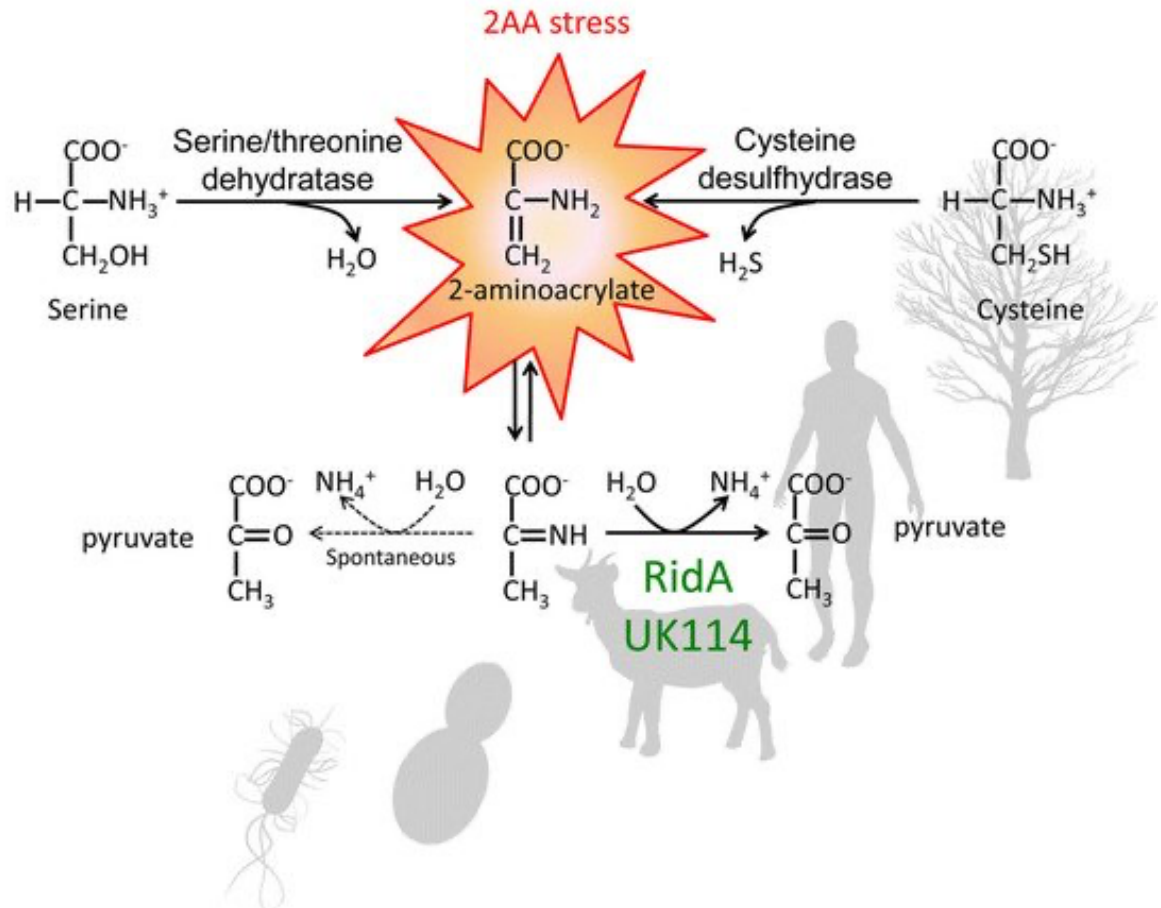


Amino Acid metabolism

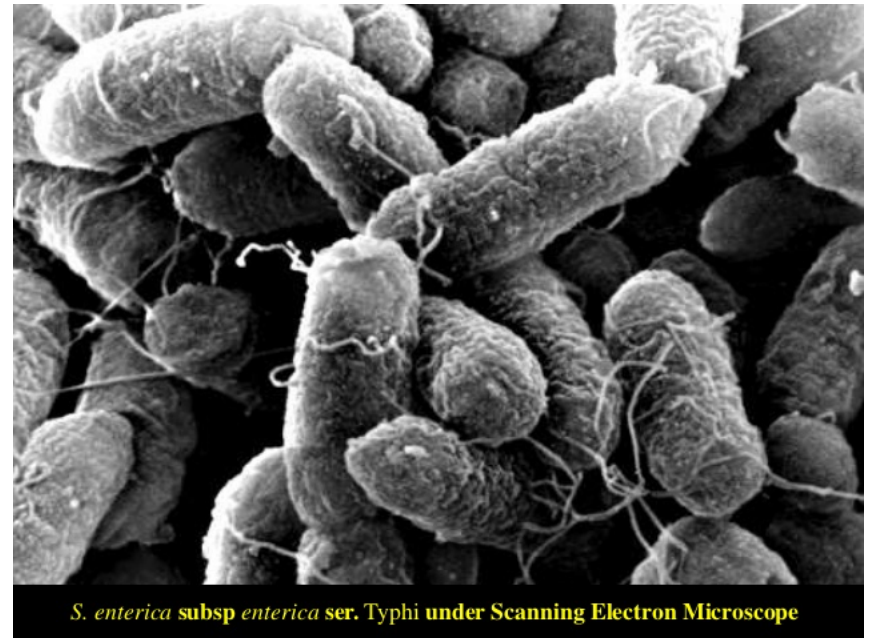
RidA catalyzes the hydrolytic deamination of enamine/imine intermediates

