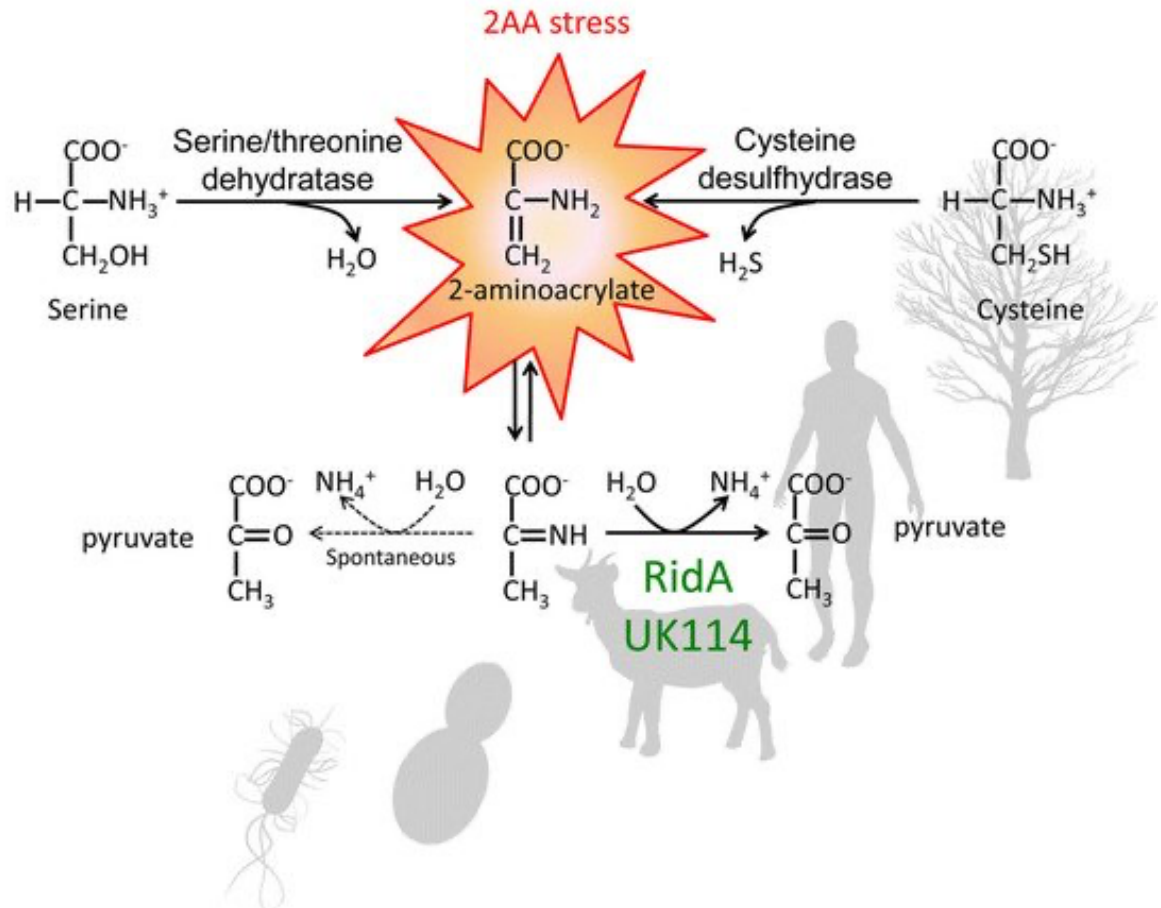# Amino Acid metabolism
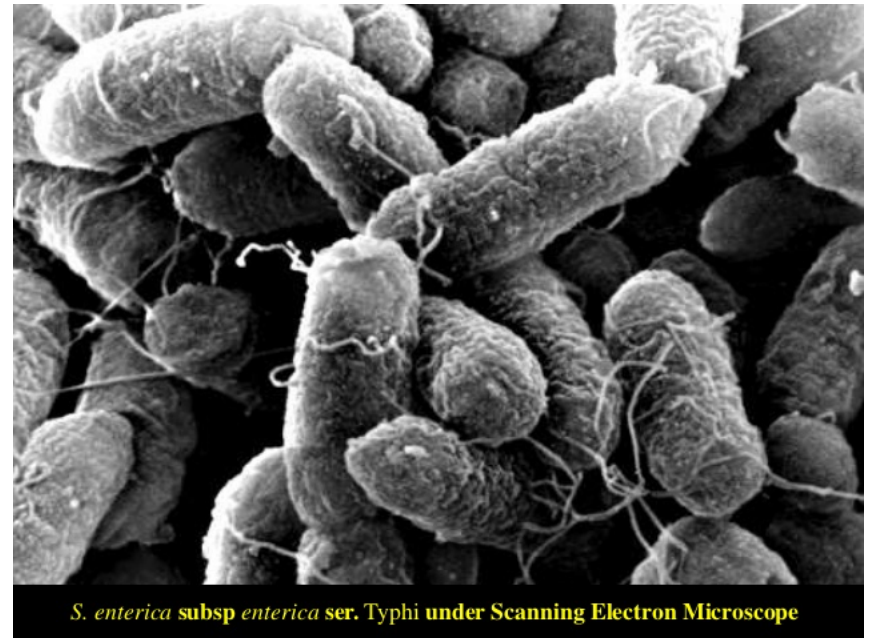
RidA catalyzes the hydrolytic deamination of enamine/imine intermediates

