

FIT2086 Lecture 12

Revision

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- Assignment #2
 - Everyone did well
 - From Clayton cohort:
 - Wanshu Li and Alex Hughes got 30/30 after bonus marks
 - Mukund Premkumar got 30/30 before bonus marks – well done!
- Assignment #3
 - Due this coming Sunday
 - Submit one PDF file and appropriate R files
- Subject Evaluation of Teaching and Units (SETU)
 - Those who have not yet done so, can you please fill out the SETU feedback
 - Greatly appreciated!

Subject Outcomes – Revision

- On completion of this unit, students should be able to:
 - 1 perform exploratory data analysis with descriptive statistics on given datasets; ✓
 - 2 construct models for inferential statistical analysis; ✓
 - 3 produce models for predictive statistical analysis; ✓
 - 4 perform fundamental random sampling, simulation and hypothesis testing for required scenarios; ✓
 - 5 implement a model for data analysis through programming and scripting; ✓
 - 6 interpret results for a variety of models. ✓

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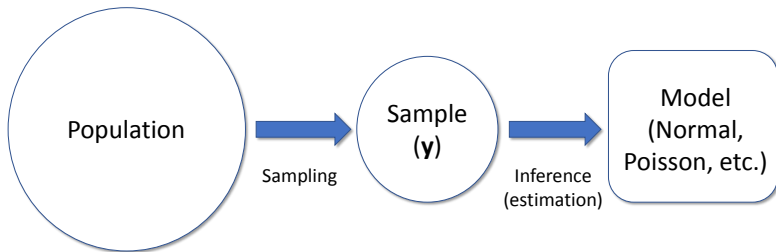
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Revision from Lecture 1



- **Population:** A large collection of objects or items with measureable attributes
- **Sample:** A finite number of recordings of attributes of items from a population
- **Model:** A mathematical or algorithmic description of the population learned/inferred from the sample

Revision from Lecture 2 (1)

- $\mathbb{P}(X = x, Y = y)$ is **joint** probability of $X = x$ and $Y = y$.
 - Sum-rule (**marginal** probability):

$$\mathbb{P}(X = x) = \sum_y \mathbb{P}(X = x, Y = y)$$

- **Conditional** probability

$$\mathbb{P}(X = x | Y = y) = \frac{\mathbb{P}(X = x, Y = y)}{\mathbb{P}(Y = y)}$$

- Cumulative distribution function (for ordered x):

$$\mathbb{P}(X \leq x) = \sum_{x \leq x} \mathbb{P}(X = x)$$

- Also: $\mathbb{P}(X > x) = 1 - \mathbb{P}(X \leq x)$.

Revision from Lecture 2 (2)

- Let $\mathbb{P}(X = x) \equiv p(x)$; **expectation** and **variance** of $f(X)$:

$$\mathbb{E}[f(X)] = \sum_x p(x)f(x)$$

$$\mathbb{V}[f(X)] = \mathbb{E}[(X - \mathbb{E}[f(X)])^2]$$

with integral replacing sum for continuous RVs.

- Some useful rules:
 - $\mathbb{E}[f(X) + g(Y)] = \mathbb{E}[f(X)] + \mathbb{E}[g(Y)]$
 - $\mathbb{E}[cf(X)] = c\mathbb{E}[f(X)]$
 - $\mathbb{V}[cf(X)] = c^2\mathbb{V}[f(X)]$
- If X, Y are **independent** RVs
 - $\mathbb{E}[f(X)g(Y)] = \mathbb{E}[f(X)]\mathbb{E}[g(Y)]$
 - $\mathbb{V}[f(X) + g(Y)] = \mathbb{V}[f(X)] + \mathbb{V}[g(Y)]$

Revision from Lecture 2 (3)

- Parametric distributions as models of populations
- **Normal** distribution; $X \in \mathbb{R}$, $X \sim N(\mu, \sigma^2)$

$$\mathbb{E}[X] = \mu, \quad \mathbb{V}[X] = \sigma^2$$

- **Bernoulli** distribution; $X \in \{0, 1\}$, $X \sim \text{Be}(\theta)$

$$\mathbb{E}[X] = \theta, \quad \mathbb{V}[X] = \theta(1 - \theta)$$

- **Binomial** distribution; $X \in \{0, 1, \dots, n\}$, $X \sim \text{Bin}(\theta, n)$

$$\mathbb{E}[X] = n\theta, \quad \mathbb{V}[X] = n\theta(1 - \theta)$$

- **Poisson** distribution; $X \in \{0, 1, 2, \dots\}$, $X \sim \text{Poi}(\lambda)$

$$\mathbb{E}[X] = \lambda, \quad \mathbb{V}[X] = \lambda$$

Revision from Lecture 3 (1)

