Introduction to Bioinformatics

Introduction to Statistics for Analysis

Haries Ramdhani. 2021.

Pipeline for Methylation Analysis

Main flow:

- Quality control
- Filtering
- Normalization
- Data exploration

Downstream Analysis:

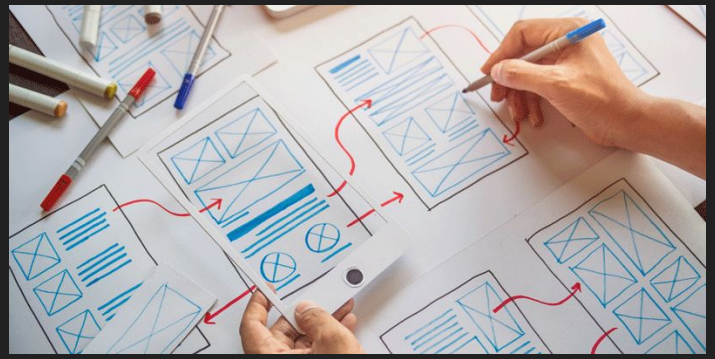
- Probe wise differential methylation analysis
- Differential variability analysis
- GO analysis
- etc.

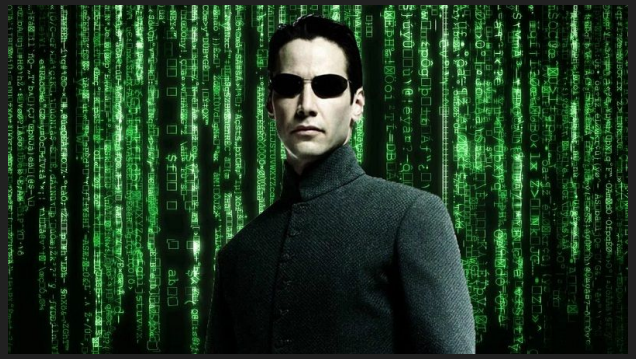
Design Matrix

This code right here is one of the most important part when we're performing differential gene exp

```
175  # this is the factor of interest
176  cellType <- factor(targets$Sample_Group)
177
178  targets
179
180  # use the above to create a design matrix
181  design <- model.matrix(~cellType, data=targets)
182  colnames(design) <- c(levels(cellType))
183
184  # fit the linear model
185  fit <- lmFit(mVals, design)
186
187  # create a contrast matrix for specific comparisons
188  contMatrix <- makeContrasts(GroupA-GroupB,
189                              levels=design)
```

What is Design Matrix?





Design Matrices

- In statistics and in particular in regression analysis, a **design matrix**, also known as **model matrix** or **regressor matrix** and often denoted by **X**, is a matrix of values of **explanatory variables** of a set of objects (Wikipedia).
- Used to define the form of a statistical model and to store observed values of the **explanatory variable**(s).
- Used in the computation process to estimate **model parameters**.

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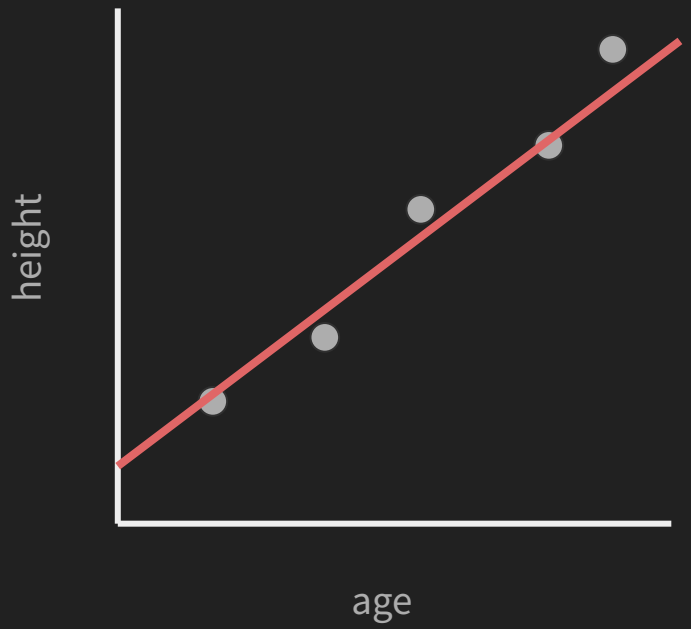
Simple Linear Model

CASE STUDY: How does human height change with age?



