

SIB
Swiss Institute of
Bioinformatics

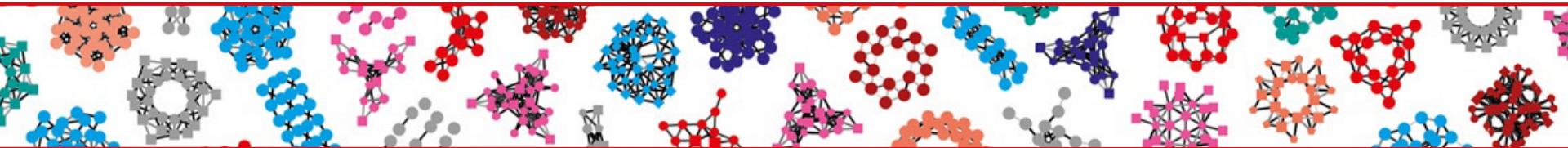
Dimensionality reduction

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Overview



01

- Principal Component Analysis

02

- Partial Least Squares

03

- Canonical Correlation Analysis

04

- Towards Nonlinearity

Questions in practice

- A real-estate agency wants to see the similarity/difference between its properties
 - Properties' characteristics: price, surface area, form, floors, bedrooms, bathrooms, entrances, garages, yards, etc.
 - Access to nearby facilities
 - Local living cost

- Patients need stratifying for clinical trials
 - Demographics
 - Lifestyle
 - Multi-omics patterns
 - etc.

What is PCA?

Several features (variables) to consider

- Relationships between features
- Risk of violation on assumptions of modeling
- Risk of overfitting the model to data

⇒ Reduce the dimension of the feature space

- *Feature selection*: find a subset of input features
- *Feature extraction*: project high-dimensional space into a space of fewer dimensions

PCA

Karl Pearson – mathematician & biostatistician (1901)

When is PCA used?

- Cannot identify features to eliminate
- Need *new* features independent of one another
- Accept that the *new* independent features are less interpretable

Y: n samples \times p features

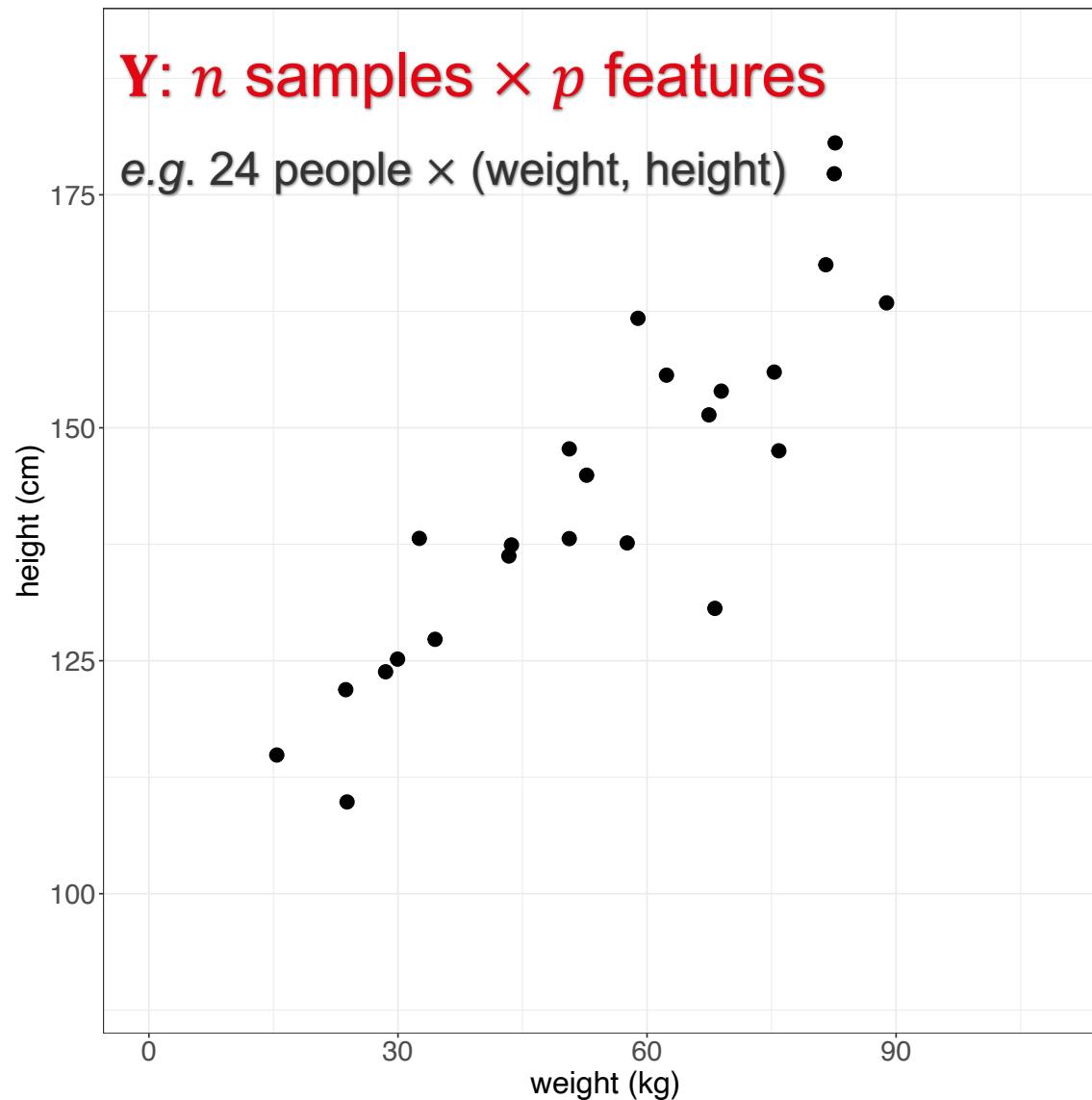
Samples

How are samples grouped together into subgroups by similarity?

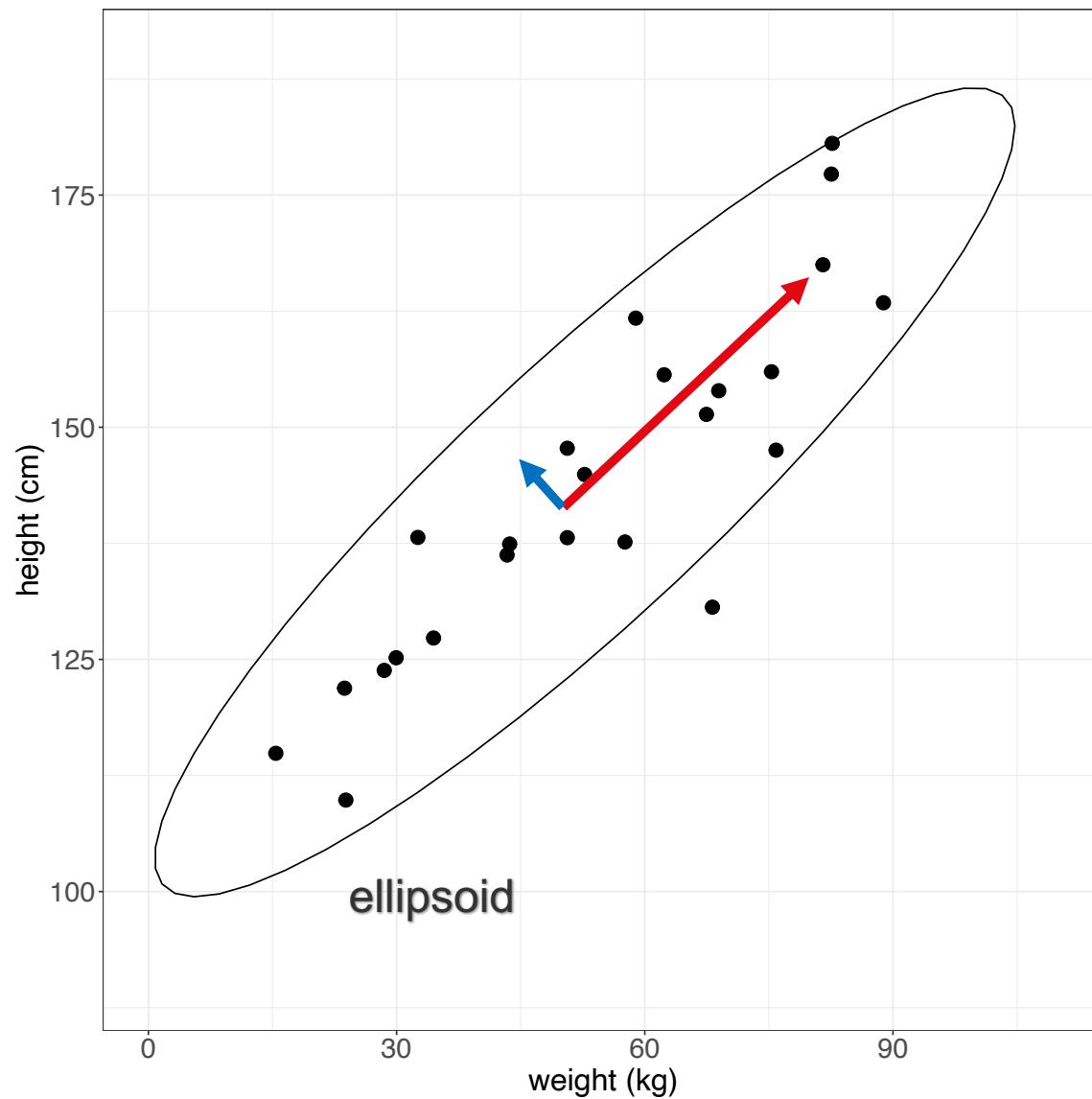
Features

What underlying factors influence the grouping?