Present in all Domains of life



Salmonella enterica

- 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

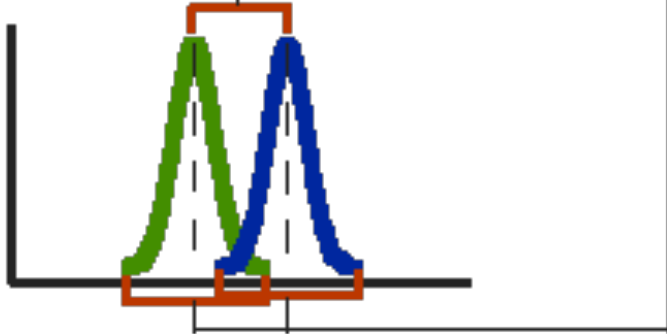
- T-test & volcano plots
- Principal component analysis

T Test

signal
noise = **difference between group means**
variability of groups

=
$$\frac{\bar{X}_T - \bar{X}_C}{SE(\bar{X}_T - \bar{X}_C)}$$

= **t-value**

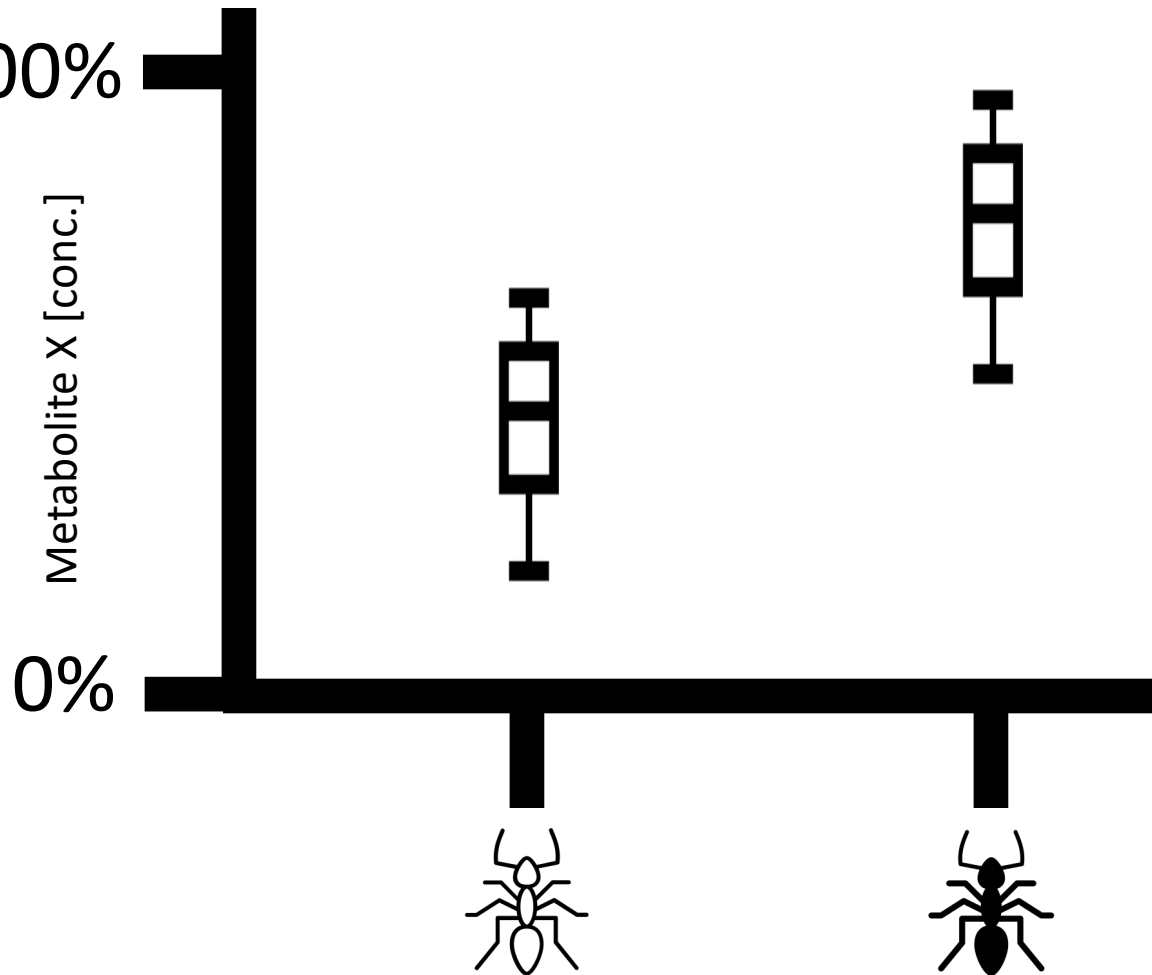


The diagram shows two overlapping normal distributions, one green and one blue, on a coordinate system. A horizontal bracket above the peaks of both distributions indicates the difference between their means. A vertical arrow points from this bracket to the 'difference between group means' part of the equation above. Another horizontal bracket below the x-axis, spanning the width of both distributions, indicates the variability of the groups. A vertical arrow points from this bracket to the 'variability of groups' part of the equation above.