- We looked at problem of parameter estimation
- Method of **maximum likelihood**

$$\hat{\theta}_{\text{ML}} = \arg \max_{\theta} \{p(\mathbf{y} \mid \theta)\}$$

- Maximum likelihood estimators for the normal

$$\hat{\mu}_{\text{ML}} = \frac{1}{n} \sum_{i=1}^n y_i, \quad \hat{\sigma}_{\text{ML}} = \sqrt{\frac{1}{n} \sum_{i=1}^n (y_i - \hat{\mu}_{\text{ML}})^2}$$

- Maximum likelihood estimator for Poisson

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Revision from Lecture 3 (2)

- Sampling distributions of estimators
- **Bias** and **variance** of an estimator

$$b_{\theta}(\hat{\theta}) = \mathbb{E} [\hat{\theta}] - \theta, \quad \text{Var}_{\theta}(\hat{\theta}) = \mathbb{V} [\hat{\theta}]$$

- **Mean squared error** of an estimator

$$\text{MSE}_{\theta}(\hat{\theta}) = b_{\theta}^2(\hat{\theta}) + \text{Var}_{\theta}(\hat{\theta})$$

- If Y_1, \dots, Y_n have $\mathbb{E} [Y_i] = \mu$ and $\mathbb{V} [Y_i] = \sigma^2$ then

$$b_{\mu}(\bar{Y}) = 0, \quad \text{Var}_{\mu}(\bar{Y}) = \frac{\sigma^2}{n}, \quad \text{MSE}_{\mu}(\bar{Y}) = \frac{\sigma^2}{n}$$

- An estimator $\hat{\theta}$ is **consistent** if

$$b_{\theta}(\hat{\theta}) \rightarrow 0, \quad \text{Var}_{\theta}(\hat{\theta}) \rightarrow 0,$$

as $n \rightarrow \infty$ for all θ .

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Example: ML Estimation of a Poisson (1)

- Recall the Poisson distribution with rate λ :

$$p(y | \lambda) = \frac{\lambda \exp(-y\lambda)}{y!}.$$

- If $\mathbf{y} = (y_1, \dots, y_n)$ are n integers, then the likelihood for a Poisson model is

$$\begin{aligned} p(\mathbf{y} | \lambda) &= \prod_{i=1}^n p(y_i | \lambda) \\ &= \left(\frac{\lambda \exp(-y_1 \lambda)}{y_1!} \right) \cdot \left(\frac{\lambda \exp(-y_2 \lambda)}{y_2!} \right) \cdots \left(\frac{\lambda \exp(-y_n \lambda)}{y_n!} \right) \\ &= \frac{\lambda^n \exp(-\lambda \sum_{i=1}^n y_i)}{\prod_{i=1}^n y_i!} \end{aligned}$$

by $e^a e^b = e^{a+b}$ and independence of y_1, \dots, y_n .

Example: ML Estimation of a Poisson (2)

- The negative log-likelihood is then

$$L(\mathbf{y} | \lambda) = -n \log \lambda + \lambda \sum_{i=1}^n y_i + \sum_{i=1}^n \log y_i!$$

- To find the ML estimator of λ we need to minimise $L(\mathbf{y} | \lambda)$, or equivalently solve

$$\frac{dL(\mathbf{y} | \lambda)}{d\lambda} = 0,$$

for λ .

Example: ML Estimation of a Poisson (3)

- The derivative is given by

$$\frac{dL(\mathbf{y} | \lambda)}{d\lambda} = -\frac{n}{\lambda} + \sum_{i=1}^n y_i \quad (1)$$

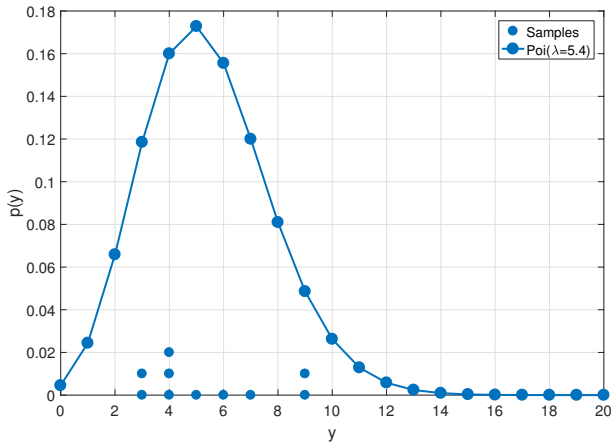
where we use $d \log x / dx = 1/x$

- Setting (1) to zero and solving for λ yields

$$\hat{\lambda} = \frac{1}{n} \sum_{i=1}^n y_i$$

- So, the ML estimator for the Poisson rate is the sample mean.
 \Rightarrow this is not always the case!

Example: ML Estimation of a Poisson (4)



Data samples and the Poisson distribution fitted by maximum likelihood with $\hat{\lambda} = 5.4$. Samples were $y = (7, 9, 3, 5, 3, 4, 4, 4, 6)$.