Present in all Domains of life

Salmonella enterica

S. enterica **subsp** *enterica* **ser.** Typhi **under Scanning Electron Microscope**

- **Gram(-) bacillus bacteria with several copies of RidA genes**

- **Has multiple RidA gene copies**

- **Does knocking out of RidA gene copies alter the metabolome?**
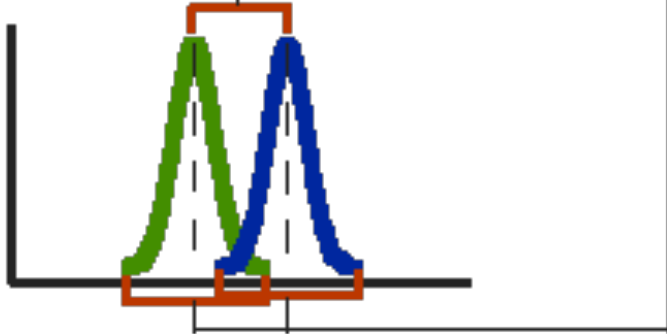- **Is it dose dependent?**

Ways to analyze the data

- T-test & volcano plots

- Principal component analysis

T Test

T Test

$$Y=MX+B$$

Metabolite X [conc.]

100%

0%
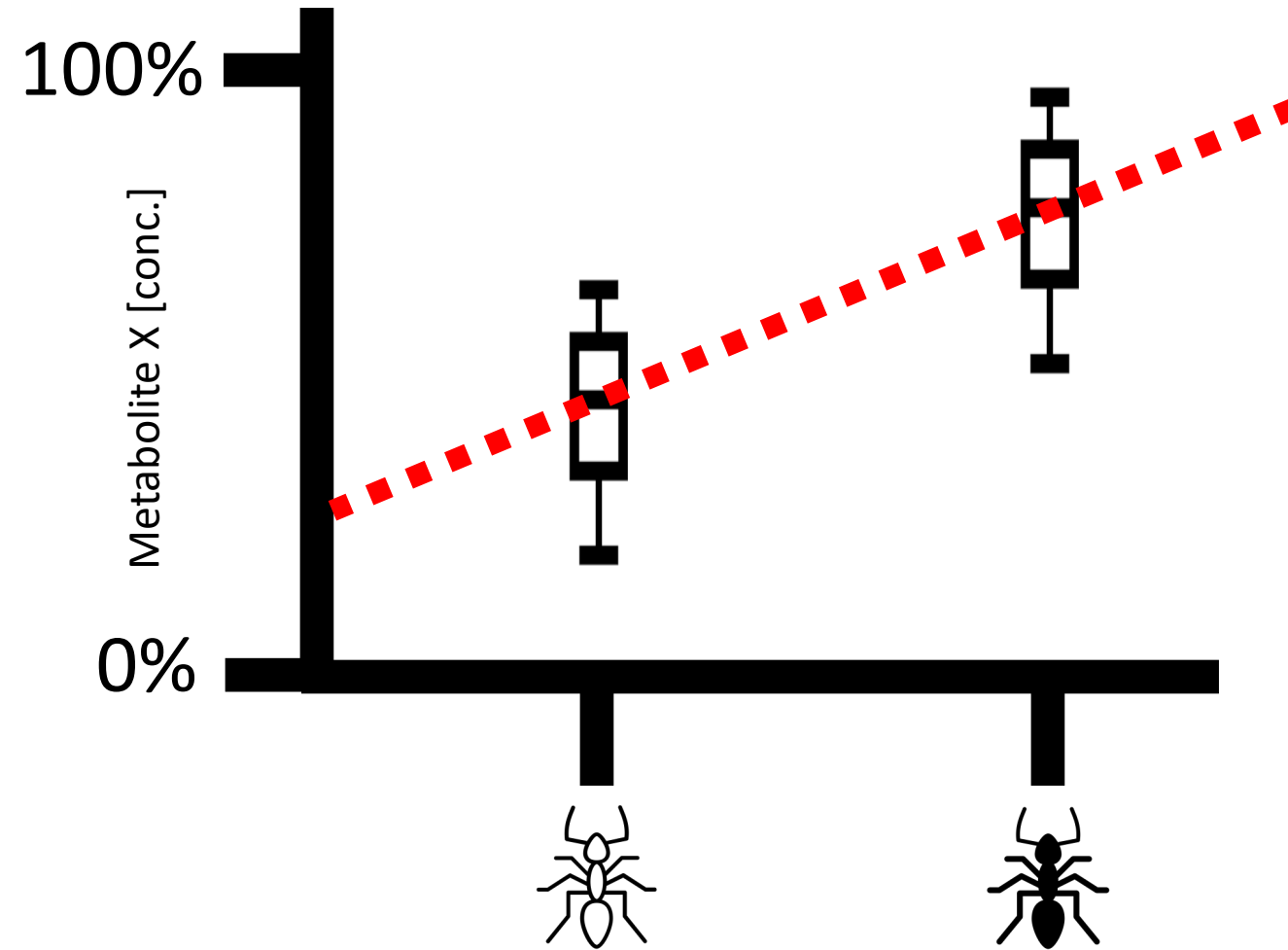
- Y is our phenotype

- X is our treatment coded as 0/1
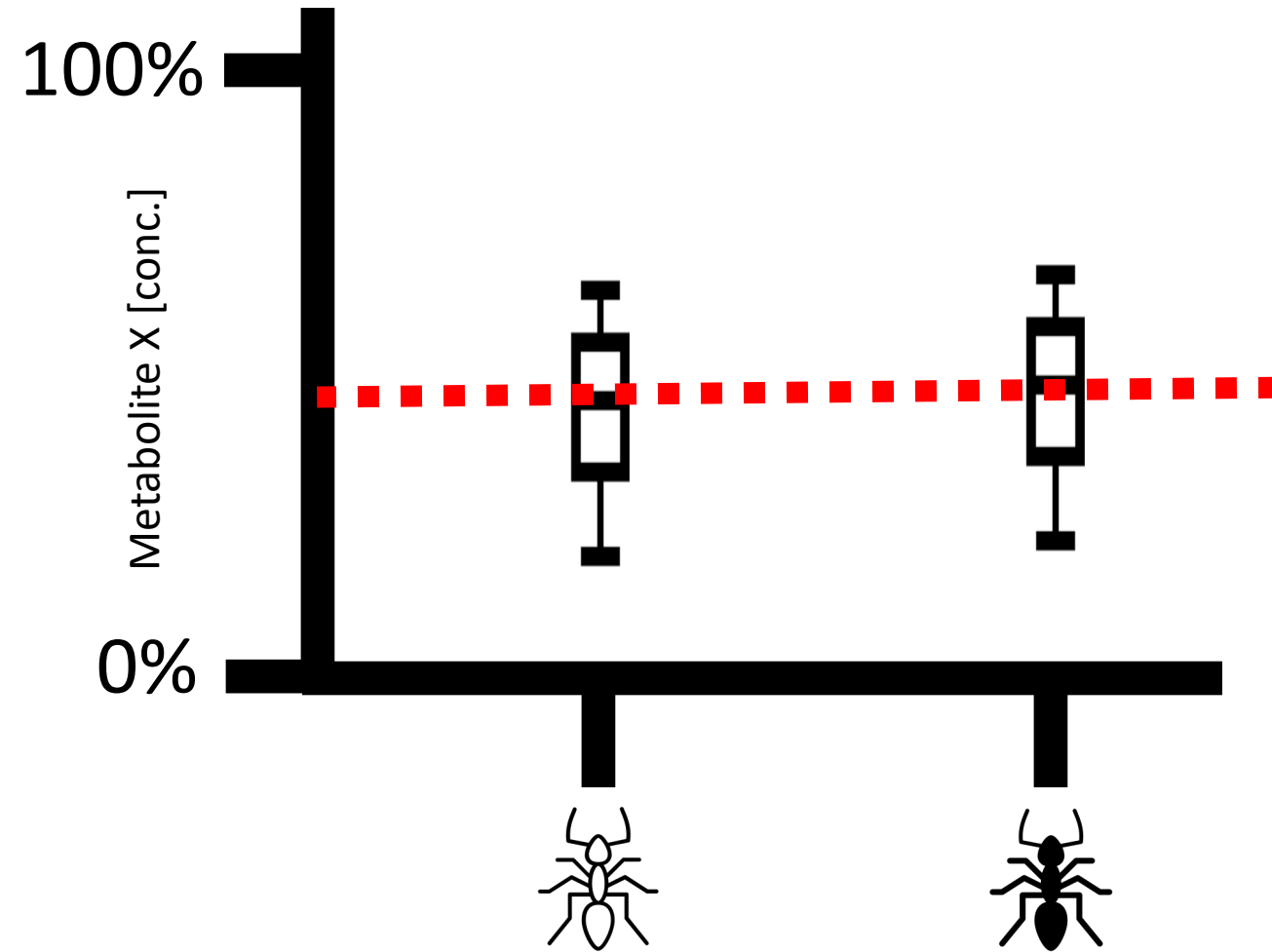
- B is intercept