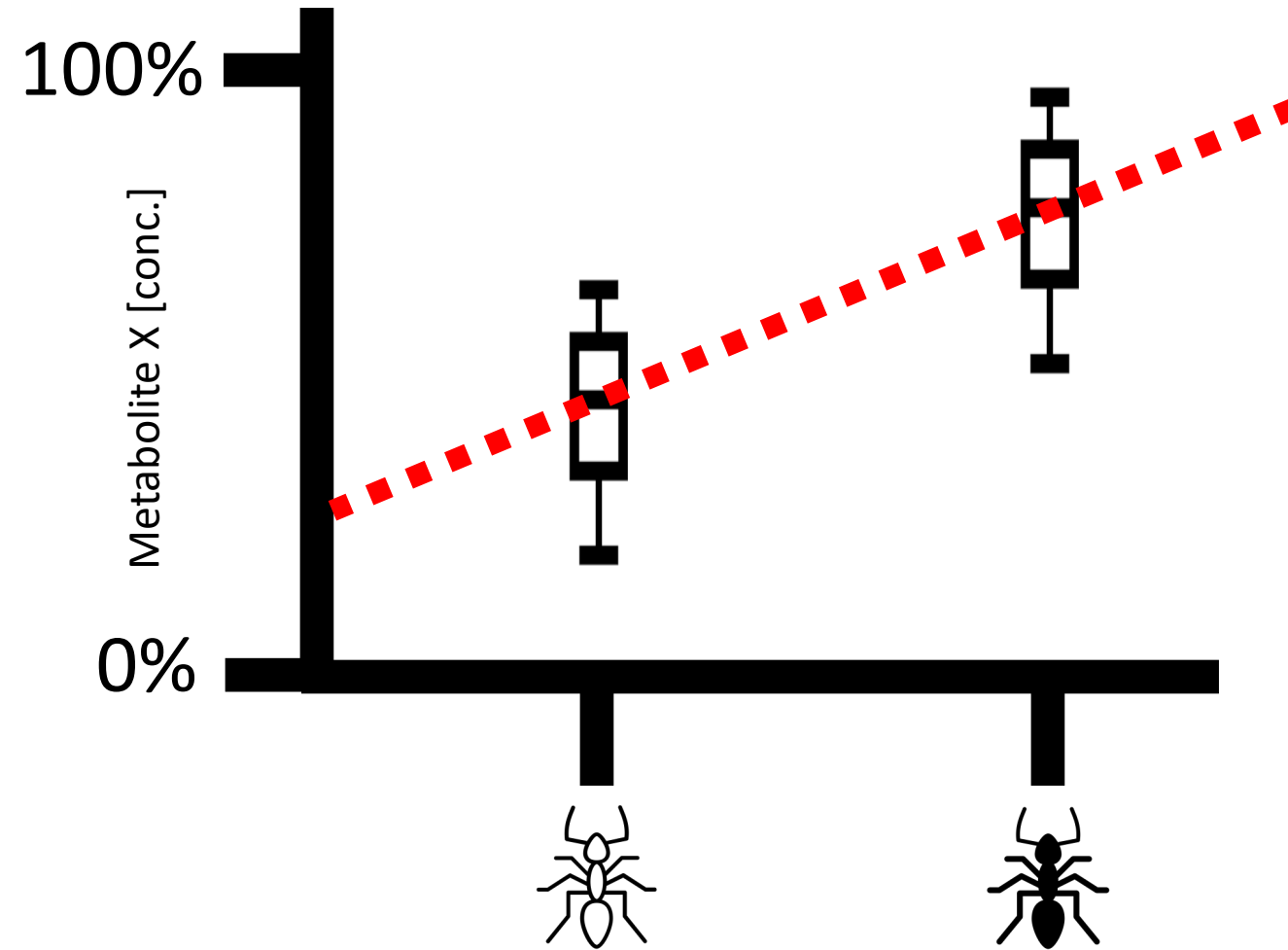
T Test

$$Y = MX + B$$

- Y is our phenotype
- X is our treatment coded as 0/1
- B is intercept
- M is slope