- **Central limit theorem:** if Y_1, \dots, Y_n are RVs with $\mathbb{E}[Y_i] = \mu$ and $\mathbb{V}[Y_i] = \sigma^2$ then

$$\sum_{i=1}^n Y_i \xrightarrow{d} N(n\mu, n\sigma^2)$$

- Implies distribution of the sample mean \bar{Y} for Y_1, \dots, Y_n with $\mathbb{E}[Y_i] = \mu$ and $\mathbb{V}[Y_i] = \sigma^2$ satisfies

$$\bar{Y} \xrightarrow{d} N\left(\mu, \frac{\sigma^2}{n}\right)$$

Confidence Intervals

- An interval estimator returns an interval of plausible values for a population parameter θ

Confidence Intervals

We use the method of **confidence intervals**.

We say the interval estimator $(\hat{\theta}_{\alpha}^{-}(\mathbf{y}), \hat{\theta}_{\alpha}^{+}(\mathbf{y}))$ generates a $100(1 - \alpha)$ -percent confidence interval, for $\alpha \in (0, 1)$, if

$$\mathbb{P} \left(\theta \in (\hat{\theta}_{\alpha}^{-}(\mathbf{y}), \hat{\theta}_{\alpha}^{+}(\mathbf{y})) \right) = 1 - \alpha,$$

where the probability is with respect to all the different samples \mathbf{y} we could draw from our population.

- $100(1 - \alpha)\%$ confidence intervals: cover the true population parameter for 95% of possible samples we could draw from our population

CI for Normal Mean, Known Variance

- Assuming the population is normally distributed with (unknown) mean μ and (known) variance σ^2 , these results yield the following 95% confidence interval for $\hat{\mu}_{\text{ML}} \equiv \bar{Y}$,

$$\left(\hat{\mu}_{\text{ML}} - 1.96 \frac{\sigma}{\sqrt{n}}, \hat{\mu}_{\text{ML}} + 1.96 \frac{\sigma}{\sqrt{n}} \right)$$

- More generally, a $100(1 - \alpha)\%$ confidence interval is given by:

$$\left(\hat{\mu}_{\text{ML}} - z_{\alpha/2} \frac{\sigma}{\sqrt{n}}, \hat{\mu}_{\text{ML}} + z_{\alpha/2} \frac{\sigma}{\sqrt{n}} \right)$$

where $z_{\alpha/2}$ is the $100(1 - \alpha/2)$ percentile of the unit normal:

- for $\alpha = 0.05$, $z_{0.025} = Q(p = 0.975) \approx 1.96$;
- for $\alpha = 0.01$, $z_{0.005} = Q(p = 0.995) \approx 2.576$;
- for general α , use $Q(p = 1 - \alpha/2)$

where $Q(\cdot)$ is the quantile function for the unit normal.

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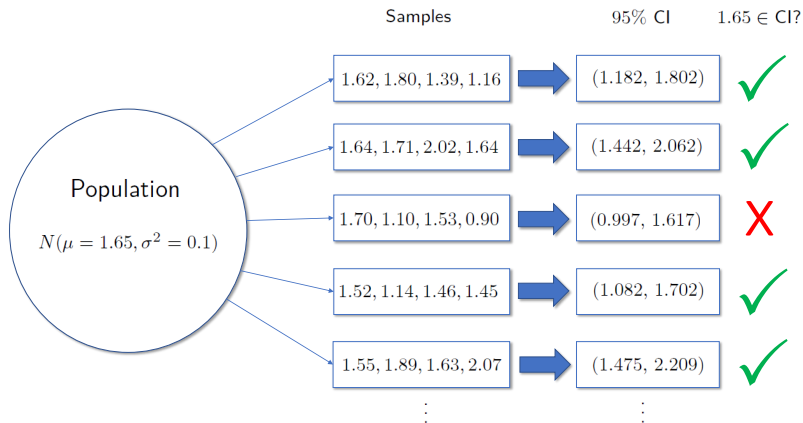
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CI for Normal Mean, Known Variance (2)



Cartoon showing multiple samples drawn from a $N(\mu = 1.65, \sigma^2 = 0.1)$ population, along with the 95% confidence intervals for each sample. 5% of possible samples will result in CIs that do not include $\mu = 1.65$.

Example: Normal Mean, Known Variance (1)

- **Example:** We have the following samples of body mass index taken people with diabetes from the Pima ethnic group

$$\mathbf{y} = (53.2, 33.6, 36.6, 42.0, 33.3, 37.8, 31.2, 43.4)$$

- Imagine we are given a value for the population variance of 43.75 which has been estimated by another, very large study of people from the Pima group.
- Task: Estimate the BMI of diabetic Pima people and construct a 95% CI
- Our best guess at the population mean BMI for Pima people with diabetes is

$$\hat{\mu}_{\text{ML}} = 38.88$$

Example: Normal Mean, Known Variance (2)

- Our 95% CI is then

$$\left(38.88 - 1.96\sqrt{43.75/8}, 38.88 + 1.96\sqrt{43.75/8} \right)$$

which is equal to

$$(34.3, 43.47)$$

- In words, we summarise our analysis by:

“The estimated mean BMI of people from the Pima ethnic group with diabetes (sample size $n = 8$) is 38.88 kg/m^2 . We are 95% confident the population mean BMI for this group is between 34.3 kg/m^2 and 43.75 kg/m^2 .”