- M is slope
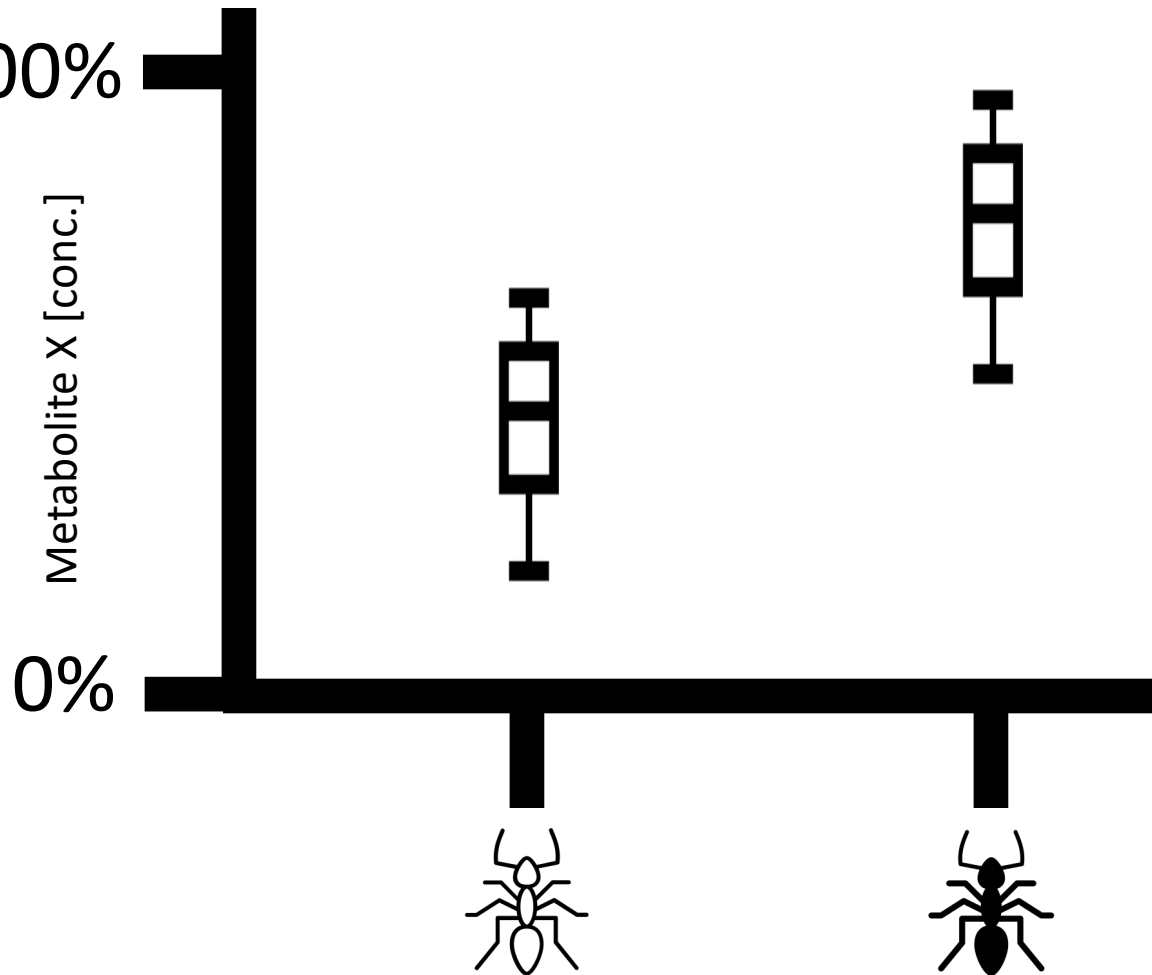
T Test

- Is the slope Nonzero?