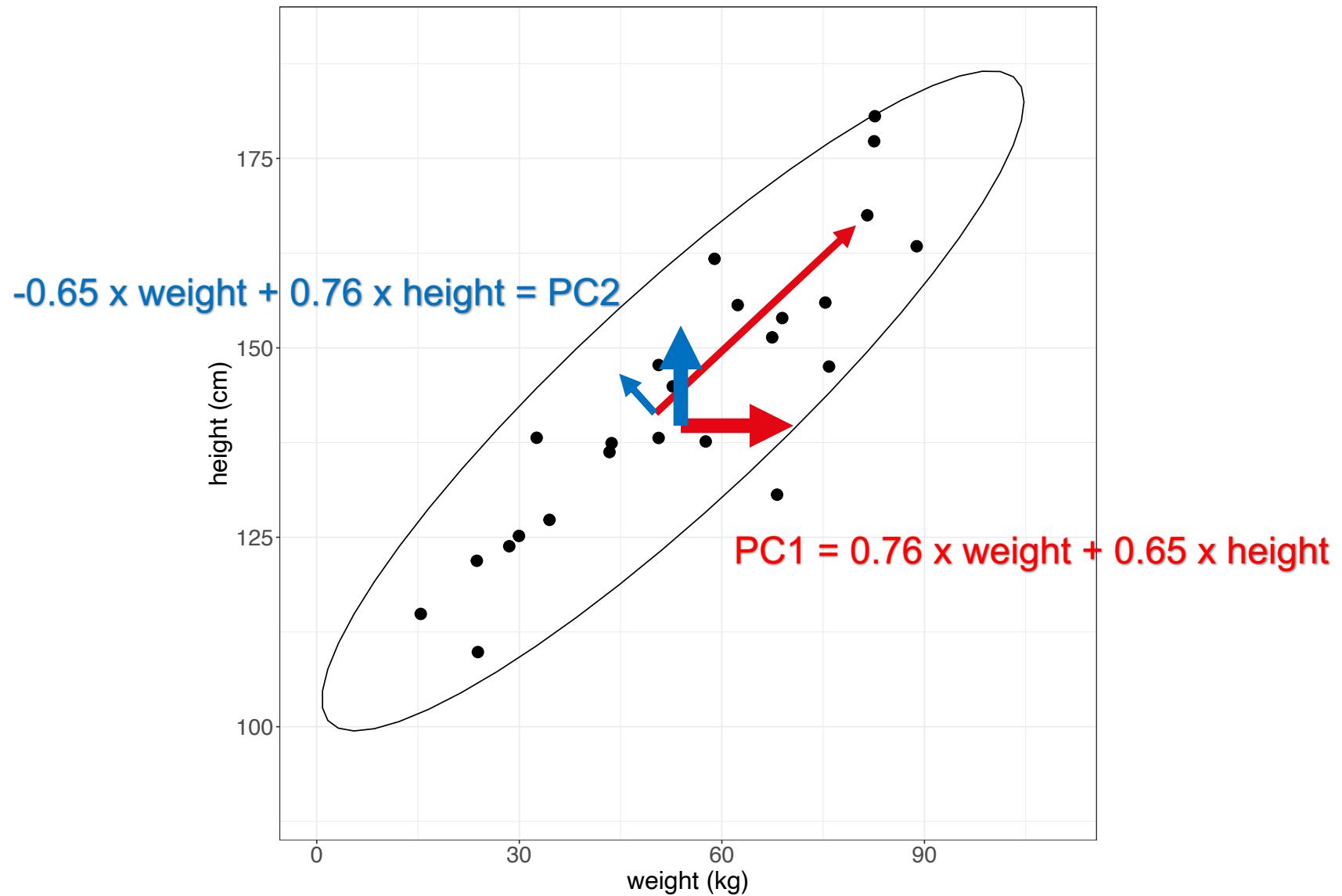
How does PCA work?



How does PCA work?



How does PCA work?



How does PCA work?

- $\mathbf{Y} = (Y_1 \ Y_2 \dots \ Y_p)$
- **REQUIRED:** cleaning
- **OPTIONAL:** normalizing
- **REQUIRED:** centering
$$\text{mean}(Y_i) = 0$$
- **RECOMMENDED:** scaling (after centering)
$$\text{var}(Y_i) = 1$$

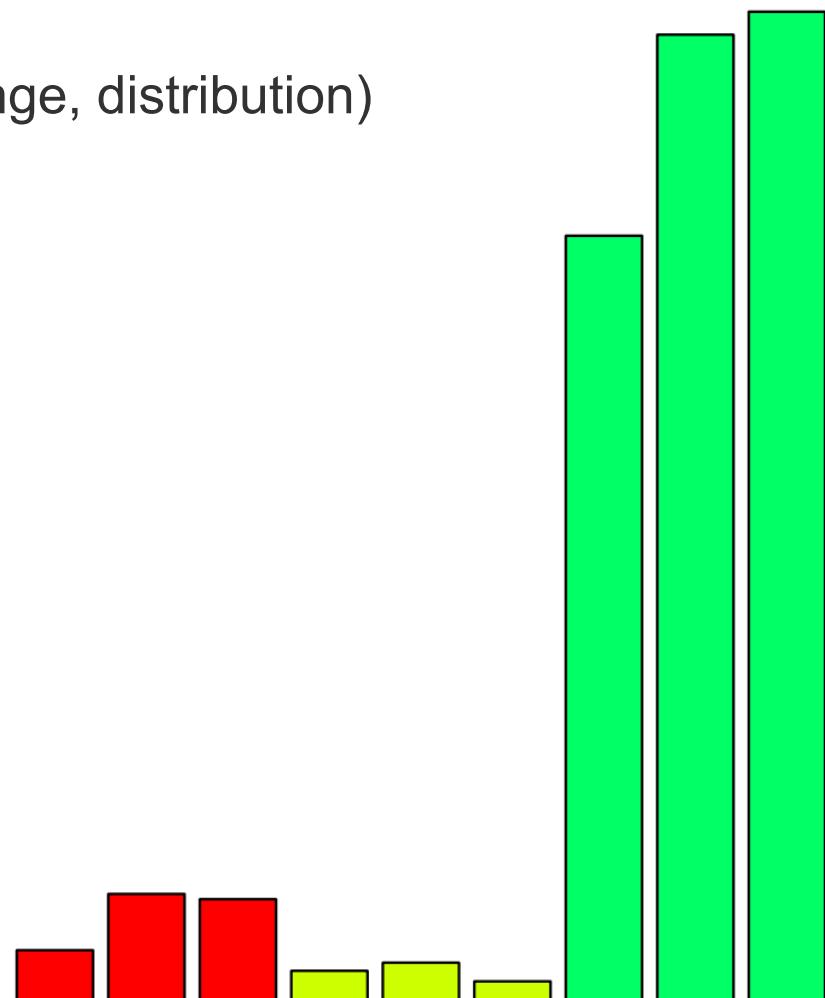
Data cleaning

GARBAGE IN, GARBAGE OUT

- Missing values: biologically or technically unidentified
⇒ *removal, imputation*
- Inconsistent data: qualitative, ill-formatted data
⇒ *reformatting, correction*
- Outlier and noisy data
⇒ *removal*
- Redundancy
⇒ *removal*

Data normalization

- Account for biases (technical variation) from sample handling to instrumentation difference
- Make samples more comparable (range, distribution)
- Various normalization techniques



Data centering

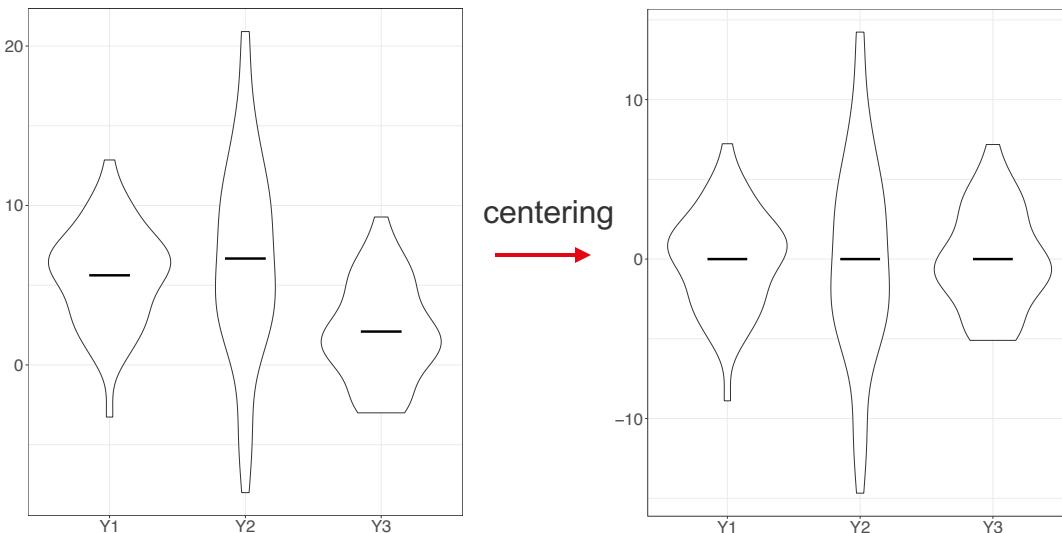
Each variable fluctuates around zero instead of its mean value

WHY: Offsets complicate models with more parameters, introduce algorithmic problems

HOW: For each variable

- Compute its mean
- Subtract the mean from all its values

$$\text{mean}(Y_i) = 0$$



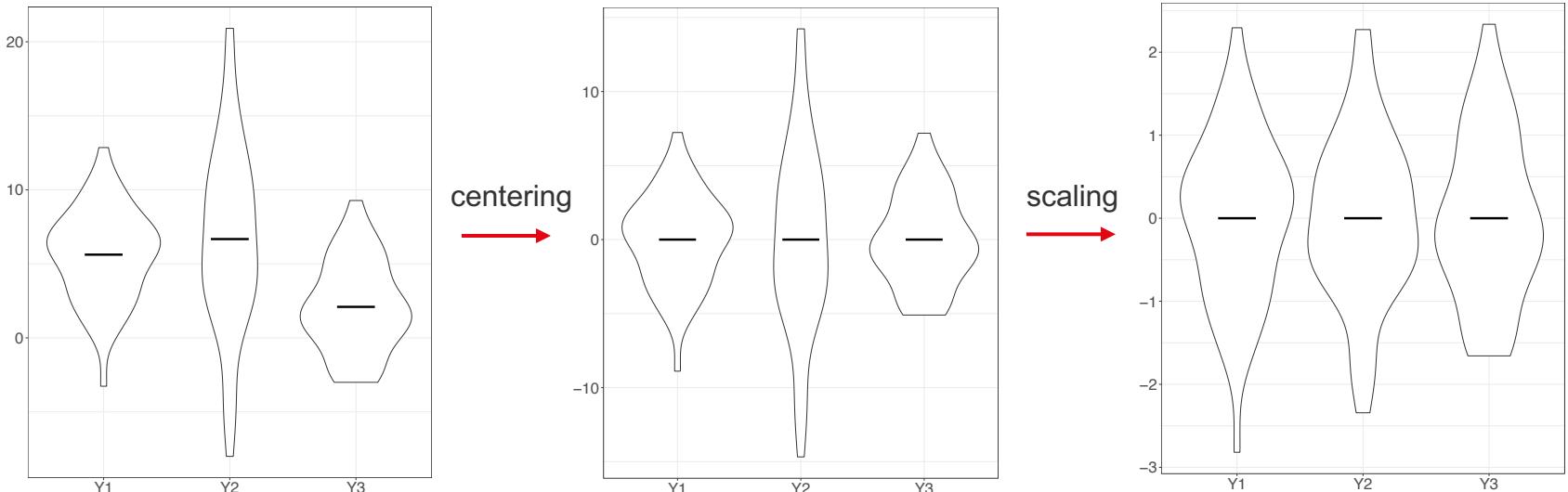
Data scaling

All variables are allocated an equivalent importance.