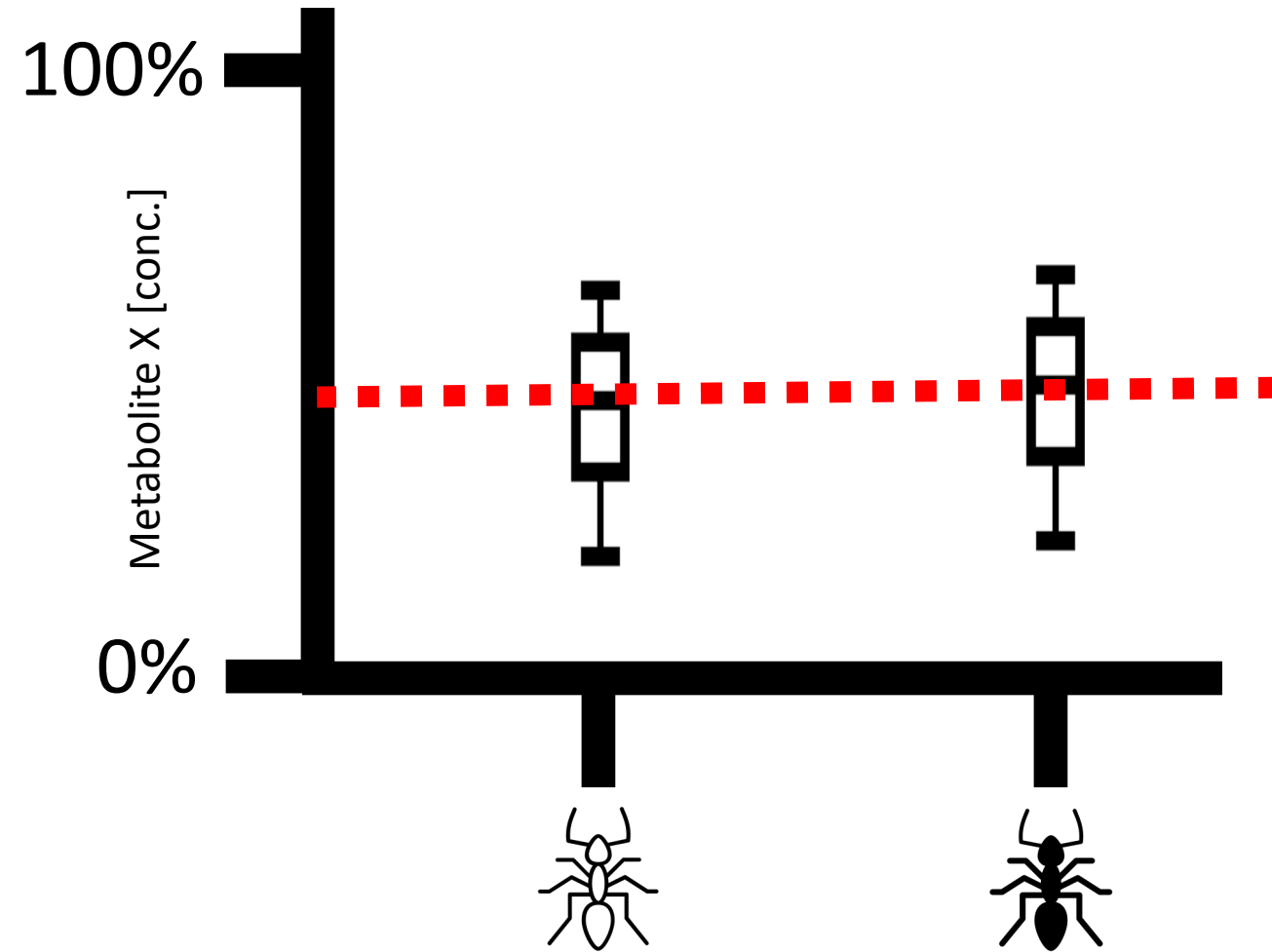


T Test



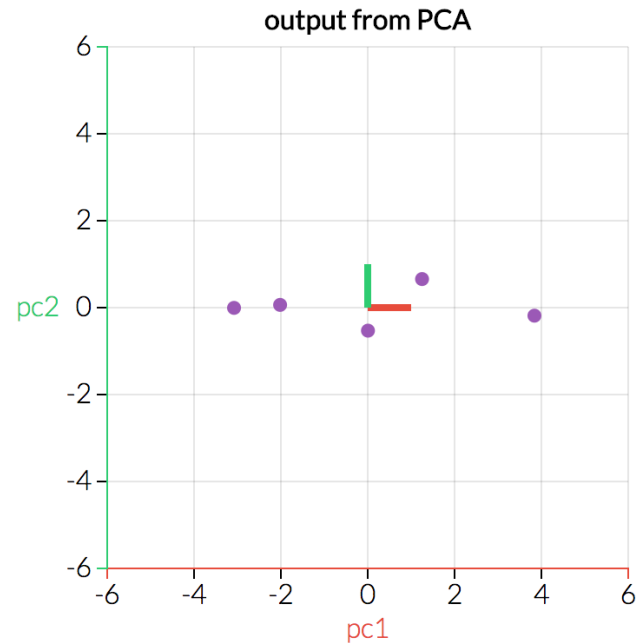