CI for Normal Mean, Unknown Variance

- Let us make our assumptions more realistic
 - $Y_1, \dots, Y_n \sim N(\mu, \sigma^2)$ with *both* μ and σ^2 **unknown**.
- We can instead estimate σ^2 and use the Student- t distribution

$$\left(\hat{\mu}_{\text{ML}} - t_{\alpha/2, n-1} \frac{\hat{\sigma}_u}{\sqrt{n}}, \hat{\mu}_{\text{ML}} + t_{\alpha/2, n-1} \frac{\hat{\sigma}_u}{\sqrt{n}} \right)$$

which achieves $100(1 - \alpha)\%$ coverage if population is Gaussian

- $\hat{\sigma}_u^2$ is the unbiased estimate of variance from our sample
- Here, $t_{\alpha/2}$ is the $100(1 - \alpha/2)$ -th percentile of the standard Student t -distribution with $n - 1$ degrees of freedom
- To compare with normal percentiles, recall $z_{0.025} = 1.96$;
 - for $n = 3$, $t_{0.025, 2} \approx 4.3$;
 - for $n = 6$, $t_{0.025, 5} \approx 2.57$;
 - for $n = 11$, $t_{0.025, 10} \approx 2.22$;

CI for Difference of Normal Means

- We have two samples \mathbf{y}_A and \mathbf{y}_B
 - Wish to get confidence interval for $\mu_A - \mu_B$ (i.e., the difference in population means)
- Instead, let us assume $\mu_A, \mu_B, \sigma_A^2, \sigma_B^2$ are all **unknown**
- Let $\hat{\sigma}_A^2$ and $\hat{\sigma}_B^2$ be unbiased estimates of the variance in sample A and B, respectively
- Then the following interval:

$$\left(\hat{\mu}_A - \hat{\mu}_B - z_{\alpha/2} \sqrt{\frac{\hat{\sigma}_A^2}{n_A} + \frac{\hat{\sigma}_B^2}{n_B}}, \hat{\mu}_A - \hat{\mu}_B + z_{\alpha/2} \sqrt{\frac{\hat{\sigma}_A^2}{n_A} + \frac{\hat{\sigma}_B^2}{n_B}} \right)$$

is an *approximate* $100(1 - \alpha)\%$ confidence interval for $\hat{\mu}_A - \hat{\mu}_B$, with the approximation getting better for increasing n_A and n_B .

- Hypothesis testing; test **null hypothesis** vs alternative

H_0 : null hypothesis

vs

H_A : alternative hypothesis

- A **test-statistic** measures how different our observed sample is from the null hypothesis
- A **p-value** quantifies the evidence against the null hypothesis
- A **p-value** is the probability of seeing a sample that results in a test statistic as extreme, or more extreme, than the one we observed, just by chance if the null was true.

Testing μ with known variance

- Assume population follows normal distribution with unknown mean and **known** variance σ^2 ; testing inequality of μ
 - First calculate the ML estimate of the mean/sample mean

$$\hat{\mu} = \frac{1}{n} \sum_{i=1}^n y_i$$

- Then calculate the z -score

$$z_{\hat{\mu}} = \frac{\hat{\mu} - \mu_0}{(\sigma/\sqrt{n})}$$

- Then calculate the p -value:

$$p = \begin{cases} 2\mathbb{P}(Z < -|z_{\hat{\mu}}|) & \text{if } H_0 : \mu = \mu_0 \text{ vs } H_A : \mu \neq \mu_0 \\ 1 - \mathbb{P}(Z < z_{\hat{\mu}}) & \text{if } H_0 : \mu \leq \mu_0 \text{ vs } H_A : \mu > \mu_0 \\ \mathbb{P}(Z < z_{\hat{\mu}}) & \text{if } H_0 : \mu \geq \mu_0 \text{ vs } H_A : \mu < \mu_0 \end{cases} .$$

where $Z \sim N(0, 1)$

Example: Testing if $\mu = \mu_0$ (1)

- For US women aged between 20 to 34 years of age, the population body mass index (BMI) has
 - an approximate mean of 26.8 kg/m^2 ; and
 - an approximate standard deviation of 4.5 kg/m^2 .

(Source: Center for Disease Control)

- We have BMI measured on a sample of women aged 20-34 from the Pima ethnic group, without diabetes:

$$\mathbf{y} = (46.8, 27.8, 32.5, 39.5, 32.8, 31.0, 26.2, 20.8)$$

- Using this data, can we say whether women aged 20-34 in this Pima cohort have the same average BMI as the general US population?