WHY: Variables with higher variances dominate those of lower variances

HOW: For each centered variable, divide all variables centered values by the scaling factor

- Unit variance scaling: standard deviation $\text{var}(Y_i) = 1$
- Pareto scaling: square root of standard deviation



Principal component

Coordinate change: $(Y_1 \ Y_2 \dots \ Y_p) \rightarrow (Z_1 \ Z_2 \dots \ Z_p)$

Linear combination:

$$Z_1 = w_{11}Y_1 + w_{12}Y_2 + \dots + w_{1p}Y_p$$

$$Z_2 = w_{21}Y_1 + w_{22}Y_2 + \dots + w_{2p}Y_p$$

...

$$Z_p = w_{p1}Y_1 + w_{p2}Y_2 + \dots + w_{pp}Y_p$$

$$\mathbf{Z}_1 = 0.8 \ Y_1 + 0.1 \ Y_2 + \dots + 0.001 \ Y_p$$

Latent variables

Principal component 1

Coordinate change: $(Y_1 \ Y_2 \dots \ Y_p) \rightarrow (Z_1 \ Z_2 \dots \ Z_p)$

Linear combination:

$$Z_1 = w_{11}Y_1 + w_{12}Y_2 + \dots + w_{1p}Y_p = \mathbf{Y}\mathbf{w}_1$$

=> projection of \mathbf{Y} onto vector \mathbf{w}_1

Find \mathbf{w}_1 ($\|\mathbf{w}_1\| = \mathbf{w}_1^T \mathbf{w}_1 = 1$) to maximize:

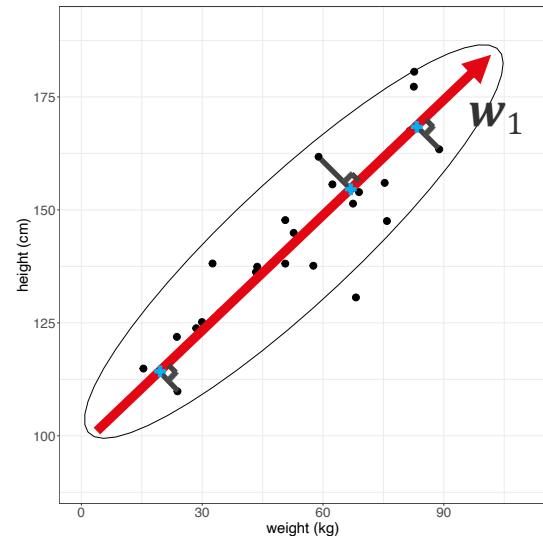
$$\text{var}(Z_1) = \mathbf{w}_1^T \text{cov}(\mathbf{Y}) \mathbf{w}_1$$

Variance-covariance matrix

$$\text{cov}(\mathbf{Y}) = \begin{pmatrix} \text{cov}(Y_1, Y_1) & \cdots & \text{cov}(Y_1, Y_p) \\ \vdots & \ddots & \vdots \\ \text{cov}(Y_p, Y_1) & \cdots & \text{cov}(Y_p, Y_p) \end{pmatrix}$$

Solution: $\max \text{var}(Z_1) = \max \text{eigenvalue of } \text{cov}(\mathbf{Y})$
at $\mathbf{w}_1 = \text{corresponding eigenvector}$

Hint: Lagrange multiplier + derivative



Principal component 2

Coordinate change: $(Y_1 \ Y_2 \dots \ Y_p) \rightarrow (Z_1 \ Z_2 \dots \ Z_p)$

Linear combination:

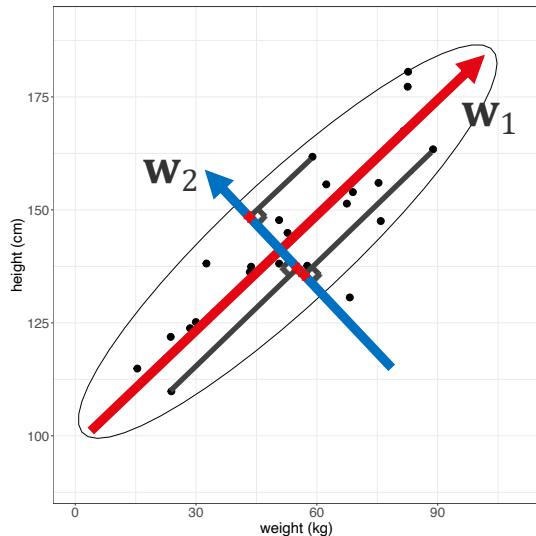
$$Z_2 = w_{21}Y_1 + w_{22}Y_2 + \dots + w_{2p}Y_p = \mathbf{Y}\mathbf{w}_2$$

=> projection of \mathbf{Y} onto vector \mathbf{w}_2

$\mathbf{w}_2 \perp \mathbf{w}_1$: independent projection

Find \mathbf{w}_2 ($\|\mathbf{w}_2\| = \mathbf{w}_2^T \mathbf{w}_2 = 1$ and $\mathbf{w}_2^T \mathbf{w}_1 = 0$) to maximize:

$$\text{var}(Z_2) = \mathbf{w}_2^T \text{cov}(\mathbf{Y}) \mathbf{w}_2$$



Solution: $\max \text{var}(Z_2) = 2^{\text{nd}}$ max eigenvalue of $\text{cov}(\mathbf{Y})$
at \mathbf{w}_2 = corresponding eigenvector

and so on

PCA implementation

\mathbf{Y} : n samples \times p features

Input: \mathbf{Y} or $\text{cov}(\mathbf{Y})$

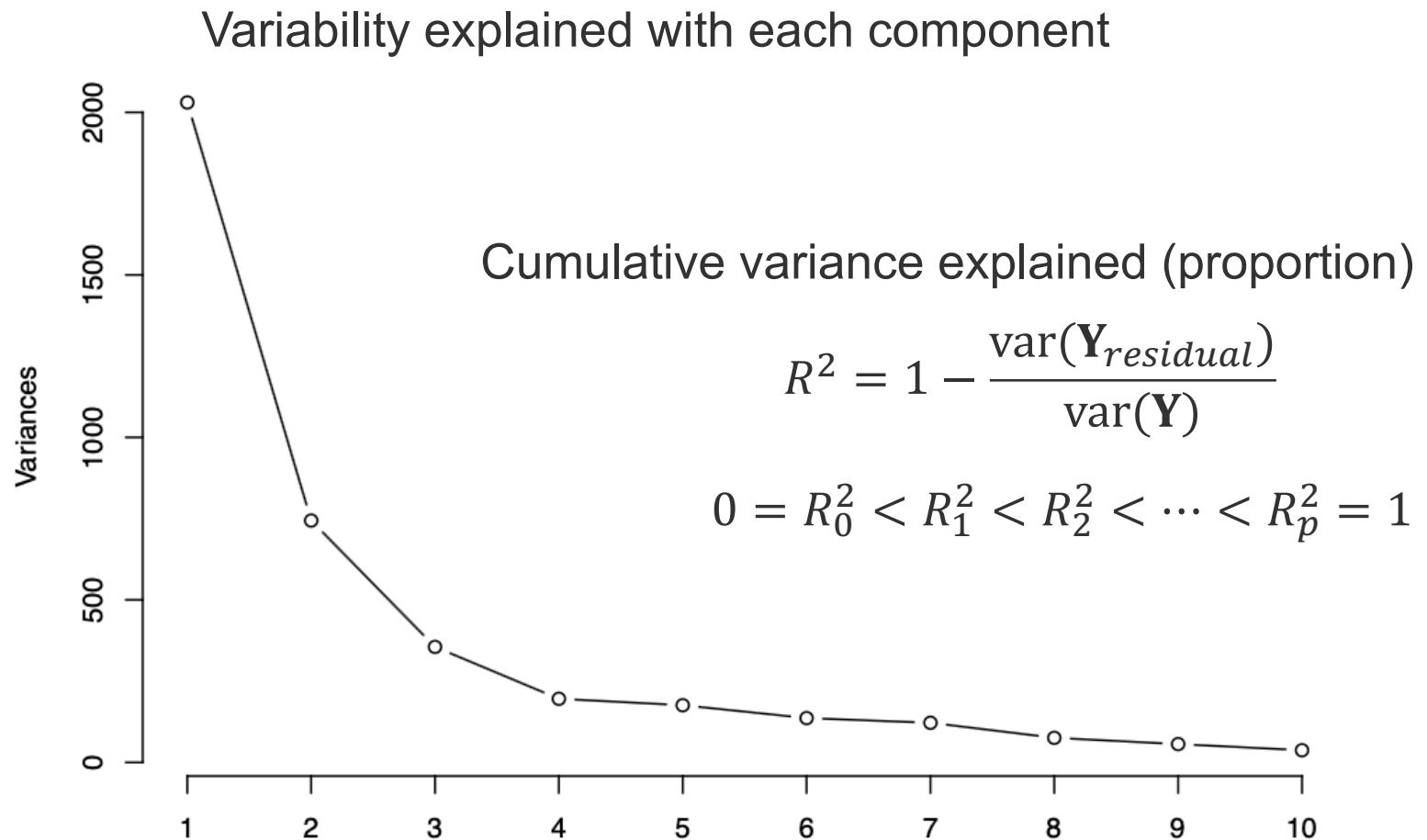
Output:

- sdev: square root of eigenvalues of $\text{cov}(\mathbf{Y})$
- scores: $(\mathbf{Z}_1 \ \mathbf{Z}_2 \ \dots \ \mathbf{Z}_p)$
- loadings/rotation: $(\mathbf{w}_1 \ \mathbf{w}_2 \ \dots \ \mathbf{w}_p)$

Why does PCA work? Why should PCA be used?

- Covariance matrix: relation between features
- Eigenvectors of covariance matrix: directions of dispersion
- Eigenvalues of covariance matrix: importance of directions
- Assumption: variability \sim signal
- Application: data exploration, visualization of underlying patterns within correlated data sets, decorrelation, detection of outliers, data compression

PCA: which number of principal components?



PCA score plot

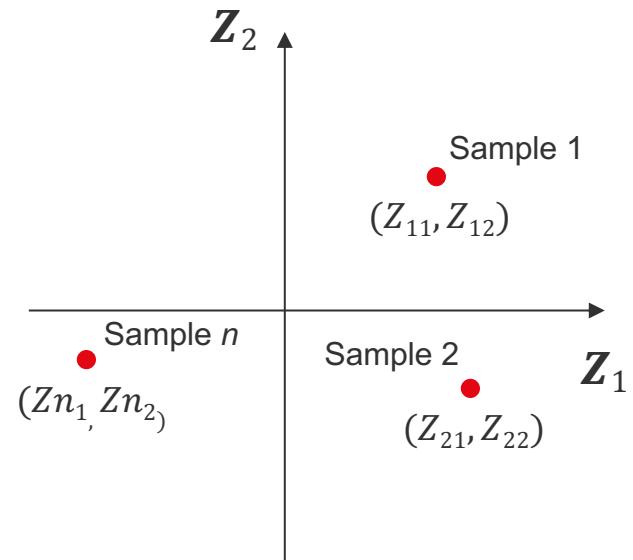
Score: **projection measures of samples** in each principal component

=> Coordinate of samples on each axis PC

$$(\mathbf{Z}_1 \ \mathbf{Z}_2 \ \dots \ \mathbf{Z}_p)$$



$$\begin{pmatrix} Z_{11} & Z_{12} \\ Z_{21} & Z_{22} \\ \vdots & \vdots \\ Z_{n1} & Z_{n2} \end{pmatrix}$$



PCA score plot

Transcriptomics dataset:

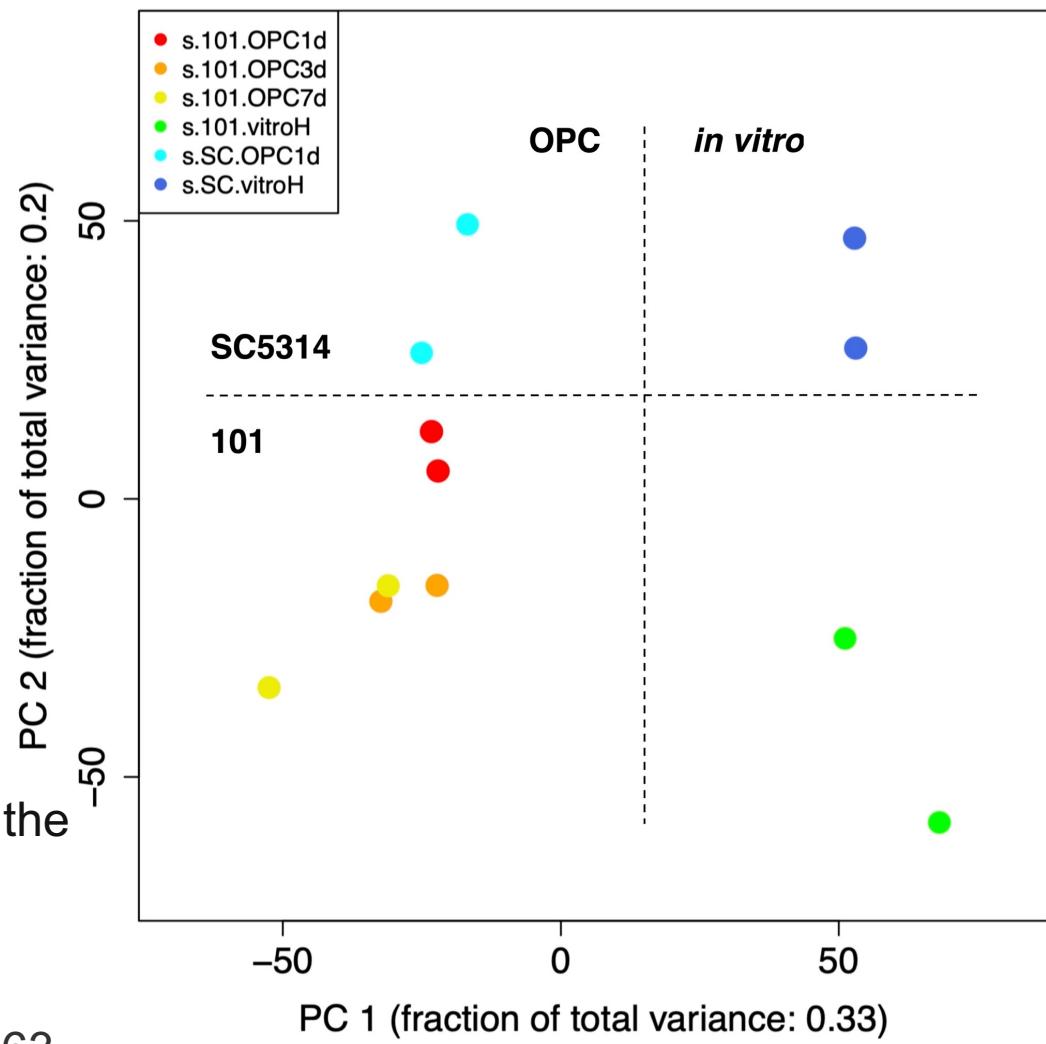
Gene expression profiles of different isolates of *Candida albicans* *in vitro* and during oral infection on mice

Candida albicans commensalism in the oral mucosa is favoured by limited virulence and metabolic adaptation

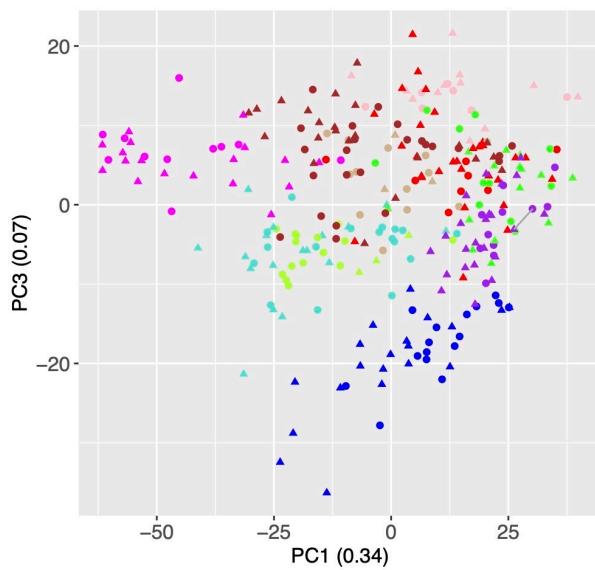
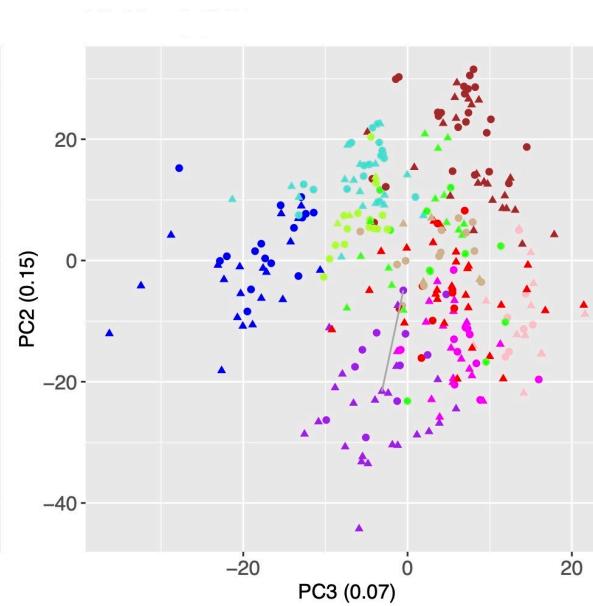
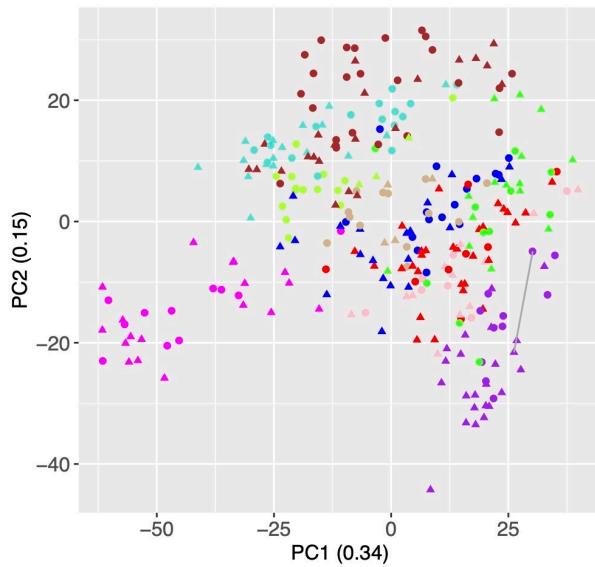
Lembert *et al.*

<https://doi.org/10.1101/2021.10.11.463>

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PCA score plot

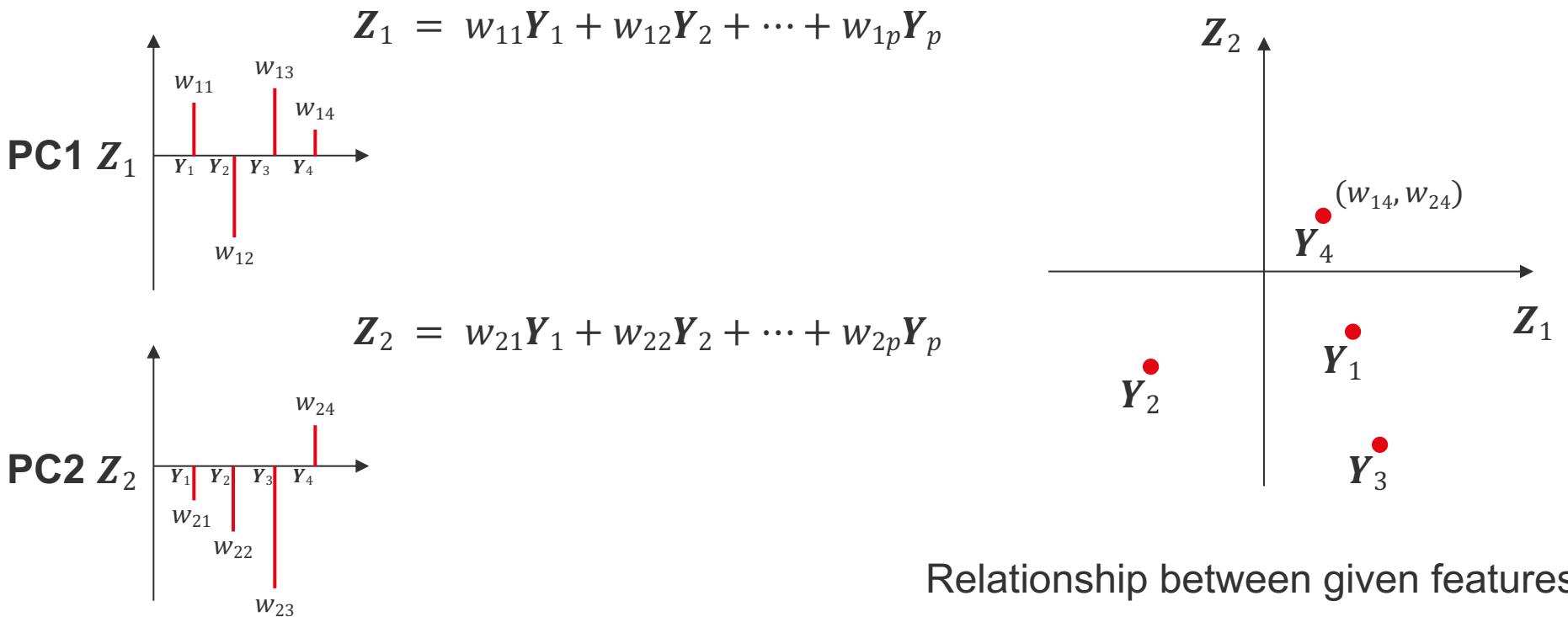


Metagenomics dataset:
Microbiome composition in patients'
lung post lung-transplantation