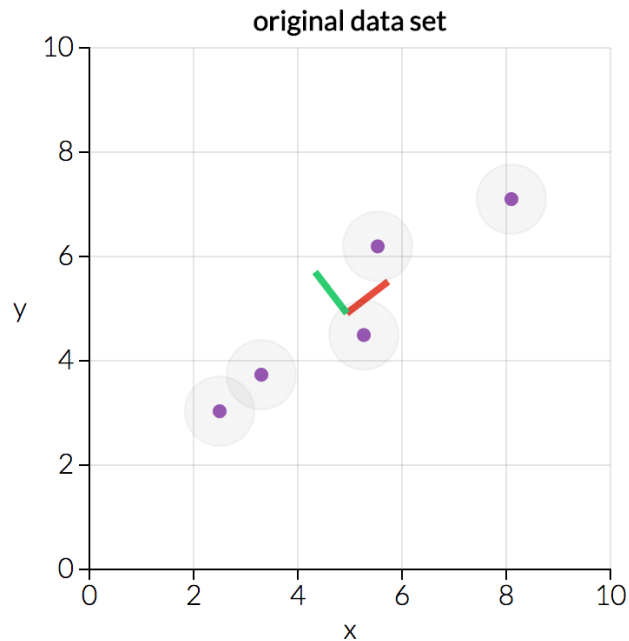
- Is the slope Nonzero?
- If yes, there is an effect
- If no, there is no effect