Example: Testing if $\mu = \mu_0$ (2)

- We want to test:
 - $H_0 : \mu = 26.8$ vs $H_A : \mu \neq 26.8$,
 μ is the population mean BMI of Pima women aged 20-34.
- The estimated mean $\hat{\mu}$ from our sample is

$$\hat{\mu} = 32.175$$

- From this we can calculate the z -score as

$$z_{\hat{\mu}} = \frac{32.175 - 26.8}{(4.5/\sqrt{8})} = 3.3784$$

- This yields a p -value of

$$\begin{aligned} 1 - \mathbb{P}(-z_{\hat{\mu}} < Z < z_{\hat{\mu}}) &= 2 * \text{pnorm}(-\text{abs}(3.3784)) \\ &= 7.29 \times 10^{-4} \end{aligned}$$

Example: Testing if $\mu = \mu_0$ (3)

- How to interpret?
- A p -value of 7.29×10^{-4} can be interpreted as follows:
If the null was true, i.e., Pima ethnic women aged 20-34 have the same BMI as the average US woman aged 20-34, then the chance of observing a sample with as an extreme, or more extreme, difference from the null as the one that we saw would be less than 1/1371.
- So quite unlikely to happen just by vagaries of sampling
 \Rightarrow strong evidence against the null.

Testing μ with unknown variance

- Then our test statistic is a t -score

$$t_{\hat{\mu}} = \frac{\hat{\mu} - \mu_0}{(\hat{\sigma}/\sqrt{n})}$$

where the unknown population σ is replaced with our estimate

- If the null was true, then

$$t_{\hat{\mu}} \sim T(n-1)$$

where $T(d)$ denotes a standard t -distribution with d degrees-of-freedom

- The p -value is then

$$p = \begin{cases} 2 \mathbb{P}(T < -|t_{\hat{\mu}}|) & \text{if } H_0 : \mu = \mu_0 \text{ vs } H_A : \mu \neq \mu_0 \\ 1 - \mathbb{P}(T < t_{\hat{\mu}}) & \text{if } H_0 : \mu \leq \mu_0 \text{ vs } H_A : \mu > \mu_0 \\ \mathbb{P}(T < t_{\hat{\mu}}) & \text{if } H_0 : \mu \geq \mu_0 \text{ vs } H_A : \mu < \mu_0 \end{cases} .$$

where $T \sim T(n-1)$.

Testing difference of means, unknown variances

- If we relax assumption that $\sigma_x^2 = \sigma_y^2$ things get hard
- An approximate p -value can be computed by substituting estimates $\hat{\sigma}_x^2$ and $\hat{\sigma}_y^2$ into the formulae for known variance
- This give us the test statistic

$$z(\hat{\mu}_x - \hat{\mu}_y) = \frac{\hat{\mu}_x - \hat{\mu}_y}{\sqrt{\frac{\hat{\sigma}_x^2}{n_x} + \frac{\hat{\sigma}_y^2}{n_y}}}$$

which is approximately $N(0, 1)$ for large samples.

- We can then find approximate p -values using:

$$p \approx \begin{cases} 2 \mathbb{P}(Z < -|z(\hat{\mu}_x - \hat{\mu}_y)|) & \text{if } H_0 : \mu = \mu_0 \text{ vs } H_A : \mu \neq \mu_0 \\ 1 - \mathbb{P}(Z < z(\hat{\mu}_x - \hat{\mu}_y)) & \text{if } H_0 : \mu \leq \mu_0 \text{ vs } H_A : \mu > \mu_0 \\ \mathbb{P}(Z < z(\hat{\mu}_x - \hat{\mu}_y)) & \text{if } H_0 : \mu \geq \mu_0 \text{ vs } H_A : \mu < \mu_0 \end{cases} .$$

- More exact but complicated procedures exist; `t.test()` in R implements some of these

Revision from Lecture 6

- Imagine we have measured $p + 1$ variables on n individuals (people, objects, things)
- We would like to predict one of the variables using the remaining p variables
- If the variable we are predicting is categorical, we are performing **classification**
 - Example: predicting if someone has diabetes from medical measurements.
- If the variable we are predicting is numerical, we are performing **regression**
 - Example: Predicting the quality of a wine from chemical and seasonal information.