- If yes, there is an effect

- If no, there is no effect

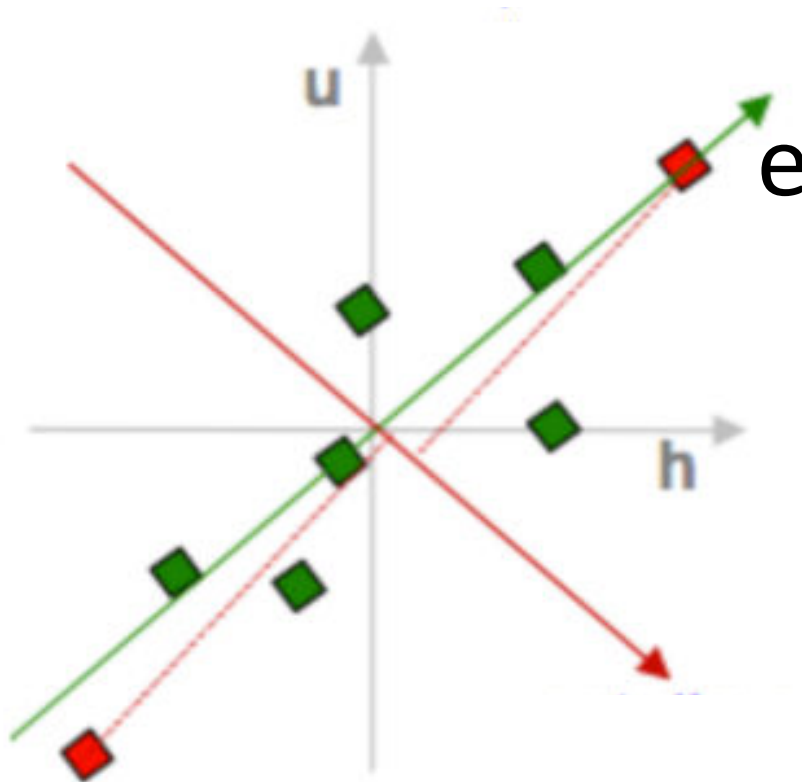# T Test

Principal Component Analyses

original data set

output from PCA
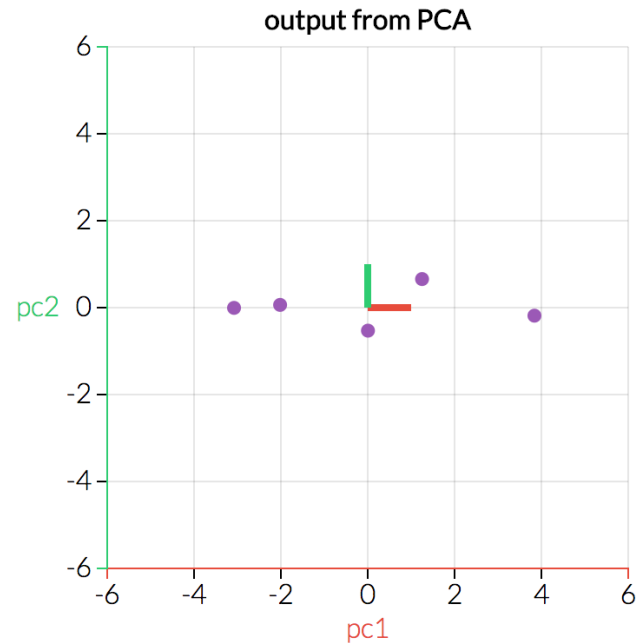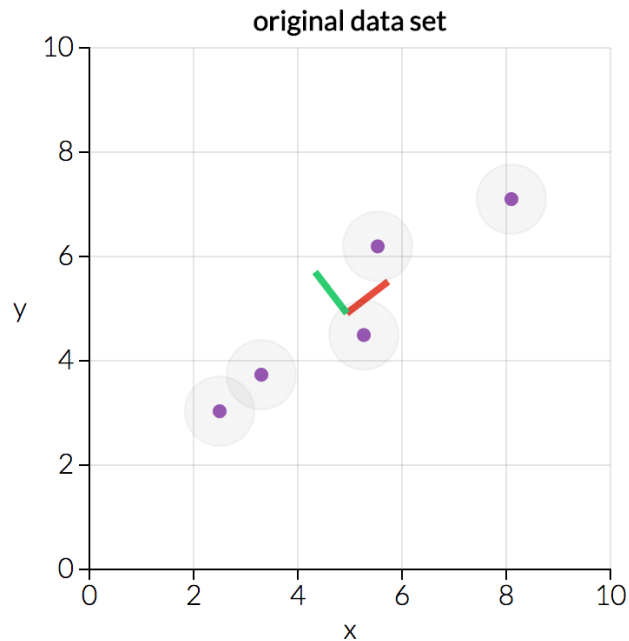
