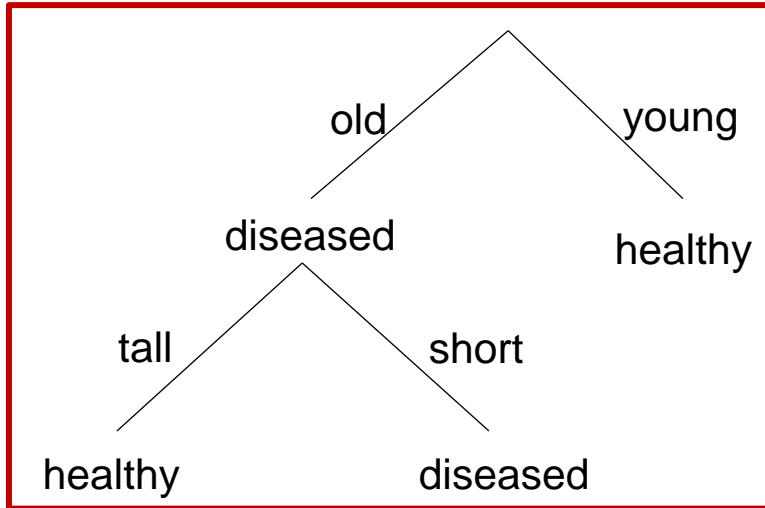
Random Forest

- Intuition of Random Forest
- The Random Forest Algorithm
- De-correlation gives better accuracy
- Out-of-bag error (OOB-error)
- Variable importance

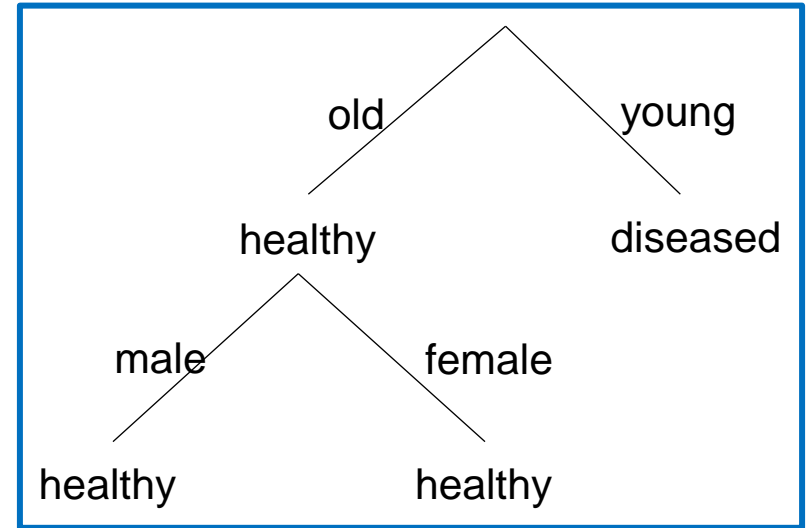


Intuition of Random Forest

Tree 1



Tree 2



New sample:

old, retired, male, short

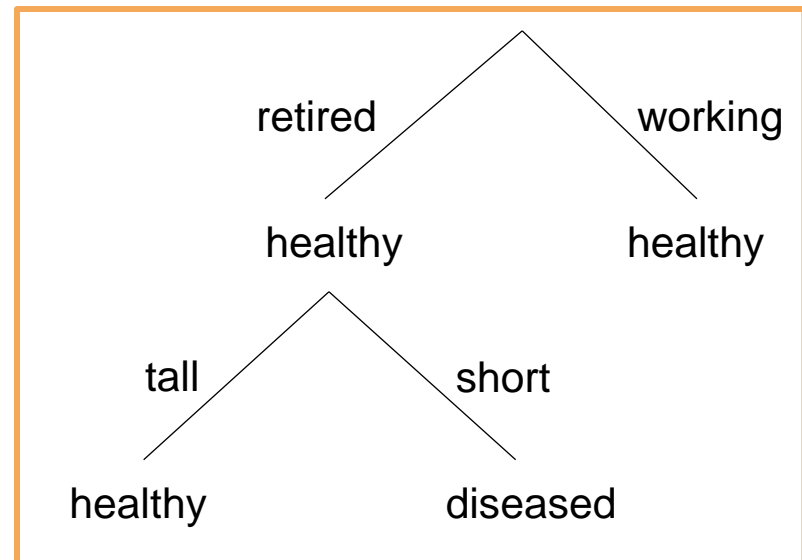
Tree predictions:

diseased, healthy, diseased

Majority rule:

diseased

Tree 3



The Random Forest Algorithm

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

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

Differences to standard tree

- Train each tree on bootstrap resample of data
(Bootstrap resample of data set with N samples:
Make new data set by drawing **with replacement** N samples; i.e., some samples will probably occur multiple times in new data set)
- For each split, consider only m randomly selected variables
- Don't prune
- Fit **B trees** in such a way and use average or majority voting to aggregate results

Why Random Forest works 1/2

- Mean Squared Error = Variance + Bias²
- If trees are sufficiently deep, they have very small bias
- How could we improve the variance over that of a single tree?