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Revision from Lecure 6 (1)

- Linear regression

$$\mathbb{E}[Y_i] = \beta_0 + \beta_1 x_{i,1} + \beta_2 x_{i,2} + \cdots + \beta_p x_{i,p}$$

- β_0 is the **intercept** (value of $\mathbb{E}[Y]$ when all predictors are zero)
 - β_j is a **coefficient** (change in $\mathbb{E}[Y]$ per unit change in $x_{j,i}$)
- Residuals (errors)

$$e_i = y_i - \beta_0 - \beta_1 x_{i,1} - \beta_2 x_{i,2} - \cdots - \beta_p x_{i,p}$$

- Residual sum-of-squares

$$\text{RSS}(\beta_0, \beta_1, \dots, \beta_p) = \sum_{i=1}^n e_i^2$$

- Least-squares estimates linear model by finding $\beta_0, \beta_1, \dots, \beta_p$ that minimise the RSS

Revision from Lecure 6 (2)

- R^2 measure of goodness-of-fit

$$R^2 = 1 - \frac{\text{RSS}}{\text{TSS}}$$

where TSS is the sum of squared errors for the mean model

- Sometimes our predictors are categorical variables
 - We turn them into $K - 1$ new predictors (**indicator variables**)
- Sometimes predictor-target relationship is nonlinear
 - Nonlinear transformations of our variables can help
 - **Polynomial transformations** offer general purpose nonlinear fits
 - We turn our variable into q new variables of the form:

$$x_{i,j} \Rightarrow x_{i,j}, x_{i,j}^2, x_{i,j}^3, \dots, x_{i,j}^q$$

Revision from Lecture 7 (1)

- We also have p predictor variables X_1, \dots, X_p
- We can build a classifier for Y using our predictors

$$P(y | x_1, x_2, \dots, x_p) = \frac{P(y, x_1, \dots, x_p)}{P(x_1, \dots, x_p)}$$

- **Naïve Bayes** assumes predictors are conditionally independent, given the value of the target

$$P(x_1, \dots, x_p | y) = \prod_{j=1}^p P(x_j | y)$$

- Naïve Bayes classifier:

$$P(y | x_1, \dots, x_p) = \frac{\prod_{j=1}^p P(x_j | y) P(y)}{P(x_1, \dots, x_p)}$$

Revision from Lecture 7 (2)

- A **logistic regression** models the conditional log-odds as

$$\log \left(\frac{\mathbb{P}(Y_i = 1 \mid x_{i,1}, \dots, x_{i,p})}{\mathbb{P}(Y_i = 0 \mid x_{i,1}, \dots, x_{i,p})} \right) = \beta_0 + \sum_{j=1}^p \beta_j x_{i,j} \equiv \eta_i$$

- Logistic regression model of conditional probability

$$\mathbb{P}(Y_i = 1 \mid x_{i,1}, \dots, x_{i,p}) = \frac{1}{1 + \exp(-\eta_i)}$$

- Estimated using maximum likelihood
- Performance measures for classification
 - Classification error
 - Sensitivity and specificity
 - Area-under-the-curve (AUC)
 - Logarithmic loss

Revision from Lecture 8 (1)

- How many predictors should we include in our linear model?
- **Underfitting**
 - Omitting important predictors
 - Leads to systematic error (“bias”) in predicting the target
- **Overfitting**
 - Including spurious predictors
 - Leads our model to “learn” noise and random variation
- Methods to trade off bias and variance
 - Hypothesis testing $\beta_j = 0$ vs $\beta_j \neq 0$
 - Multiple hypothesis testing problem, Bonferroni
 - Penalized likelihood – likelihood plus complexity penalty
 - AIC, KIC, BIC, RIC
 - **Cross-validation**

Revision from Lecture 8 (2)

- **All-subsets selection:**
 - Try all combination of predictors to model with smallest model selection criterion score
- **Forward selection algorithm:**
 - 1 Start with the empty model;
 - 2 Find the predictor that reduces info criterion by most
 - 3 If no predictor improves model, end.
 - 4 Add this predictor to the model
 - 5 Return to Step 2
- **Backwards selection** is related algorithm
 - Start with the full model and remove predictors

Revision from Lecture 8 (3)

- Statistical instability;
 - Small changes in data \Rightarrow big changes in model
- **Ridge regression**, squared penalty on coefficients

$$(\hat{\beta}_0, \hat{\beta}_\lambda) = \arg \min_{\beta_0, \beta} \left\{ \text{RSS}(\beta_0, \beta) + \lambda \sum_{j=1}^p \beta_j^2 \right\}$$

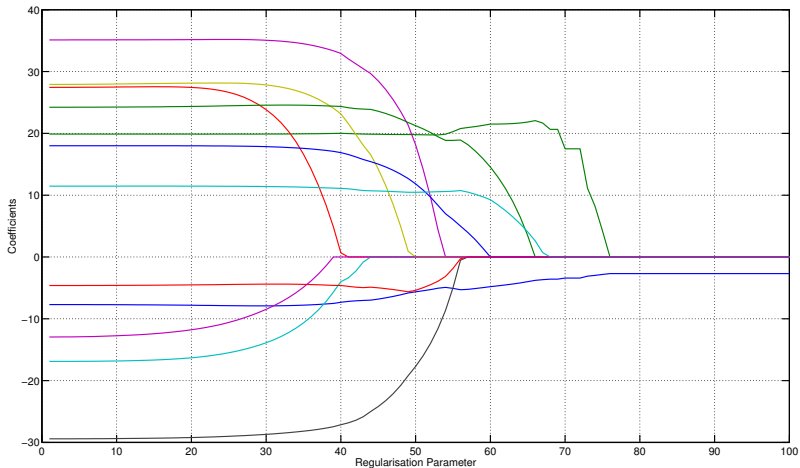
- **Lasso regression**, absolute penalty on coefficients

