Regression Modelling in `R`

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Workshop Overview

- Correlation
- Linear Regression
  - Specifying a model with `lm`
  - Interpreting the model output
  - Assessing model fit
- Multiple Regression
- Prediction
- Generalized Linear Models using `glm`
  - Logistic Regression

Mixture of theory, examples and practical exercises

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Relationships between variables

If two variables are related, we usually describe them as 'correlated'.

Usually interested in "strength" and "direction" of association

Two analysis techniques commonly used to investigate:

- *Correlation:* shows direction, and strength of association
- *Regression:* estimate how one variable: y changes when we observed changes in another: x (or more than one, x_i)

Sometimes the effects of other variables interact/mask this (*"confounding"*)

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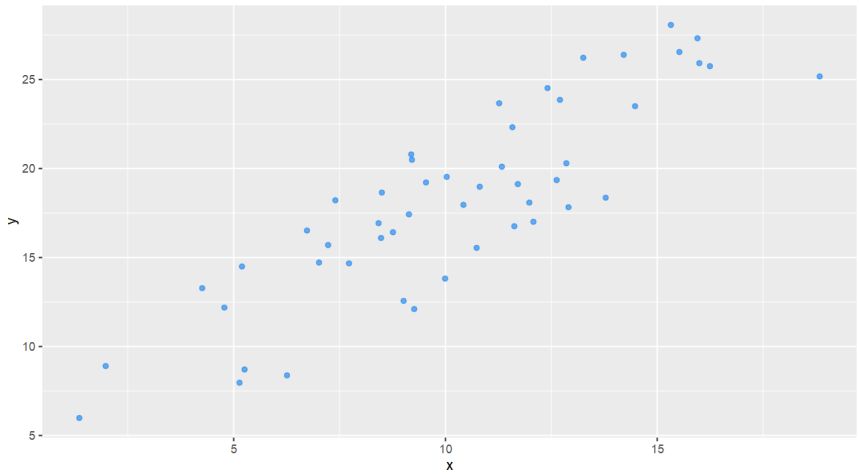
Example:

```
x <- rnorm(50, 10, 4)
y <- runif(50, min = 0.5, 10) + (1.25*x)

a<-ggplot(data.frame(x,y,z), aes(x=x,y=y))+
  geom_point(col="dodgerblue2", alpha=0.65)
a
```



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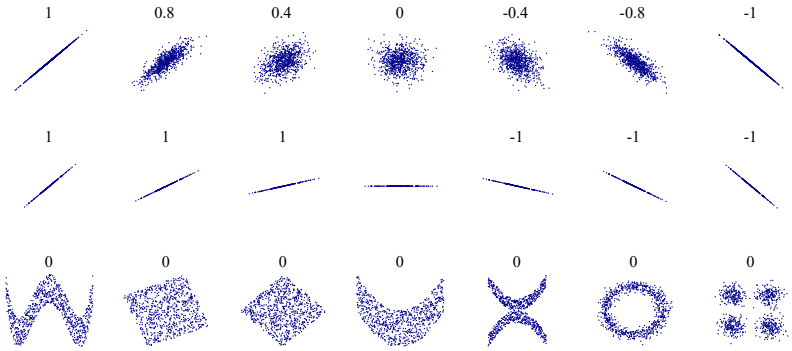
Correlation

- Measured with a correlation coefficient ('Pearson' is the most common)
- Range:
  - **-1 to 1:** Perfect negative to Perfect positive Correlation
  - **0:** No Correlation



Graphic from: Wikipedia: Correlation and dependence: By DenisBoigelot, https://commons.wikimedia.org/w/index.php?curid=15165296 [Accessed 24 Sept 2019]

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Correlation in R

Lets check the correlation in our generated data:

```
cor(x, y)
#> [1] 0.8650106

cor.test(x,y)
#>
#>     Pearson's product-moment correlation
#>
#> data:  x and y
#> t = 11.944, df = 48, p-value = 5.53e-16
#> alternative hypothesis: true correlation is not equal to 0
#> 95 percent confidence interval:
#>  0.7727115 0.9214882
#> sample estimates:
#>       cor
#> 0.8650106
```

- `cor.test` is a correlation and a t-test.
- Different types of correlation coefficient, default is 'Pearson'
- Doesn't work for different distributions, data types or more variables

