

Principal Component Analysis (PCA)

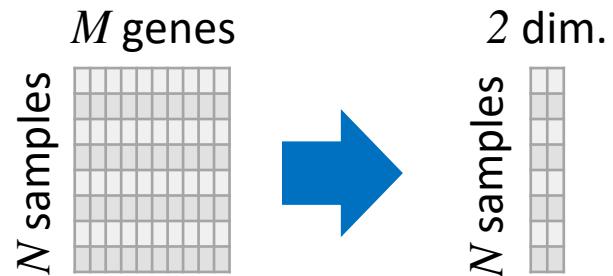
RNA-seq data analysis

Paulo Czarnewski | 13-May-2019

Why PCA?

Simplify complexity, so it becomes easier to work with.

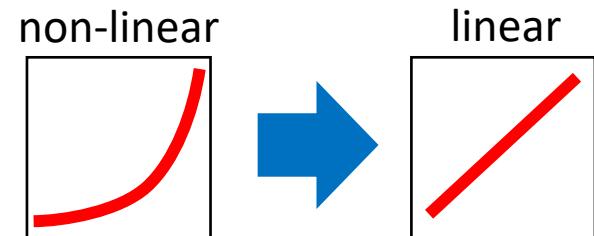
- Reduce number of features (genes)
- Need to transform non-linear relationships to linear



"Remove" redundancies in the data

Identify the most relevant information

Find and filter noise

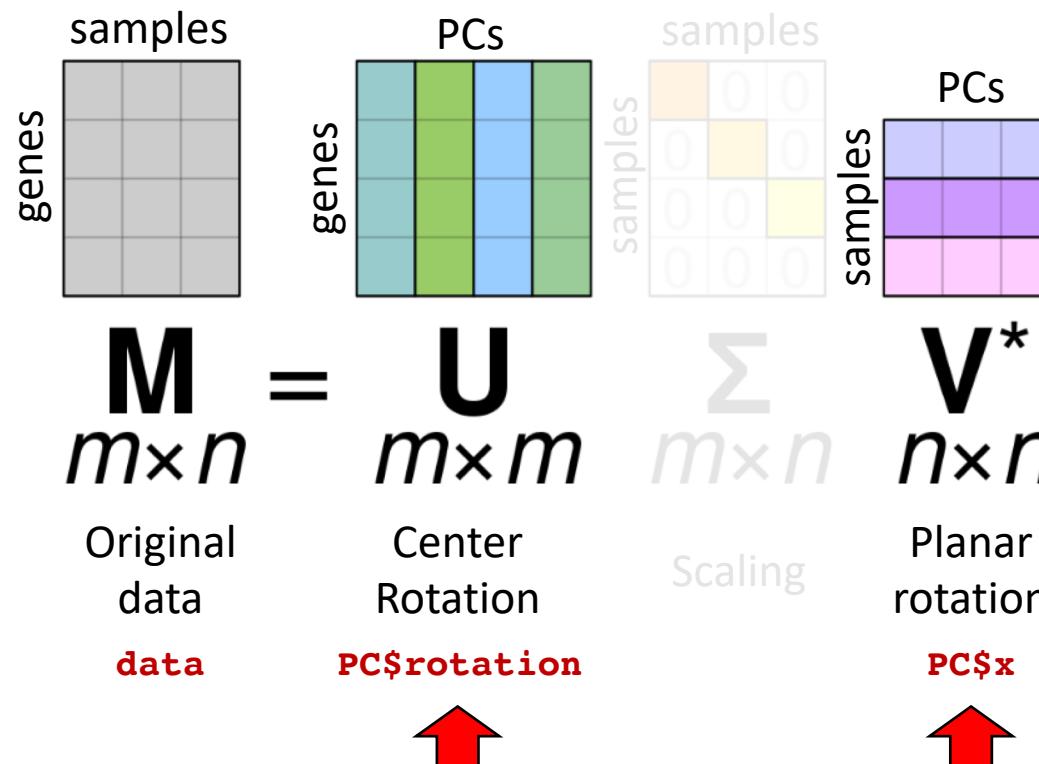


Data visualization

How PCA works

It is a LINEAR algebraic method of dimensionality reduction.

It is a case inside Singular Value Decomposition (SVD) method (data compression)
Any matrix can be decomposed as a multiplication of other matrices (Matrix Factorization).