$$(\hat{\beta}_0, \hat{\beta}_\lambda) = \arg \min_{\beta_0, \beta} \left\{ \text{RSS}(\beta_0, \beta) + \lambda \sum_{j=1}^p |\beta_j| \right\}$$

- Lasso can estimate coefficients to be zero, ridge cannot
- Vary λ to get a “path” of different complexity models
 - $\lambda = 0$ most complex, $\lambda = \infty$ least complex
- Use cross validation to choose a good λ

Lasso Regression (3)

- Example lasso regression coefficient path



Revision from Lecture 9 (1)

- Machine learning methods
- Cross validation for model selection
 - Withhold data to estimate prediction error
 - K -fold CV divides data up into K equal sized groups
 - Train on $K - 1$ folds, predict on the remaining fold
- Decision Trees
 - Split the data up by asking questions of the predictors
 - Number of leaves determines complexity of tree
 - Easy to interpret, flexible
- Methods for learning trees
 - Greedy growing of trees – find best split at each step
 - Backwards pruning of large tree
 - Use CV to select number of leaves in the tree

Revision from Lecture 9 (2)

- Trees have low bias, high variance
- One solution: **random forests**
 - Grow many trees with guided random search
 - Aggregate predictions from the trees
 - Stable, low variance, but loses interpretability
- **k -nearest neighbours** (kNN) methods
 - Assume individuals similar in predictors are similar in targets
 - Find k “most similar” individuals in data to new individual
 - Use their targets to predict target for new individual
- Use CV to select k , other tuning parameters

K -fold Cross Validation

- Outer loop: try different model complexities γ

- ① For $i = 1$ to m

- ① Partition data into K equal sized, disjoint subsets

$$\mathbf{y}^{(1)}, \mathbf{y}^{(2)}, \mathbf{y}^{(3)}, \dots, \mathbf{y}^{(K)}$$

- ② For $k = 1$ to K

- ① Fit model $\mathcal{M}(\gamma)$ to all $\mathbf{y}^{(i)}$ except for $i = k$

- ② Use fitted model to predict onto $\mathbf{y}^{(k)}$

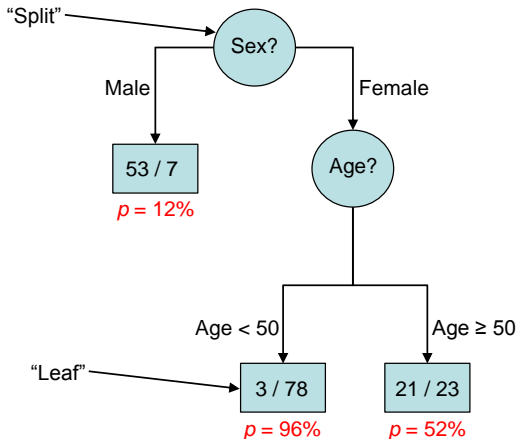
- ③ Calculate and accumulate prediction errors

- ② Average all m accumulated prediction errors

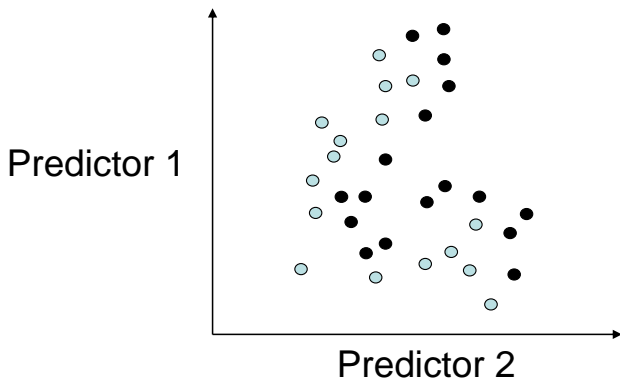
- Once this is done, we have CV errors for each complexity γ
 \Rightarrow choose the γ with the smallest estimated error
- The larger the m , the more stable the estimates (but slower)