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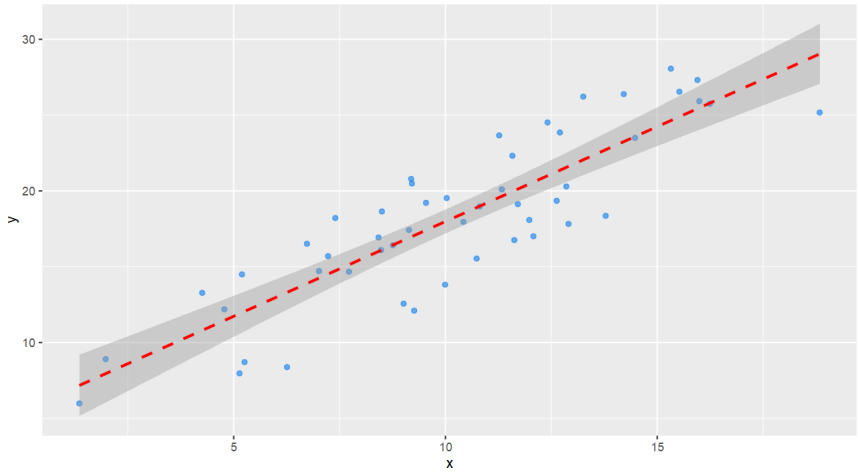
Regression models (1)

Regression gives us more options than correlation:

```
z <- lm(y~x)
print(a<- a + geom_smooth(method="lm", col="red", linetype=2))
```



$$y = \alpha + \beta x + \epsilon$$

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Regression equation

$$y = \alpha + \beta_i x_i + \epsilon$$

- y - is our 'outcome', or 'dependent' variable
- α - is the 'intercept', the point where our line crosses y-axis
- β - is a coefficient (weight) applied to x
- x - is our 'predictor', or 'independent' variable
- i - is our index, we can have i predictor variables, each with a coefficient
- ϵ - is the remaining ('residual') error

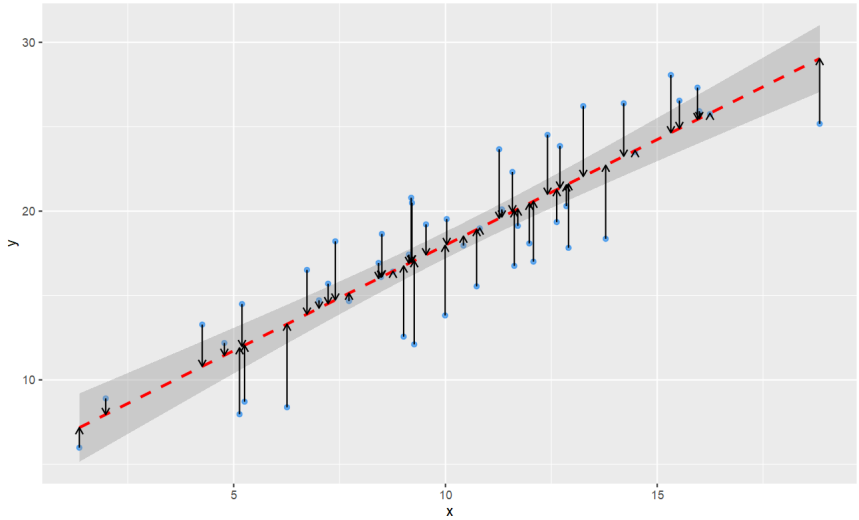
We are making some assumptions:

- Linear relations
- Data points are independent (not correlated)
- Normally distributed error
- Homoskedastic (error doesn't vary across the range)

Ordinary Least Squares 'OLS'

- 'Residual' distance between prediction and data point (ϵ).
- Sum would be zero, so we square and minimise *'sum of the squares'*

```
a + geom_segment(aes(xend=c(x), yend=c(z)), size=0.5, arrow=arrow(length=unit(0.2,"cm")))
```



Regression models (3)

- We created an `lm` object called `z`. You can then use that object with other functions like `summary`, `predict`, `plot` etc.

```
summary(z)
#>
#> Call:
#> lm(formula = y ~ x)
#>
#> Residuals:
#>     Min      1Q  Median      3Q     Max
#> -4.9575 -2.2614  0.4444  2.4475  4.1663
#>
#> Coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)   5.4776     1.1386   4.811 1.53e-05 ***
#> x             1.2507     0.1047  11.944 5.53e-16 ***
#> ---
#> Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
#>
#> Residual standard error: 2.77 on 48 degrees of freedom
#> Multiple R-squared:  0.7482,    Adjusted R-squared:  0.743
#> F-statistic: 142.7 on 1 and 48 DF,  p-value: 5.53e-16
```

- We can test fit using f-tests, prediction error or the R^2 .
- R^2 is the proportion of variation in y, explained by x .