PCA loading plot

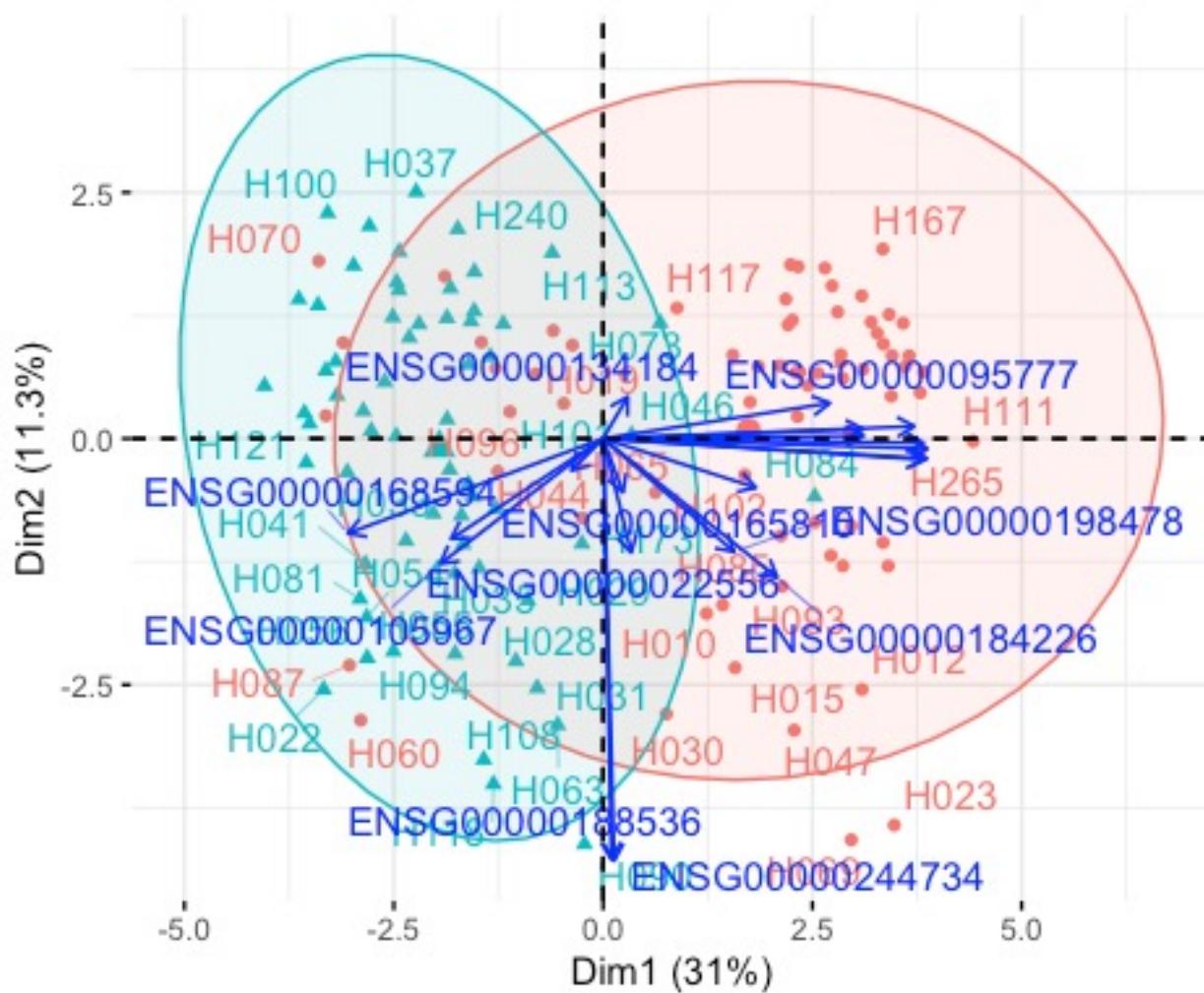
Loading: **contribution of given features** to each principal component

- ⇒ Coordinate of given features on each axis PC
- ⇒ Highly correlated features: similar weights in the loading vectors; close together in the loading plots of all dimensions.



PCA biplot

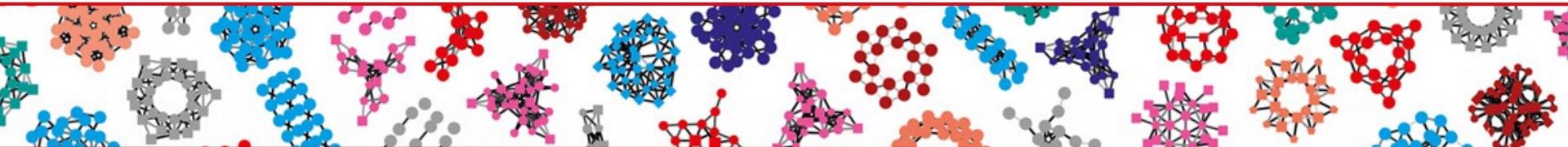
Score plot + Loading plot



Exercise PCA

1. Load the `nutrimouse` data from the `mixOmics` R package and investigate its structure.
2. Take the gene expression dataset in *samples x variables* matrix format. Investigate their distribution.
3. Perform PCA and investigate variances, sample distribution and variable relationship with plots.
4. Visually investigate the sample distribution with coloring by metadata or expression of certain genes.
5. (Optional) PCA on lipidomic dataset

Overview



01

—• Principal Component Analysis

02

—• Partial Least Squares

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—• Towards Nonlinearity

Questions in practice

- A real-estate agency wants to know why some properties were sold quickly and some not.
 - Properties' characteristics: price, surface area, form, floors, bedrooms, bathrooms, entrances, garages, yards, etc; Access to nearby facilities; Local living cost
 - Properties' sold status

- Relation between lifestyle and clinical measurements of patients
 - Lifestyle
 - Clinical measurements

What is PLS?

Herman Wold – econometrician (1966)

Two sets of variables (features) to consider

- Many (predictors or independent/explanatory variables) vs One (response or dependent variable)
- Many vs Many

Reduce the dimension of the two variable spaces

- *Variable extraction*: project high-dimensional space into a space of fewer dimensions

Find the relation between the two sets of variables: covariance

PLS: also Projection to Latent Structures

When is PLS used?

- Cannot identify variables to eliminate
- Need *new* variables independent of one another
- Accept that the *new* independent variables are less interpretable

X: n samples $\times p$ variables

Y: n samples $\times q$ variables

Samples

Variables

How is variation in
both response and
predictor

What underlying
factors explain both
variation?

Predict variables in **Y** using variables in **X**

How does PLS work?

- **PCA objective: calculate latent variables**
 - best explaining variance in **X**
- **PLS objective: calculate latent variables**
 - best explaining variance in **X**
 - best explaining variance in **Y**
 - having greatest relationship between **X** and **Y**

Components 1

Coordinate change:

$$\begin{aligned}(X_1 & \ X_2 \dots \ X_p) \rightarrow (U_1 \ U_2 \dots \ U_p) \\ (Y_1 & \ Y_2 \dots \ Y_q) \rightarrow (V_1 \ V_2 \dots \ V_q)\end{aligned}$$

Linear combination:

$$\begin{aligned}U_1 &= w_{11}X_1 + w_{12}X_2 + \dots + w_{1p}X_p = \mathbf{X}w_1 \\ V_1 &= c_{11}Y_1 + c_{12}Y_2 + \dots + c_{1q}Y_q = \mathbf{Y}c_1\end{aligned}$$

=> projection of \mathbf{X} onto vector w_1 and \mathbf{Y} onto vector c_1

Find w_1, c_1 ($\|w_1\| = \|c_1\| = w_1^T w_1 = c_1^T c_1 = 1$) to maximize:

$$\text{cov}(U_1, V_1) = \text{cor}(U_1, V_1) \sqrt{\text{var}(U_1)} \sqrt{\text{var}(V_1)}$$

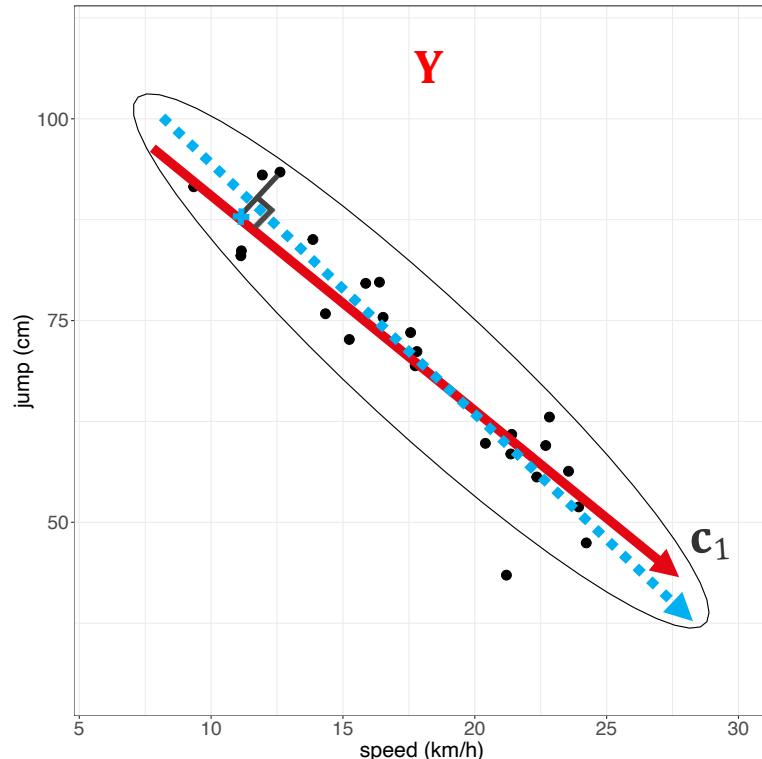
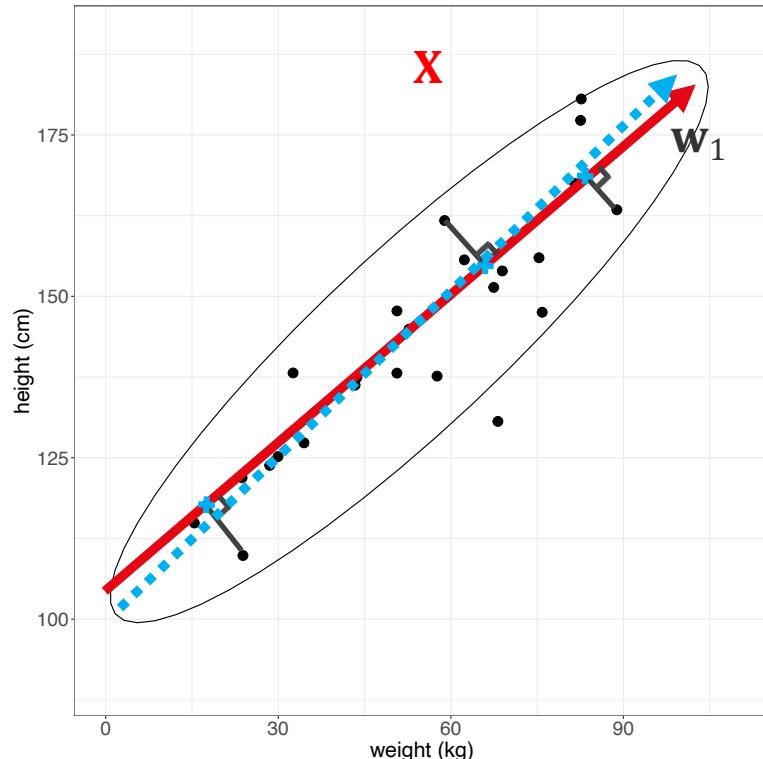
- best explaining variance in \mathbf{X} , given by $\sqrt{\text{var}(U_1)} = U_1^T U_1$
- best explaining variance in \mathbf{Y} , given by $\sqrt{\text{var}(V_1)} = V_1^T V_1$
- having greatest relationship between \mathbf{X} and \mathbf{Y} , given by $\text{cor}(U_1, V_1)$