Decision Trees

- Example tree: predicting high blood pressure

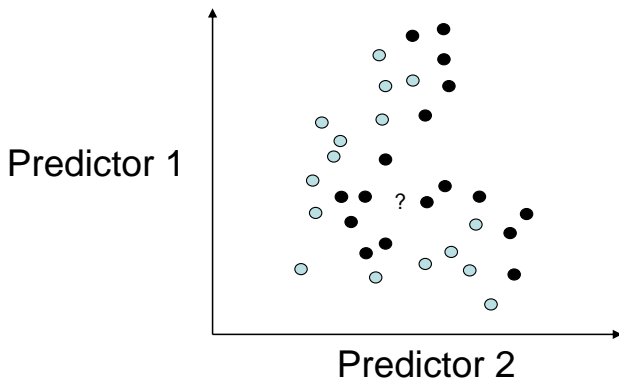


k -Nearest Neighbours Example 1 (1)



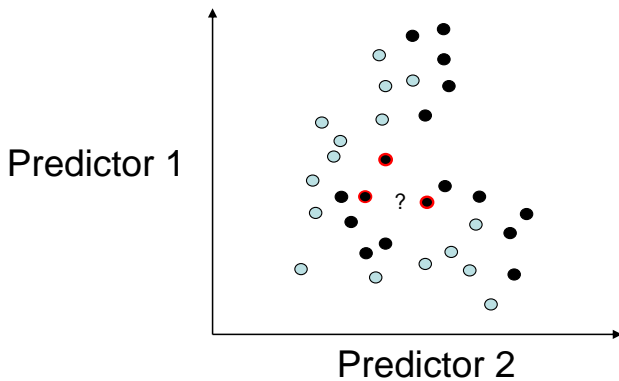
Example data set: black are individuals with disease, blue are those without

k -Nearest Neighbours Example 1 (2)



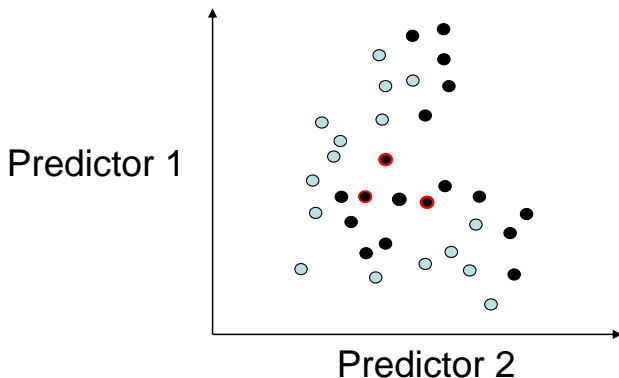
We want to predict the disease status of the individual marked with a "?" using a k nearest neighbour method with $k = 3$ neighbours

k -Nearest Neighbours Example 1 (3)



We find the closest $k = 3$ individuals

k -Nearest Neighbours Example 1 (4)



They all have the disease, so we predict that our new individual will also have the disease

Revision from Lecture 10 (1)

- **Unsupervised Learning**
- n individuals, q attributes
 - No “target”; instead, discover structure inherent in data
- **Clustering**
 - Model the population as K distinct sub-populations
 - Learn both K and the subpopulation parameters
- **k -means** clustering algorithm
 - Allocate individuals to closest clusters
 - Re-estimate cluster centres
 - Iterate until convergence

Revision from Lecture 10 (2)

- **Mixture modelling**

- Models data as a **mixture of probability distributions** (subpopulations)

$$p(y_{i,j}) = \sum_{k=1}^K \alpha_k p(y_{i,j} | \theta_{k,j})$$

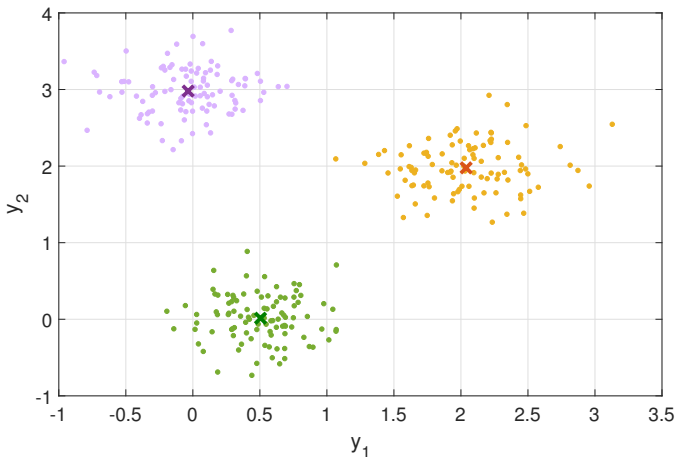
- Each subpopulation characterised by distributions
- “Soft” assignment of individuals to classes
- Intrinsic classification

- **Matrix completion**

- Missing entries in our data matrix
- Try to estimate the values of the missing data
- Applications: imputation, recommender systems
- Mixture modelling approach, k -NN approaches

K -means Clustering

- Find the centroids that minimise within-cluster sum-of-squares



Summary

- I have put some links up in Lecture 12 to books/book chapters you can read if you want to learn more about data science
- FIT3154 Advanced data analysis is a good follow up if you enjoyed this
 - More focus on machine learning, including neural networks/deep learning
- Good luck in the exam!