Interpretation

We can now read this as:

- *"For each increase of 1 in x, y increases by 1.25, starting at 5.48."*

A common addition is to **"mean-centre and scale"** our variables:

Original Scaled Interpretation

```
z <- lm(y~x)
summary(z)
#>
#> Call:
#> lm(formula = y ~ x)
#>
#> Residuals:
#>     Min      1Q  Median      3Q     Max
#> -4.9575 -2.2614  0.4444  2.4475  4.1663
#>
#> Coefficients:
#>             Estimate Std. Error t value Pr(>|t|)
#> (Intercept)   5.4776     1.1386   4.811 1.53e-05 ***
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#>
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#> Multiple R-squared:  0.7482,    Adjusted R-squared:  0.743
#> F-statistic: 142.7 on 1 and 48 DF,  p-value: 5.53e-16
```
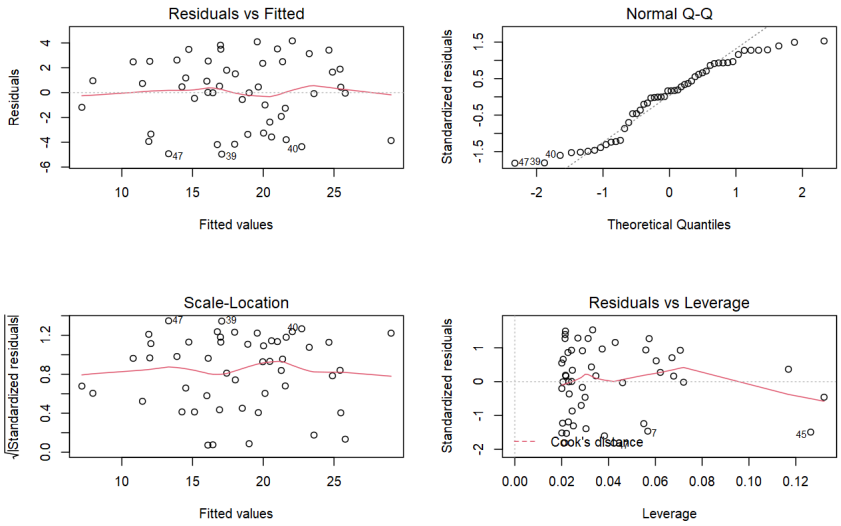


Regression diagnostics (5)

A common check is to plot residuals:

```
plot(z)
```



Exercise 1: Linear regression with a single predictor

More than one predictor?

Our plots in earlier slides make sense in 2 dimensions, but regression is not limited to this.

If we add more predictos, our interpretation of each coefficient becomes:

- *"The change in y whilst holding all others parameters constant"*

We can add more predictors with the `+`:

```
lm(y ~ x1 + x2 + x3 + xi)
```

Categorical variables

How do we enter categorical variables into a model?

- Models won't understand text, and numbers are numeric, so we use `factor` variables?

`Factors` are 'dummy coded:'

- *'pivotted' to binary columns*
- Contain a reference level: with categories: "A", "B" & "C", we get:

```
a<- data.frame(Category = factor(c("A", "B", "C", "C", "A", "B")))
model.matrix(~., a)
#>   (Intercept) CategoryB CategoryC
#> 1           1         0         0
#> 2           1         1         0
#> 3           1         0         1
#> 4           1         0         1
#> 5           1         0         0
#> 6           1         1         0
#> attr(,"assign")
#> [1] 0 1 1
#> attr(,"contrasts")
#> attr(,"contrasts")$Category
#> [1] "contr.treatment"
```


Exercise 2: Linear regression with multiple predictors

What about non-linear data?

- Data are not necessarily linear. Death is binary, LOS is a count etc.
- We can use the Generalized Linear Model (GLM):

$$g(\mu) = \alpha + \beta x$$

Where μ is the expectation of Y, and g is the link function

- The link function transforms the data before fitting a model
- Can't use OLS for this, so we use 'maximum-likelihood'
- Many of the methods for `lm` are common to `glm`, but we can't use R^2
- Other measures include AUC ('C-statistic'), and AIC or likelihood ratio tests.

Generalized Linear Models

- `family` argument was set to `binomial` for binary outcomes.

```
library(COUNT)
data(medpar)

glm_binomial <- glm(died ~ factor(age80) + los + factor(type), data=medpar, family="binomial")

sjPlot::tab_model(glm_binomial, show.df = TRUE, show.obs = TRUE, show.se = TRUE, show.r2 = FALSE)
```

			1=Died;0=Alive		
Predictors	*Odds Ratios*	*std. Error*	*CI*	*p*	*df*
(Intercept)	0.55	0.10	0.46 – 0.67	<0.001	Inf
factor(age80)1	1.93	0.13	1.50 – 2.48	<0.001	Inf
Length of Stay	0.96	0.01	0.95 – 0.98	<0.001	Inf
factor(type)2	1.52	0.14	1.14 – 2.02	0.004	Inf
factor(type)3	2.61	0.23	1.66 – 4.12	<0.001	Inf
Observations	1495				

```
ModelMetrics::auc(glm_binomial)
#> [1] 0.6372224
```