We start with correlated high dimensional data
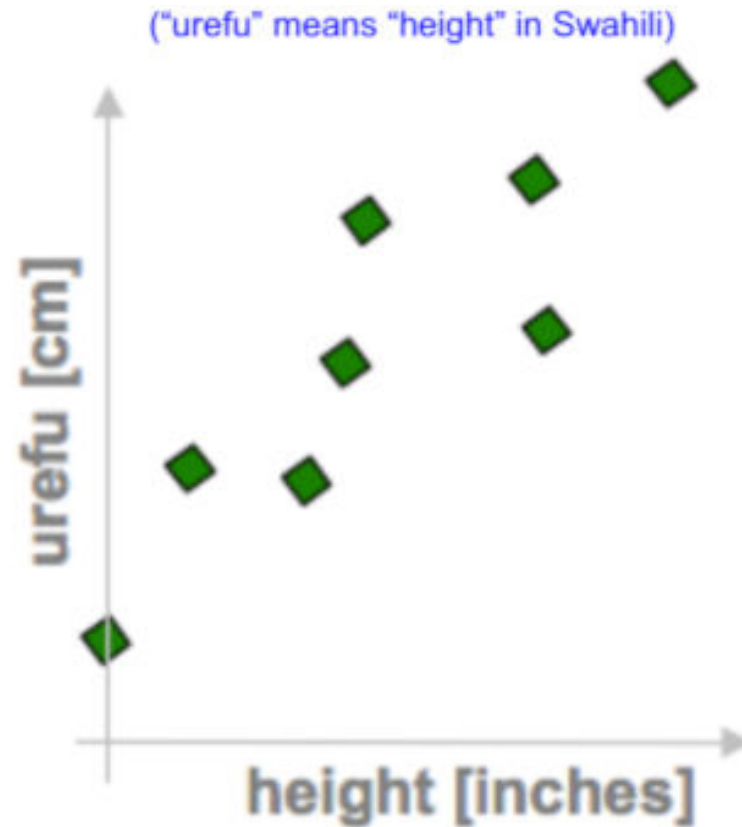
Center the points and identify line with highest variance
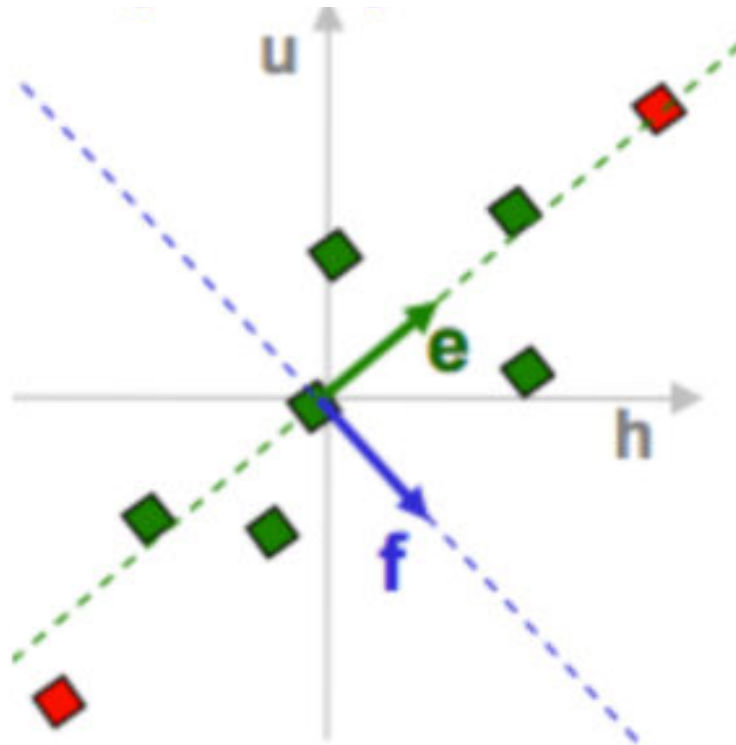
Compute the Covariance matrix