Following components

- X-space: component 2 orthogonal to component 1
- Y-space:
 - Regression mode: not necessarily orthogonal (\mathbf{Y} is deflated to the information from \mathbf{X})
 - Canonical mode: orthogonal (\mathbf{Y} is deflated to the information from \mathbf{Y})
- **Algorithm:** iterative process
 - For component 1:
 w_1 = eigenvector corresponding to max eigenvalue of $\mathbf{X}^T \mathbf{Y} \mathbf{Y}^T \mathbf{X}$
 c_1 = eigenvector corresponding to max eigenvalue of $\mathbf{Y}^T \mathbf{X} \mathbf{X}^T \mathbf{Y}$
 - For component 2:
 w_2 = eigenvector corresponding to max eigenvalue of
 $\mathbf{X}_{\text{deflated2}}^T \mathbf{Y}_{\text{deflated2}} \mathbf{Y}_{\text{deflated2}}^T \mathbf{X}_{\text{deflated2}}$
 $\mathbf{X}_{\text{deflated1}} = \mathbf{X}, \mathbf{X}_{\text{deflated2}} = \mathbf{X} - \mathbf{U}_1 \mathbf{U}_1^T \mathbf{X}_{\text{deflated1}}, \text{ etc.}$
 - And so on, at most $\min(p, q)$

Scores

- Maximum covariance between X-space scores (e.g. projection of \mathbf{X} onto vector \mathbf{w}_1) and Y-space scores (e.g. \mathbf{Y} onto vector \mathbf{c}_1)
- Usually close components but not necessarily identical to PCA components
=> affected scores
- Visualize clusters, outliers, interesting patterns in sample distribution



Loadings

- Highly correlated variables: similar weights in the loading vectors; close together in the loading plots of all dimensions.
 - Loading plot: superimpose loading plots from X and Y
- ⇒ Relationship between X variables, between Y variables, between all variables
- **Loadings**: weights on *deflated (residual)* matrices
 - **Loadings-star**: weights on input matrices

$$\begin{aligned} U_1 &= Xw_1^* = X_{\text{deflated1}}w_1: & X_{\text{deflated1}} &= X, & w_1^* &= w_1 \\ U_2 &= Xw_2^* = X_{\text{deflated2}}w_2: & X_{\text{deflated2}} &= X - U_1U_1^T X_{\text{deflated1}}, & w_2^* &\neq w_2 \end{aligned}$$

=> Interpret **Loadings-star** rather than Loadings when investigating relationships in PLS

Variability explained with components

- Cumulative variance explained for each space

$$R_X^2 = 1 - \frac{\text{var}(\mathbf{X}_{\text{deflated}})}{\text{var}(\mathbf{X})}$$

$$R_Y^2 = 1 - \frac{\text{var}(\mathbf{Y}_{\text{deflated}})}{\text{var}(\mathbf{Y})}$$

- Plot of R_X^2 and R_Y^2 for each variable

$$R_{X,k}^2 = 1 - \frac{\text{var}(\mathbf{X}_{\text{deflated},k})}{\text{var}(\mathbf{X}_k)}$$

$$R_{Y,k}^2 = 1 - \frac{\text{var}(\mathbf{Y}_{\text{deflated},k})}{\text{var}(\mathbf{Y}_k)}$$

PLS implementation

X: n samples $\times p$ variables Y: n samples $\times q$ variables

Input: X, Y

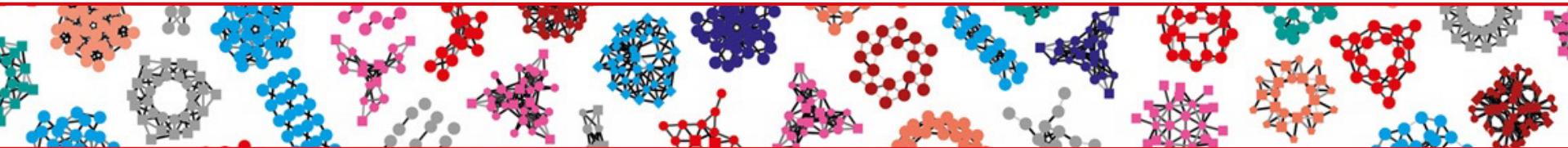
Output:

- cor: correlations
- variates: $(U_1 \ U_2 \dots \ U_{ncomp}), (V_1 \ V_2 \dots \ V_{ncomp})$
- loadings: $(w_1 \ w_2 \dots \ w_{ncomp}), (c_1 \ c_2 \dots \ c_{ncomp})$
- loadings-star
- proportion of explained variance
- correlation between variates and input data

Exercise PLS

1. Perform PLS (`mixOmics::pls`) and investigate its output, sample distribution and variable relationship with plots.
2. Observe the difference between the two modes *regression* and *canonical* of PLS.

Overview



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—• Towards Nonlinearity

Questions in practice

- **Relation between lifestyle and clinical measurements of patients**
 - Lifestyle
 - Clinical measurements

- **Relation between two omics profiles**

CCA versus PLS

- PLS

$$\max_{w,c} \text{cov} (\mathbf{X}w, \mathbf{Y}c)$$

subject to $\|w\| = \|c\| = 1$

- CCA (Harold Hotelling – statistician/economic theorist (1936))

$$\max_{w,c} \text{cor} (\mathbf{X}w, \mathbf{Y}c)$$

subject to $\text{var}(\mathbf{X}w) = \text{var}(\mathbf{Y}c) = 1$

Components 1

Coordinate change:

$$\begin{aligned}(X_1 & \ X_2 \dots \ X_p) \rightarrow (U_1 \ U_2 \dots \ U_p) \\ (Y_1 & \ Y_2 \dots \ Y_q) \rightarrow (V_1 \ V_2 \dots \ V_q)\end{aligned}$$

Linear combination:

$$\begin{aligned}U_1 &= w_{11}X_1 + w_{12}X_2 + \dots + w_{1p}X_p = \mathbf{X}w_1 \\ V_1 &= c_{11}Y_1 + c_{12}Y_2 + \dots + c_{1q}Y_q = \mathbf{Y}c_1\end{aligned}$$

=> projection of \mathbf{X} onto vector w_1 and \mathbf{Y} onto vector c_1

Find w_1, c_1 ($\text{var}(\mathbf{X}w_1) = \text{var}(\mathbf{Y}c_1) = w_1^T \mathbf{X}^T \mathbf{X} w_1 = c_1^T \mathbf{Y}^T \mathbf{Y} c_1 = 1$) to maximize:

$$\text{cor}(U_1, V_1)$$

How does CCA works?

Solution:

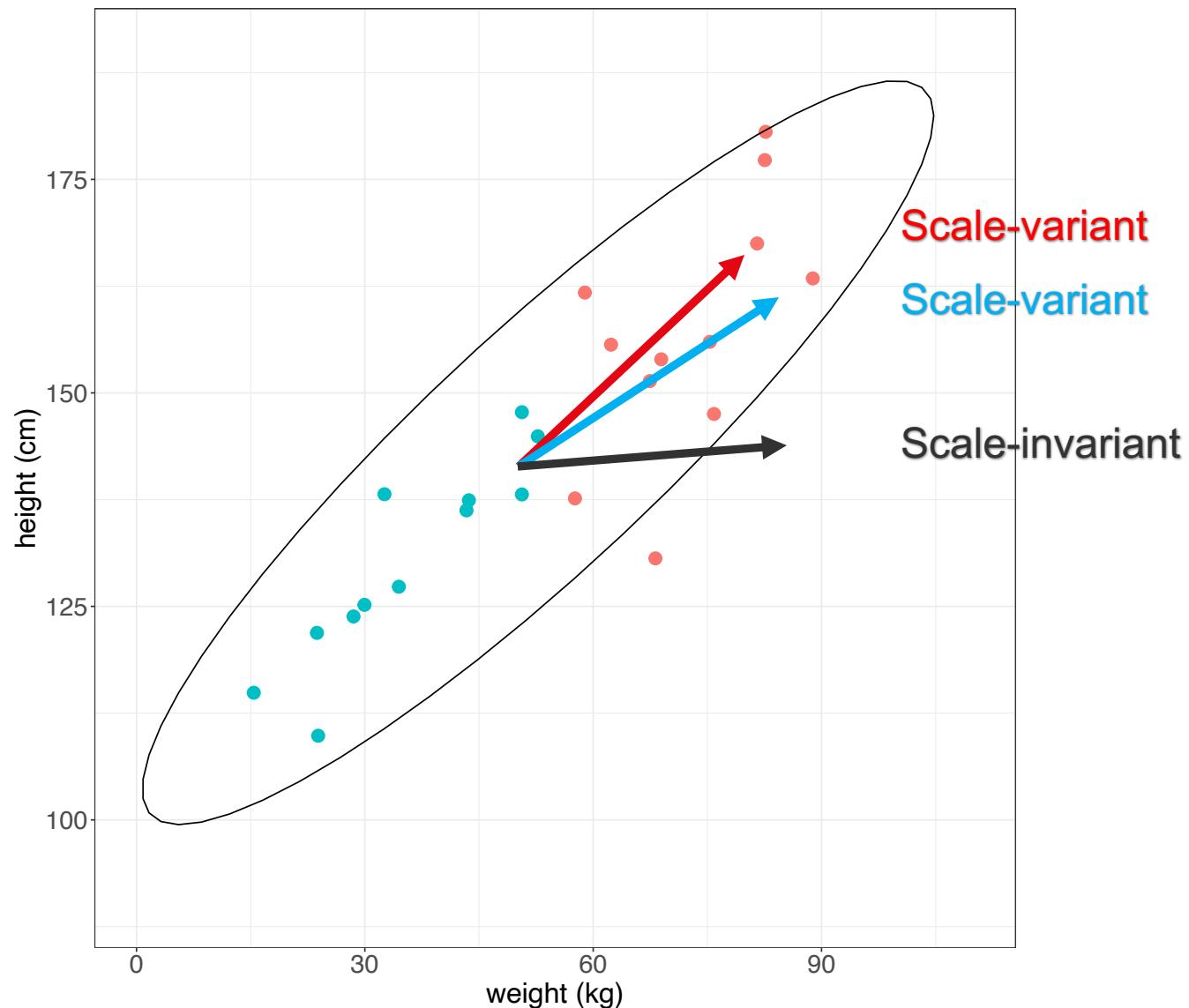
$$\begin{aligned}\max \text{cor}(\mathbf{U}_1, \mathbf{V}_1) &= \sqrt{\max \text{ eigenvalue of } \text{cov}(\mathbf{X})^{-1} \text{cov}(\mathbf{X}, \mathbf{Y}) \text{cov}(\mathbf{Y})^{-1} \text{cov}(\mathbf{Y}, \mathbf{X})} \\ &= \sqrt{\max \text{ eigenvalue of } \text{cov}(\mathbf{Y})^{-1} \text{cov}(\mathbf{Y}, \mathbf{X}) \text{cov}(\mathbf{X})^{-1} \text{cov}(\mathbf{X}, \mathbf{Y})} \\ \text{at } \mathbf{w}_1, \mathbf{c}_1 &= \text{corresponding eigenvectors}\end{aligned}$$