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Interactions

- 'Interactions' are where predictor variables affect each other.
- Can add these with `*` or `:` (check help for which to use)

```
glm_binomial2 <- glm(died ~ factor(age80) * los + factor(type), data=medpar, family="binomial")

sjPlot::tab_model(glm_binomial2, show.df = TRUE, show.obs = TRUE, show.se = TRUE, show.r2 = FALSE)
```

			1=Died;0=Alive		
Predictors	*Odds Ratios*	*std. Error*	*CI*	*p*	*df*
(Intercept)	0.57	0.10	0.47 – 0.70	<0.001	Inf
factor(age80)1	1.69	0.21	1.13 – 2.56	0.011	Inf
Length of Stay	0.96	0.01	0.94 – 0.98	<0.001	Inf
factor(type)2	1.52	0.14	1.14 – 2.01	0.004	Inf
factor(type)3	2.62	0.23	1.67 – 4.14	<0.001	Inf
factor(age80)1:los	1.01	0.02	0.98 – 1.05	0.419	Inf
Observations	1495				

```
ModelMetrics::auc(glm_binomial2)
#> [1] 0.6376572
```


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Interpretation

- Our model coefficients in `lm` were straight-forward multipliers
- `glm` is similar, but it is on the scale of the link-function.
  - log scale for `poisson` models, or logit (log odds) scale for `binomial`
- Common to transform output back to response scale
- giving Incident Rate Ratios for `poisson`, or Odds Ratios for `binomial`

```
cbind(Link=coef(glm_binomial2), Response=exp(coef(glm_binomial2)))
#>                              Link  Response
#> (Intercept)         -0.56160376 0.5702937
#> factor(age80)1       0.52537865 1.6910991
#> los                 -0.04073769 0.9600809
#> factor(type)2        0.41743940 1.5180694
#> factor(type)3        0.96477095 2.6241865
#> factor(age80)1:los   0.01450661 1.0146123
```

Exercise 3: Generalized Linear Model (GLM)

Prediction (1)

- We can then use our model to predict our expected Y:
- Need to decide what scale to predict on: `link` or `response`

```
library(dplyr)
medpar$preds <- predict(glm_binomial2, type="response")

top_n(medpar,5) %>% knitr::kable(format = "html")
```

	los	hmo	white	died	age80	type	type1	type2	type3	provnum	preds
558	1	0	1	1	1	3	0	0	1	030017	0.7114250
919	5	0	1	1	1	3	0	0	1	030061	0.6894160
1464	2	0	1	1	1	3	0	0	1	032000	0.7060100
1486	5	0	1	1	1	3	0	0	1	032002	0.6894160
1488	4	0	1	1	1	3	0	0	1	032002	0.6950045

Prediction (2)

- Lets see the 10 cases with the highest predicted risk of death:

```
medpar %>% arrange(desc(preds)) %>% top_n(10) %>% knitr::kable(format = "html")
#> Selecting by preds
```

	los	hmo	white	died	age80	type	type1	type2	type3	provnum	preds
558	1	0	1	1	1	3	0	0	1	030017	0.7114250
1464	2	0	1	1	1	3	0	0	1	032000	0.7060100
1488	4	0	1	1	1	3	0	0	1	032002	0.6950045
919	5	0	1	1	1	3	0	0	1	030061	0.6894160
1486	5	0	1	1	1	3	0	0	1	032002	0.6894160
955	6	0	1	0	1	3	0	0	1	030061	0.6837716
896	9	0	1	0	1	3	0	0	1	030061	0.6665153
941	9	0	1	0	1	3	0	0	1	030061	0.6665153
1084	10	0	1	1	1	3	0	0	1	030069	0.6606596
1482	11	0	1	1	1	3	0	0	1	032000	0.6547543

Exercise 4: Predicting from models

Summary

- Correlation shows the direction and strength of association
- Regression allows us to quantify the relationships
- We can use a single, or multiple, predictors
- Regression coefficients explain how much a change in x affects y
- R^2 is a common measure of in linear models, C-statistic/AUC/ROC in logistic models
- Generalized Linear Model (`glm`) allow linear models on a transformed scale, e.g. logistic regression for binary variables
- Interactions terms allow us to examine confounded predictors
- We can predict from our model objects, but must remember the link-function scale in `glm`

Exercise 5: Predicting 10-year CHD risk in Framingham data