T Test

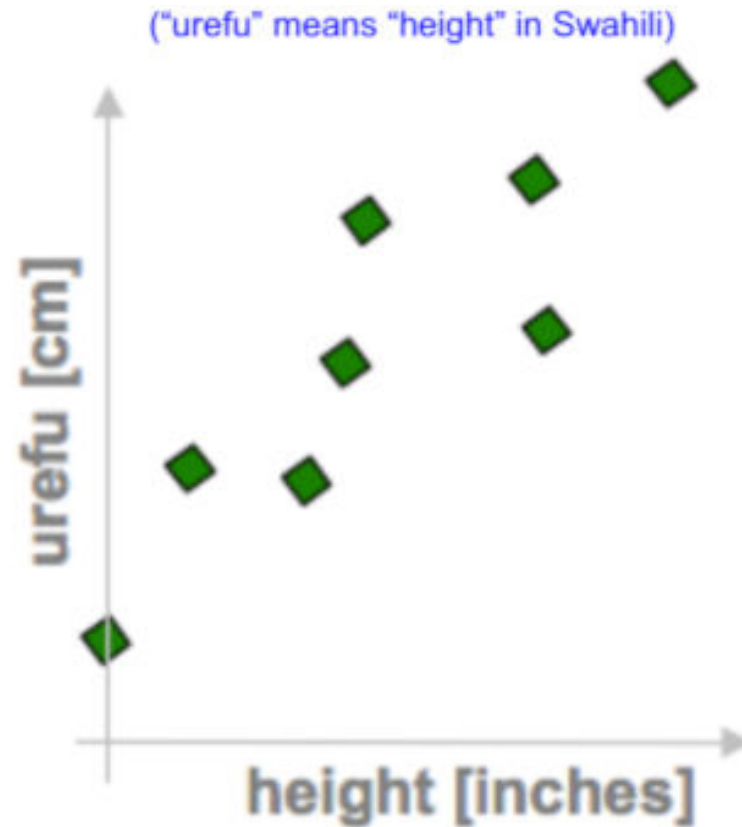


- Is the slope Nonzero?
- If yes, there is an effect
- If no, there is no effect

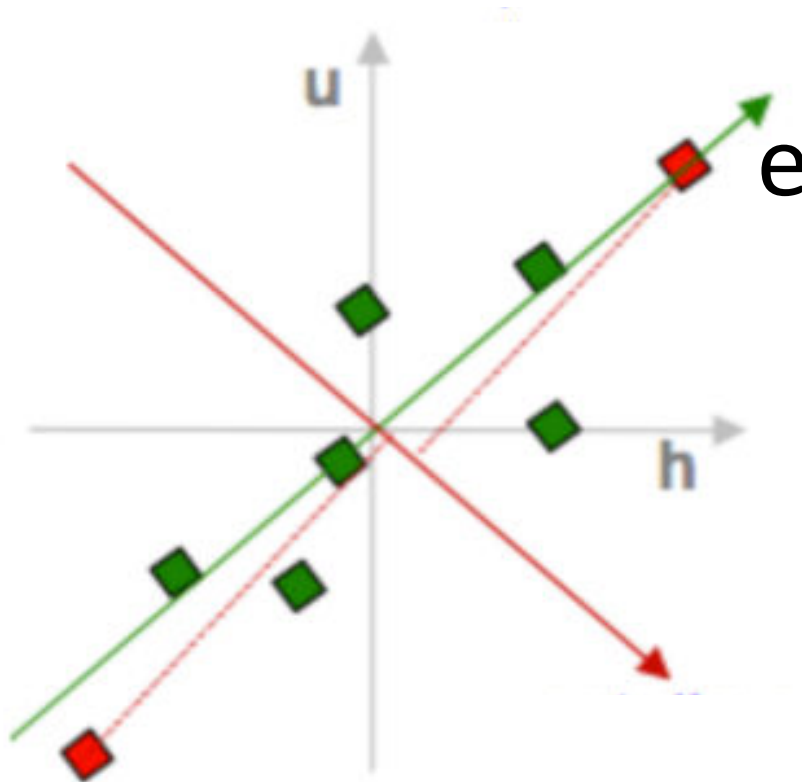
Principal Component Analyses



We start with correlated high dimensional data



Center the points and identify line
with highest variance



Compute the Covariance matrix

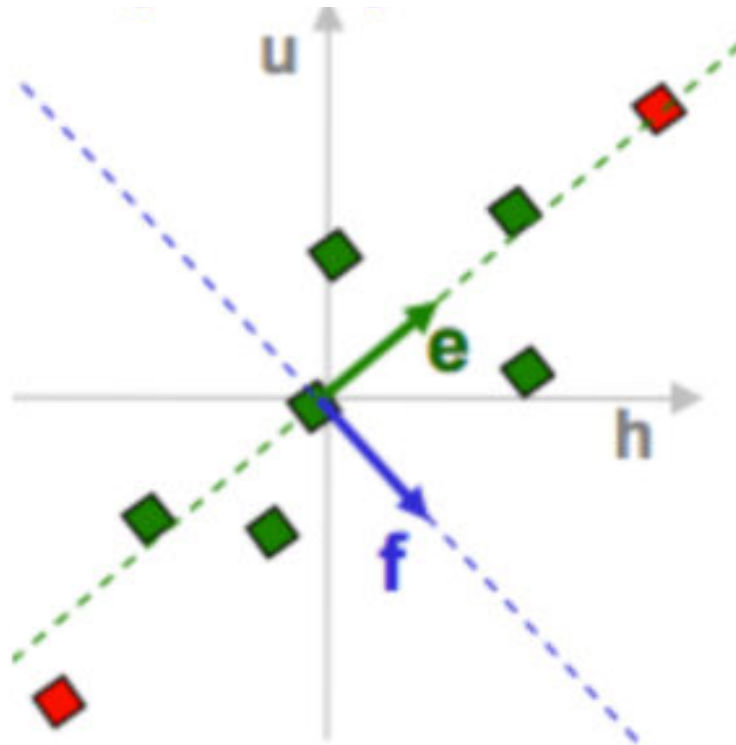
$$\begin{array}{cc} & \begin{matrix} h & u \end{matrix} \\ \begin{matrix} h \\ u \end{matrix} & \begin{pmatrix} 2.0 & 0.8 \\ 0.8 & 0.6 \end{pmatrix} \end{array} \rightarrow \text{cov}(h, u) = \frac{1}{n} \sum_{i=1}^n h_i u_i$$