Hint: Lagrange multiplier + derivative

$$\begin{aligned}\max \text{cor}(\mathbf{U}_2, \mathbf{V}_2) &= 2^{\text{nd}} \max \text{ eigenvalue} \\ \text{at } \mathbf{w}_2, \mathbf{c}_2 &= \text{corresponding eigenvectors}\end{aligned}$$

and so on

CCA versus PLS versus PCA



CCA implementation

X: n samples $\times p$ variables Y: n samples $\times q$ variables

Input: X, Y

Output:

- cor: correlations
- variates: $(U_1 \ U_2 \dots \ U_{ncomp}), (V_1 \ V_2 \dots \ V_{ncomp})$
- loadings: $(w_1 \ w_2 \dots \ w_{ncomp}), (c_1 \ c_2 \dots \ c_{ncomp})$
- proportion of explained variance
- correlation between variates and input data

Regularized CCA

Solution:

$$\begin{aligned}\max \text{cor}(\mathbf{U}_1, \mathbf{V}_1) &= \sqrt{\max \text{ eigenvalue of } \text{cov}(\mathbf{X})^{-1} \text{cov}(\mathbf{X}, \mathbf{Y}) \text{cov}(\mathbf{Y})^{-1} \text{cov}(\mathbf{Y}, \mathbf{X})} \\ &= \sqrt{\max \text{ eigenvalue of } \text{cov}(\mathbf{Y})^{-1} \text{cov}(\mathbf{Y}, \mathbf{X}) \text{cov}(\mathbf{X})^{-1} \text{cov}(\mathbf{X}, \mathbf{Y})}\end{aligned}$$

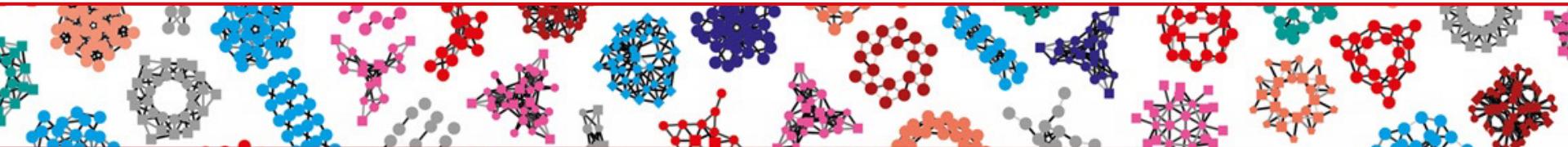
What if $\text{cov}(\mathbf{X})$ or $\text{cov}(\mathbf{Y})$ is not invertible? (*singularity* problem)

- Constant variables
⇒ remove
- Multicollinear variables (esp. when more variables than samples ($p > n$))
⇒ regularized CCA: $\text{cov}(\mathbf{X}) \leftarrow \text{cov}(\mathbf{X}) + \lambda_x \mathbf{I}$, $\text{cov}(\mathbf{Y}) \leftarrow \text{cov}(\mathbf{Y}) + \lambda_y \mathbf{I}$
⇒ tuning for optimal values of λ_x, λ_y

Exercise CCA

1. Perform CCA (`mixOmics::rcc`) between 20 genes and all lipids. Investigate correlations, sample distribution and variable relationship with plots.
2. Perform CCA with scaled datasets and observe the difference
3. Perform regularized CCA with all genes and lipids.

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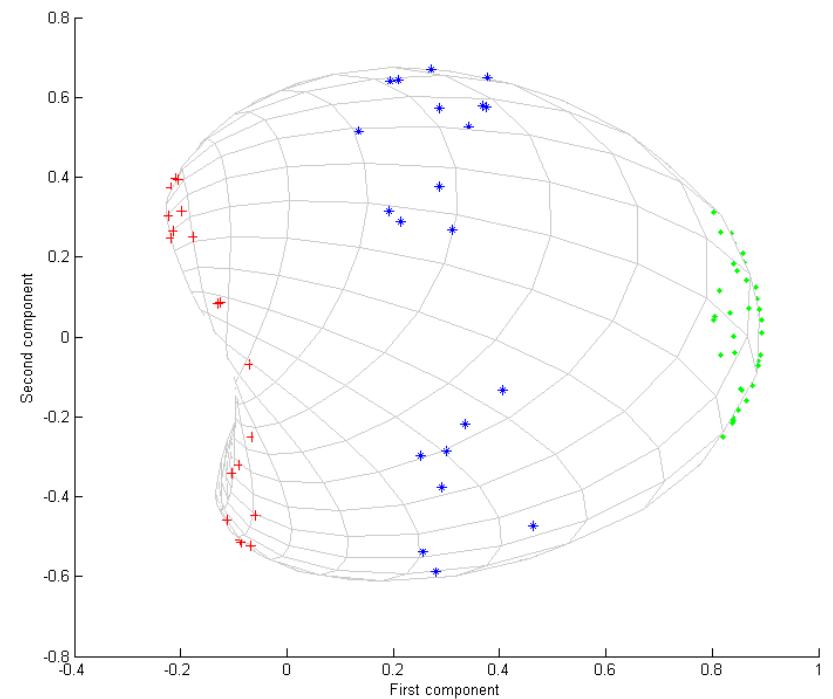
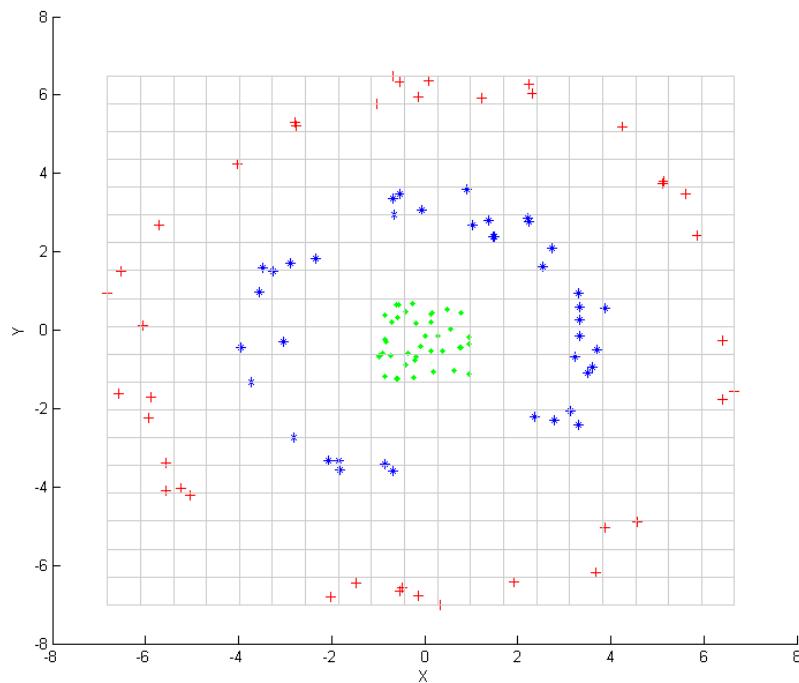
—• Canonical Correlation Analysis

04

—• Towards Nonlinearity

Towards Nonlinearity

Map data points that cannot be linearly separated into a space of higher dimension: **Kernel PCA**



$$k(x, y) = \left(e^{-\frac{\|x-y\|^2}{2\sigma^2}} \right)$$

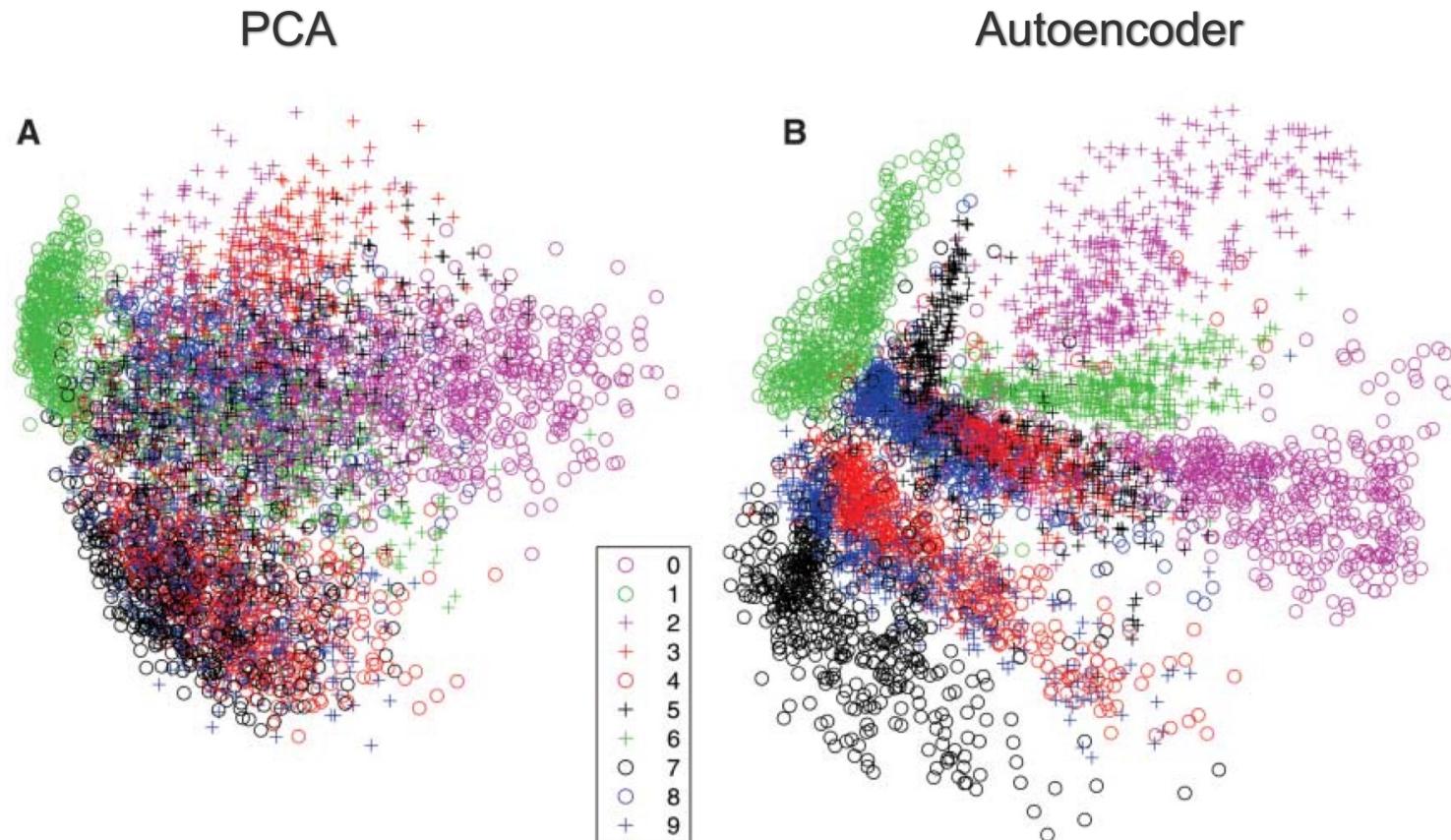
https://commons.wikimedia.org/wiki/File:Kernel_pca_input.png