Why Random Forest works 2/2

$$\begin{aligned}
 \text{Var} \left(\frac{1}{B} \sum_{i=1}^B T_i(c) \right) &= \frac{1}{B^2} \sum_{i=1}^B \sum_{j=1}^B \text{Cov}(T_i(x), T_j(x)) \\
 &= \frac{1}{B^2} \sum_{i=1}^B \left(\sum_{j \neq i}^B \text{Cov}(T_i(x), T_j(x)) + \text{Var}(T_i(x)) \right) \\
 &= \frac{1}{B^2} \sum_{i=1}^B \left((B-1)\sigma^2 \cdot \rho + \sigma^2 \right) \\
 &= \frac{B(B-1)\rho\sigma^2 + B\sigma^2}{B^2} \\
 &= \frac{(B-1)\rho\sigma^2}{B} + \frac{\sigma^2}{B} \\
 &= \rho\sigma^2 - \frac{\rho\sigma^2}{B} + \frac{\sigma^2}{B} \\
 &= \rho\sigma^2 + \frac{\sigma^2(1-\rho)}{B}
 \end{aligned}$$

i=j

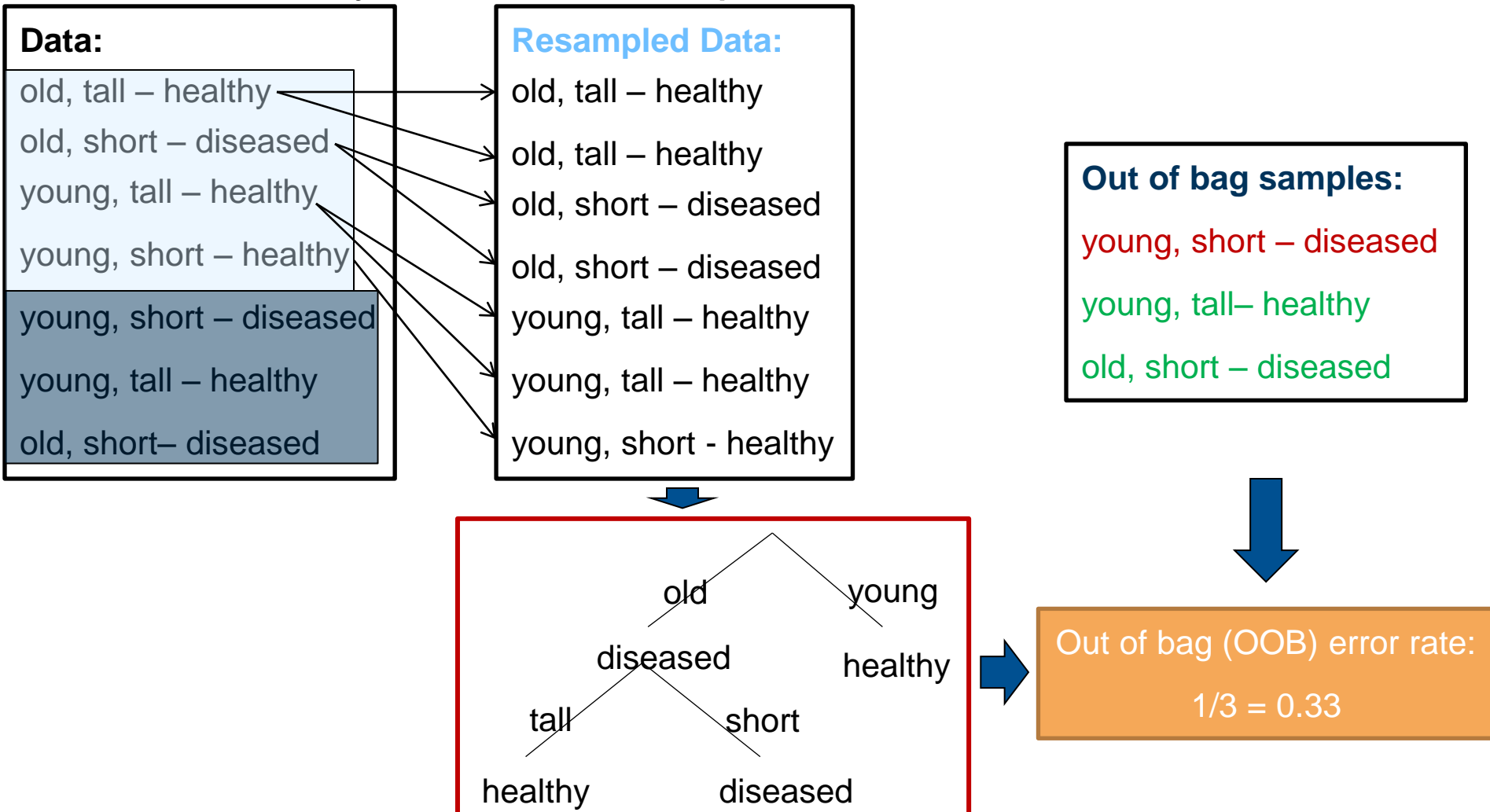
Decreases, if ρ decreases, i.e., if m decreases