Calculate eigenvectors and eigenvalues

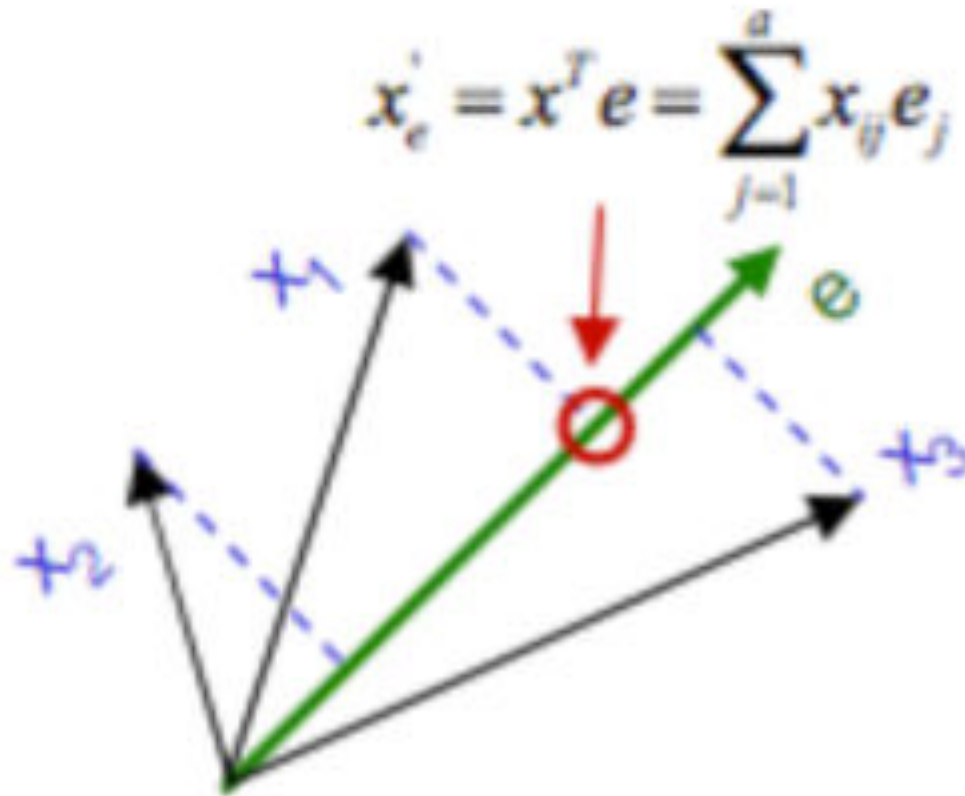
$$\begin{pmatrix} 2.0 & 0.8 \\ 0.8 & 0.6 \end{pmatrix} \begin{pmatrix} e_h \\ e_u \end{pmatrix} = \lambda_e \begin{pmatrix} e_h \\ e_u \end{pmatrix}$$

$$\begin{pmatrix} 2.0 & 0.8 \\ 0.8 & 0.6 \end{pmatrix} \begin{pmatrix} f_h \\ f_u \end{pmatrix} = \lambda_f \begin{pmatrix} f_h \\ f_u \end{pmatrix}$$