https://commons.wikimedia.org/wiki/File:Kernel_pca_output.png

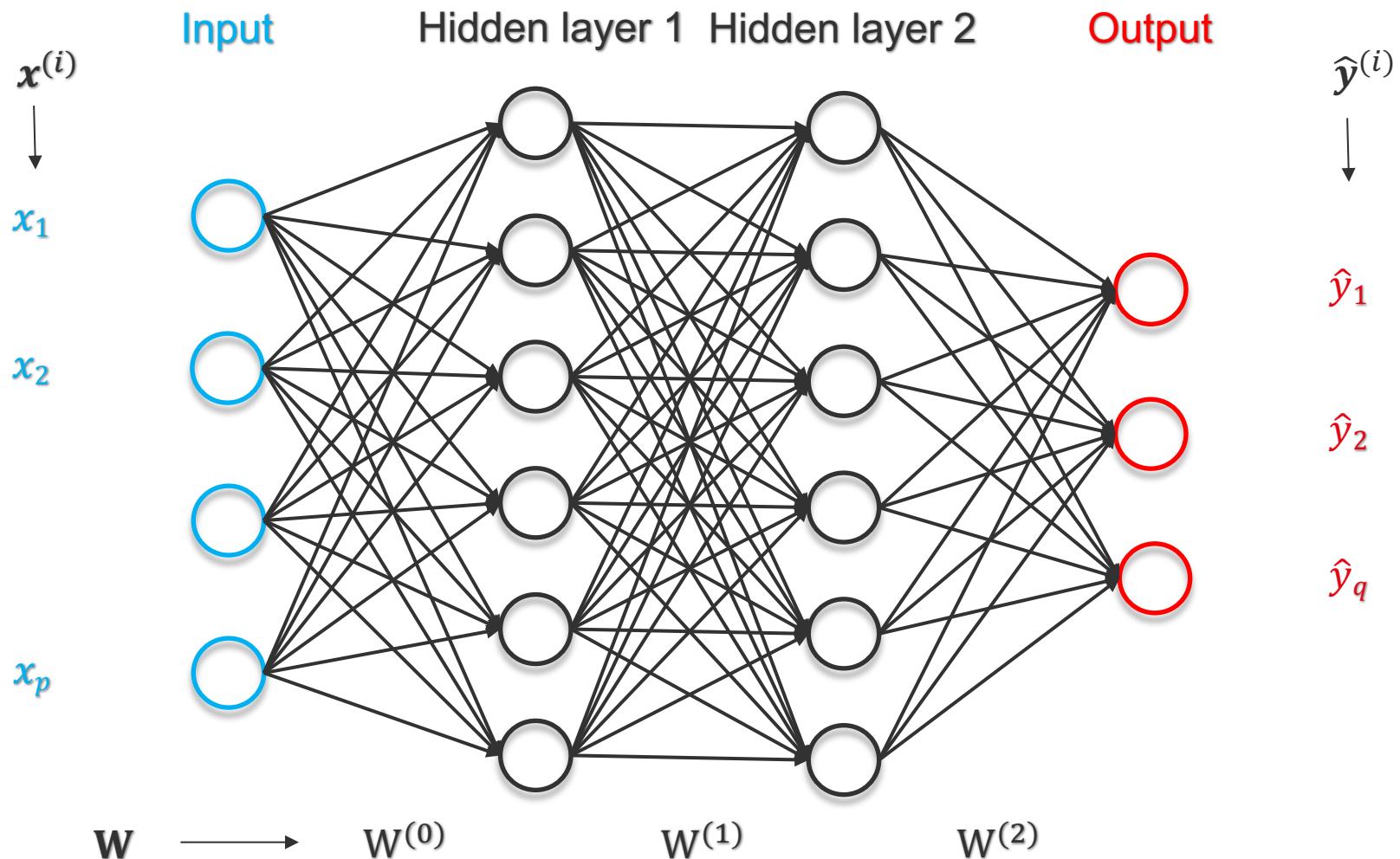
https://commons.wikimedia.org/wiki/File:Kernel_pca_output_gaussian.png

Towards Nonlinearity

Generalize principal components from straight lines to curves:
Autoencoder



Neural Networks



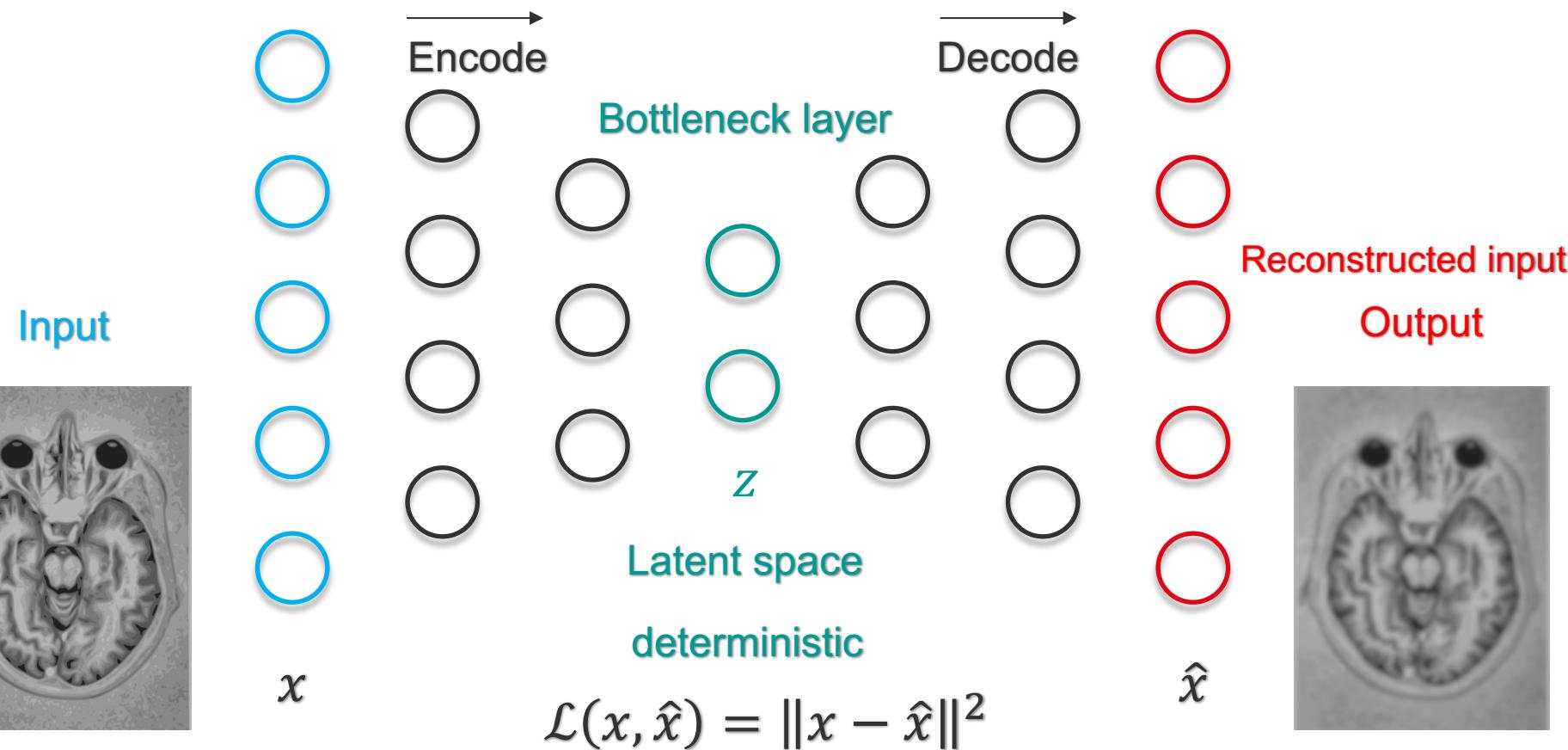
Loss optimization

$$\mathbf{W}^* = \operatorname{argmin}_{\mathbf{W}} \frac{1}{n} \sum_{i=1}^n \mathcal{L}(f(\mathbf{x}^{(i)}, \mathbf{W}), \mathbf{y}^{(i)})$$

Activation functions on linear regressions

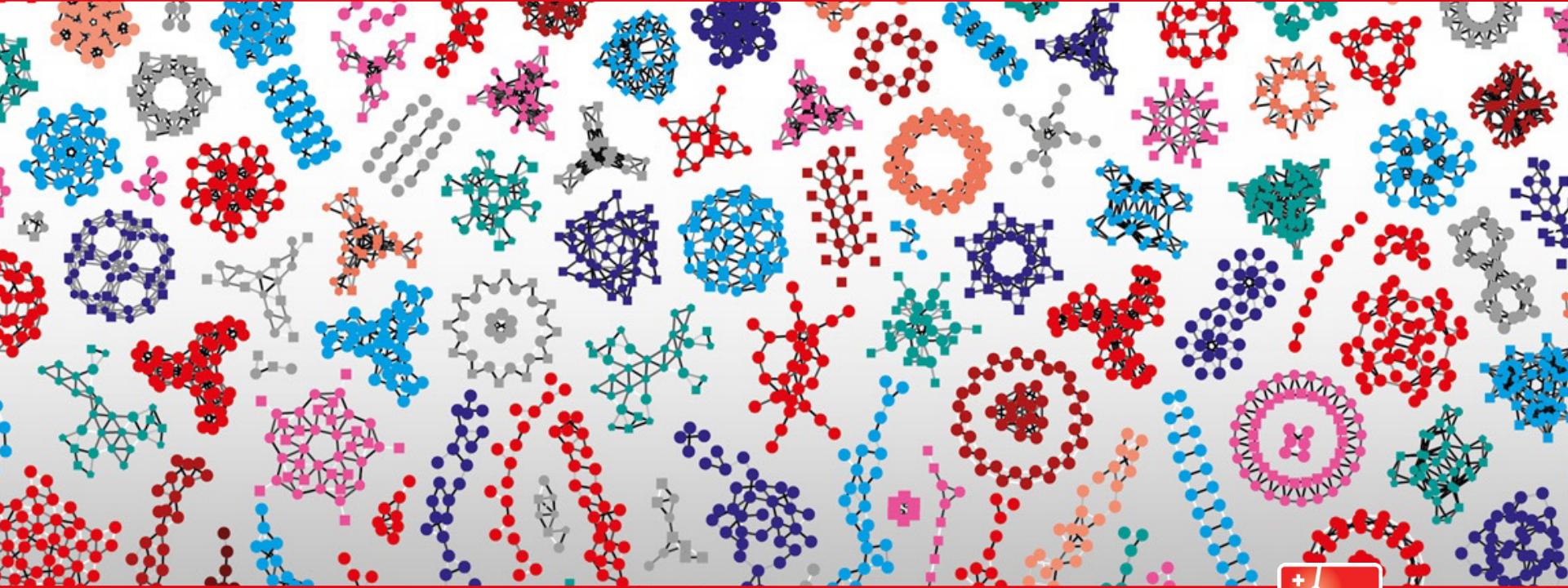
Autoencoder

- Learning a lower-dimensional feature representation (compression) from unlabeled training data and learning a reconstruction back



Autoencoder application

- Image compression, denoising and generation, recommendation system, anomaly detection, feature extraction
- Life sciences
 - dimensionality reduction (clustering) in sequencing data
 - multi-omics and biomedical data integration



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Thank you