De-correlation gives better accuracy

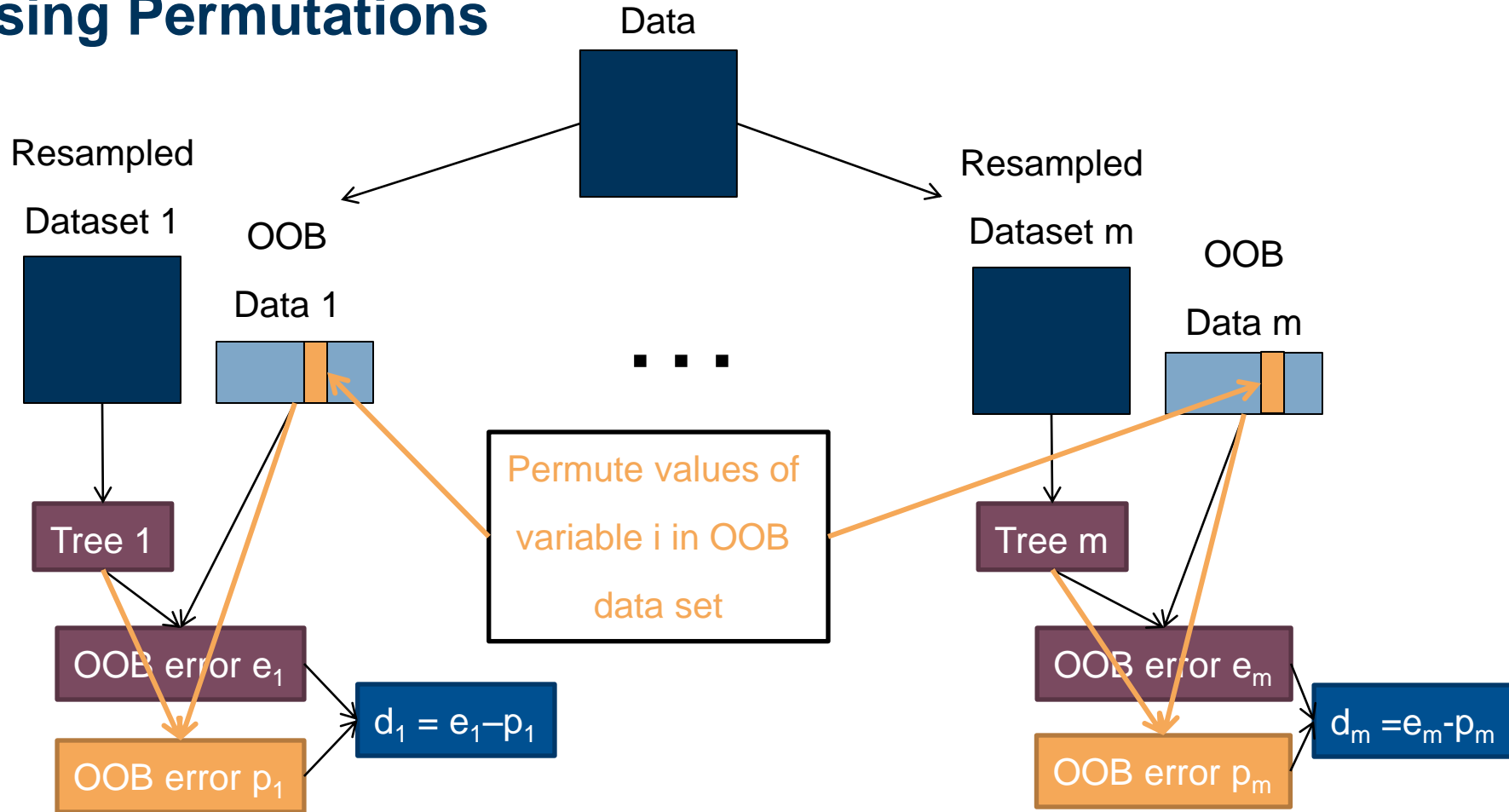
Decreases, if number of trees B increases (irrespective of ρ)

Estimating generalization error: Out-of bag (OOB) error

- Similar to leave-one-out cross-validation, but almost without any additional computational burden



Variable Importance for variable i using Permutations



$$\left. \begin{aligned} \bar{d} &= \frac{1}{m} \sum_{i=1}^m d_i \\ s_d^2 &= \frac{1}{m-1} \sum_{i=1}^m (d_i - \bar{d})^2 \end{aligned} \right\} v_i = \frac{\bar{d}}{s_d}$$

**Thank you for your attention
and
all the best for the exams!**