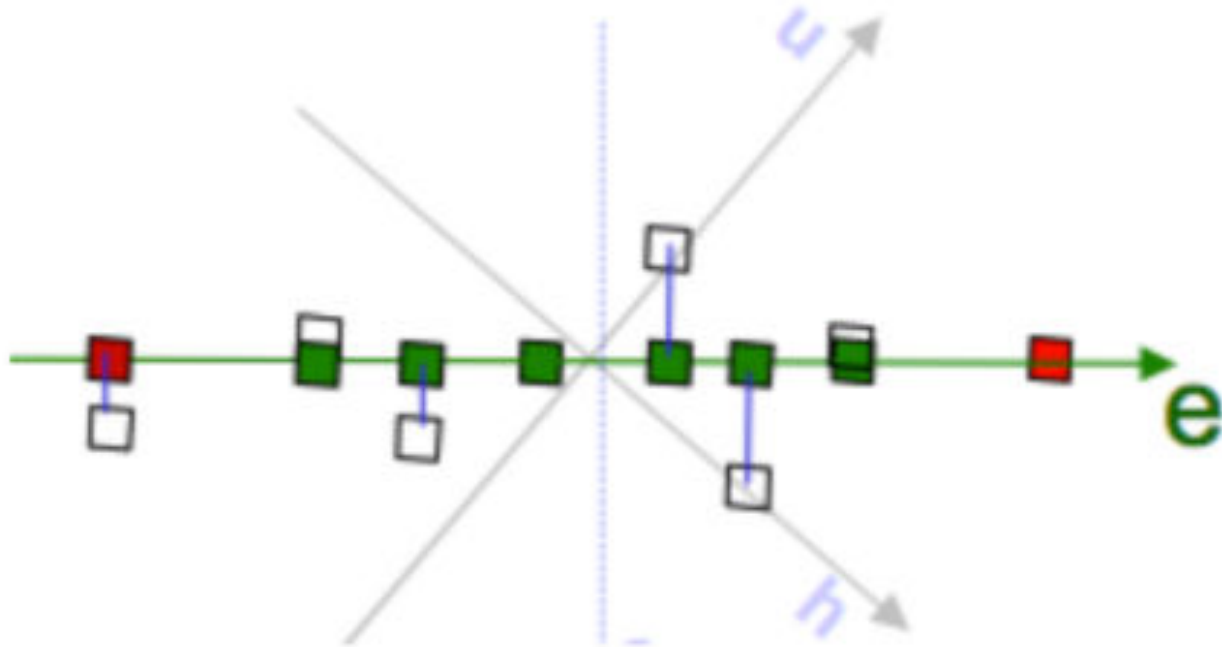
Pick a set of eigenvectors with highest eigenvalues



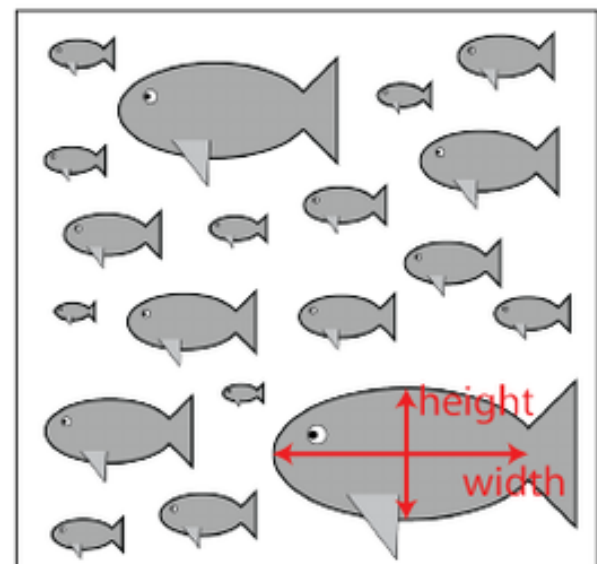
Project data points to eigenvectors



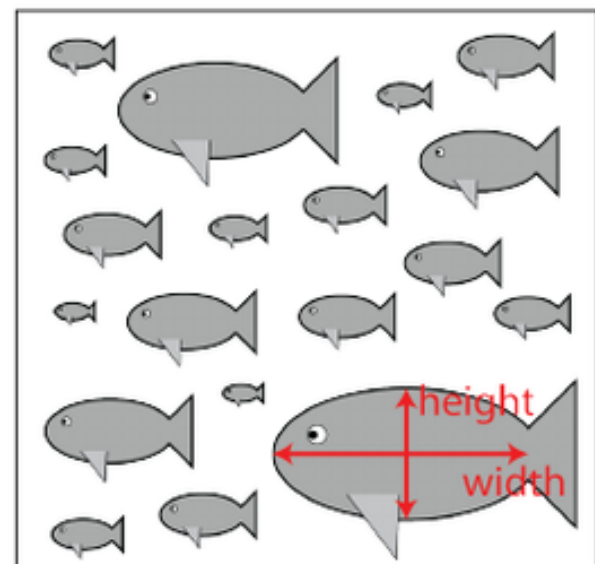
Finished!



A



A



B