$$
\begin{array}{c}
\quad\quad h \quad\quad u \\
\begin{array}{c} h \\ u \end{array}
\begin{pmatrix} 2.0 & 0.8 \\ 0.8 & 0.6 \end{pmatrix}
\end{array}
\rightarrow \mathrm{cov}(h,u) = \frac{1}{n}\sum_{i=1}^{n} h_i u_i
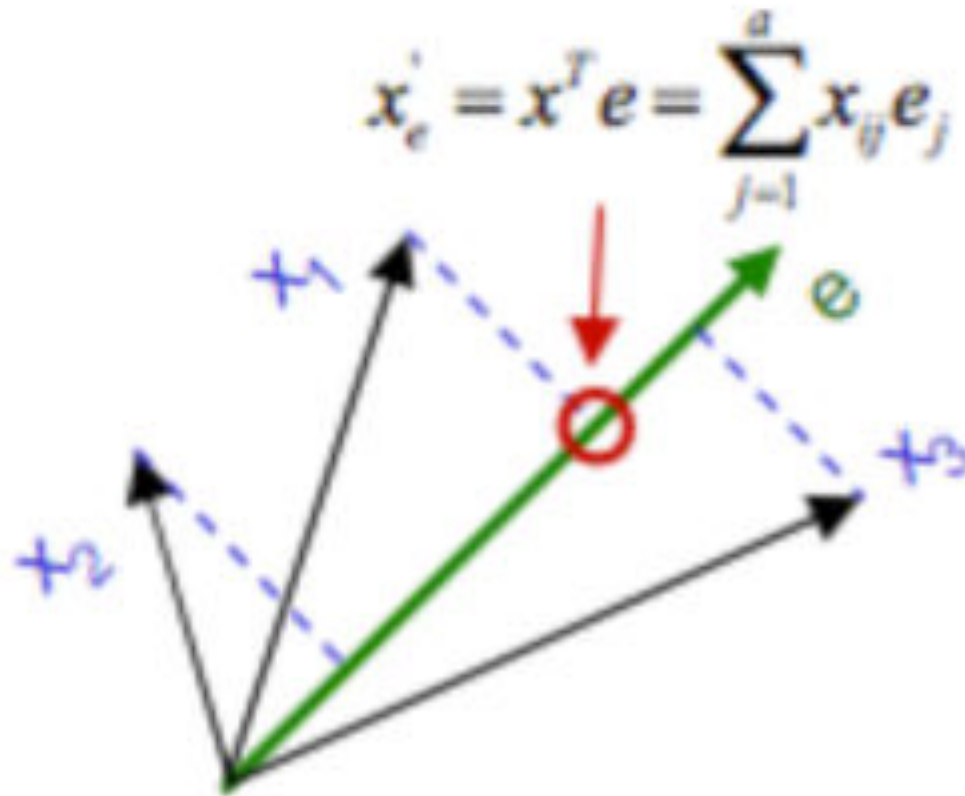$$

Calculate eigenvectors and eigenvalues

$$\begin{pmatrix} 2.0 & 0.8 \\ 0.8 & 0.6 \end{pmatrix} \begin{bmatrix} e_h \\ e_u \end{bmatrix} = \lambda_e \begin{bmatrix} e_h \\ e_u \end{bmatrix}$$