$$Y = mx + b$$

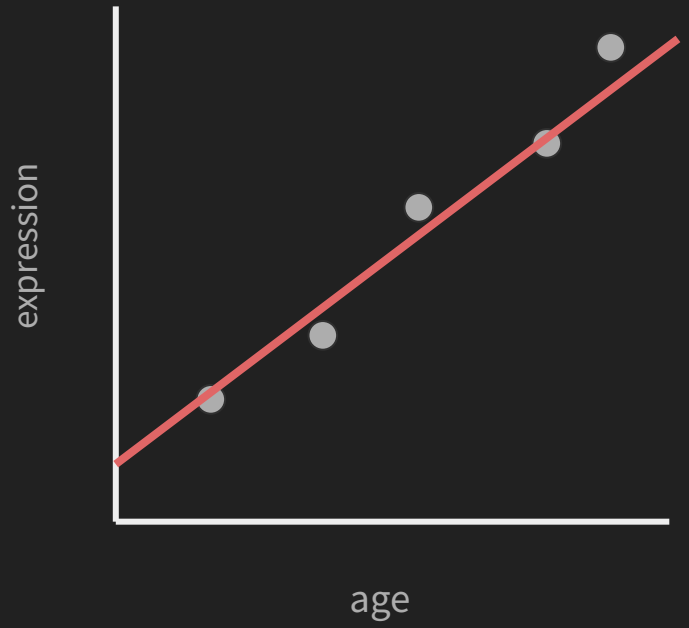
$$height = \beta_0 + \beta_1 age$$

Simple Linear Model

- There are two types of explanatory variable that we can use when we are performing differentially gene expression analysis or differentially methylated probe analysis, they are:
    - Covariates : Continuous variable, quantitative (age, weight, measurement from PCR)
    - Factors : Categorical variable associated with samples (disease status, genotype, cell type or treatment)

Simple Linear Model

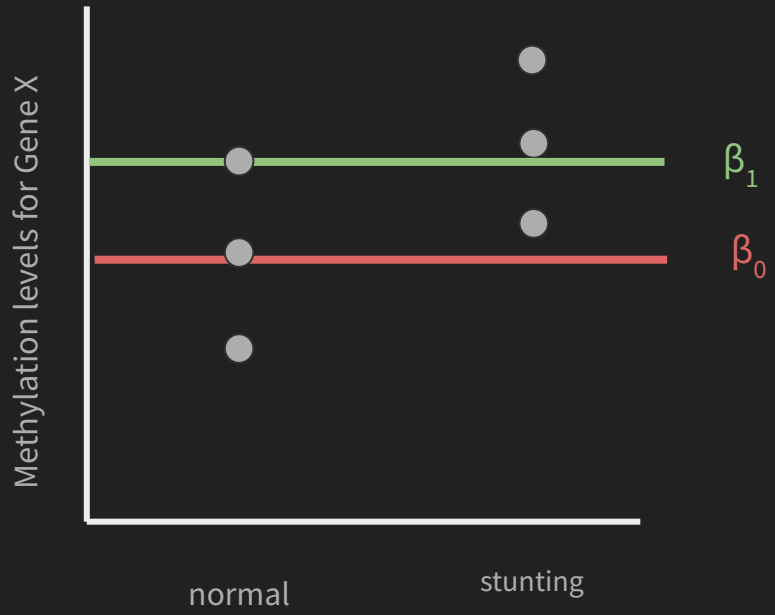
- For covariates, it is pretty straightforward, we can draw a straight line to the model that can describe the relationship



$$\text{Expression} = \beta_0 + \beta_1 \text{age}$$

Simple Linear Model

- For factors, there are two different types of model. The first one is the means model.



Means Model

Methylation levels = β_0 normal + β_1 stunting

Simple Linear Model

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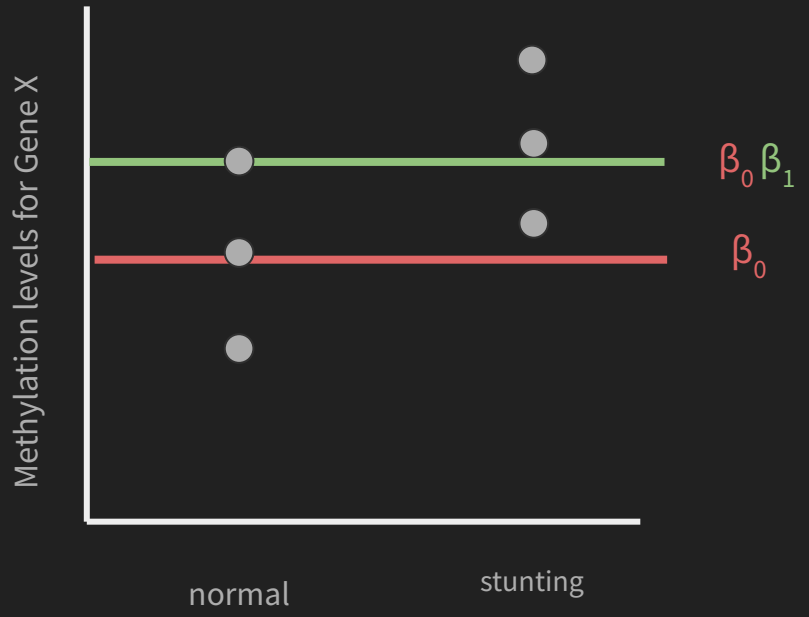

Means Reference Model

Methylation levels = β_0 + $\beta_1$stunting