$$\begin{pmatrix} 2.0 & 0.8 \\ 0.8 & 0.6 \end{pmatrix} \begin{bmatrix} f_h \\ f_u \end{bmatrix} = \lambda_f \begin{bmatrix} f_h \\ f_u \end{bmatrix}$$
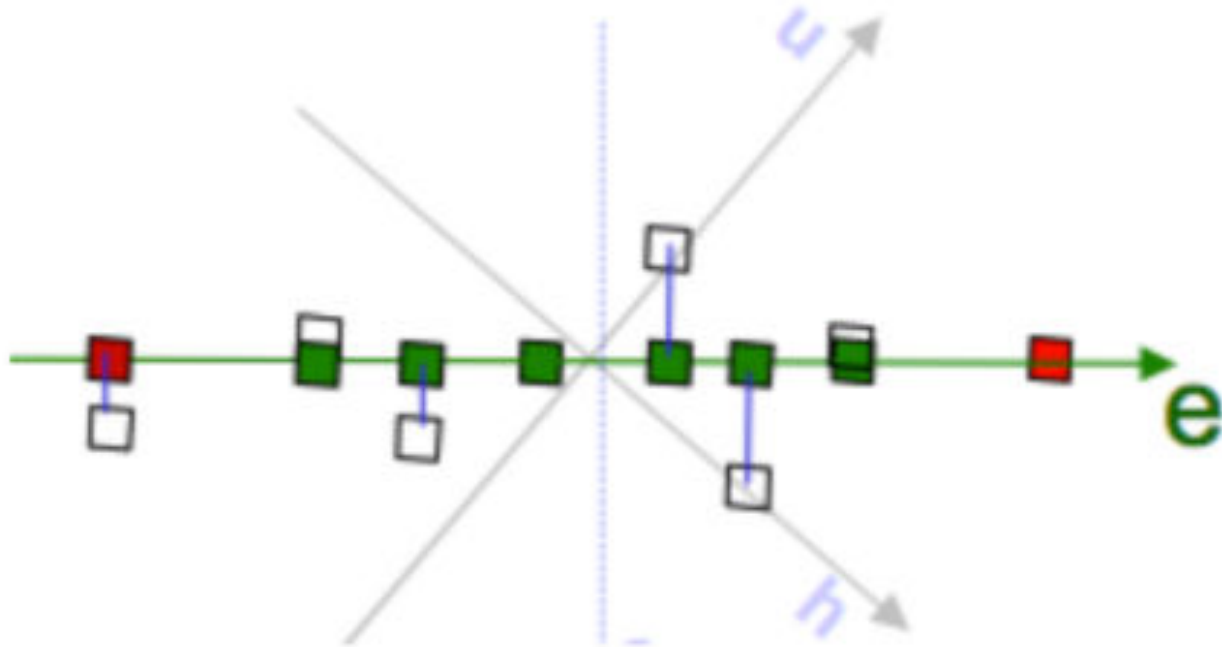
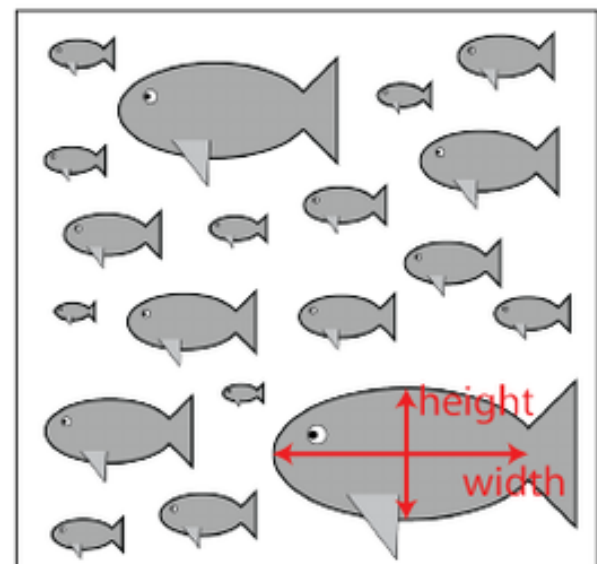# Pick a set of eigenvectors with highest eigenvalues
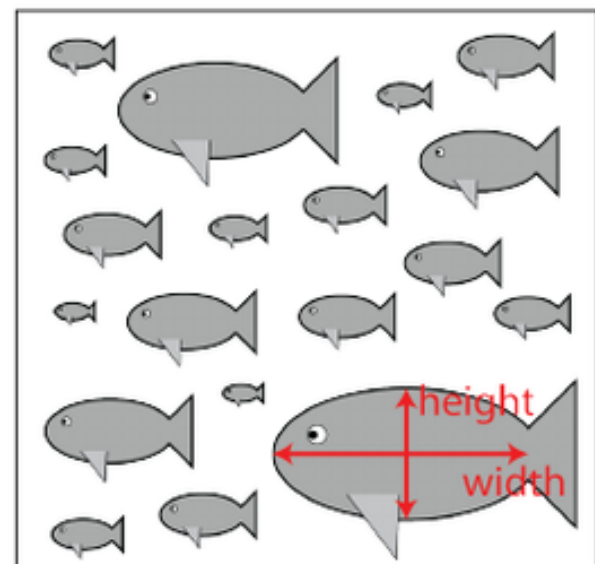
Project data points to eigenvectors

$$x_e^{'} = x^T e = \sum_{j=1}^{d} x_{ij} e_j$$

Finished!

A

A

B

height
width

height

width

first shape score

V