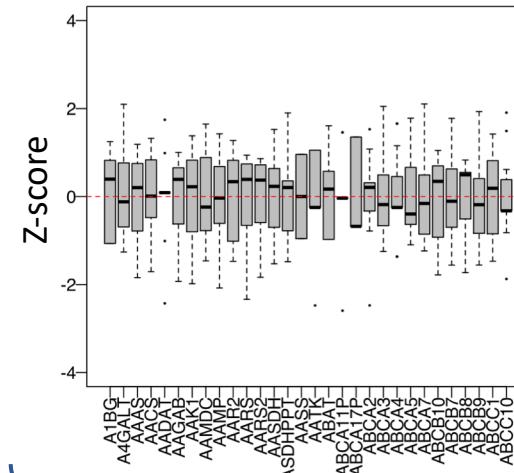
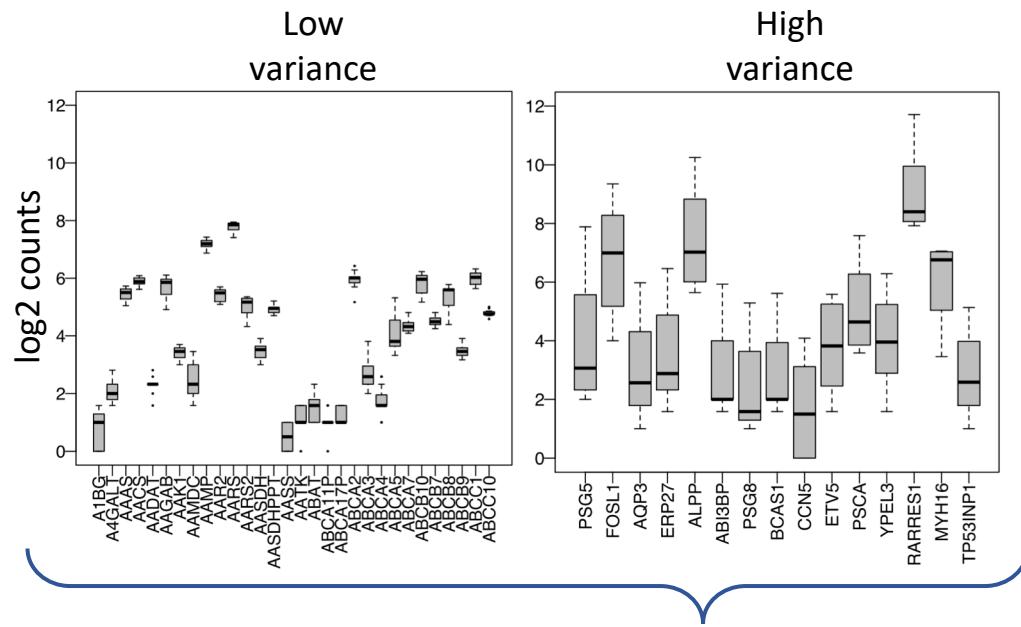
```
PC <- prcomp( data )
PC$
```

◆ sdev
◻ rotation
◆ center
◆ scale
◻ x

Data transformation and scaling

Before applying PCA, the data should be first transformed to a linear scale (i.e. log)

Each feature should be scaled to have a similar center (zero) and similar deviation.



$$\mathbf{M}_{m \times n} = \mathbf{U}_{m \times m} \mathbf{\Sigma}_{m \times n} \mathbf{V}^*_{n \times n}$$

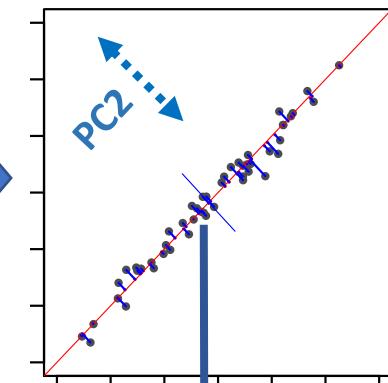
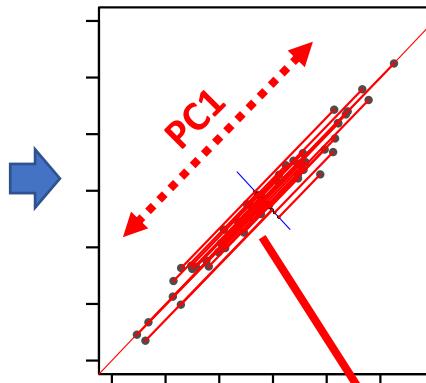
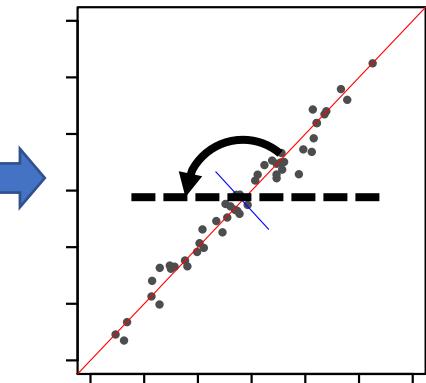
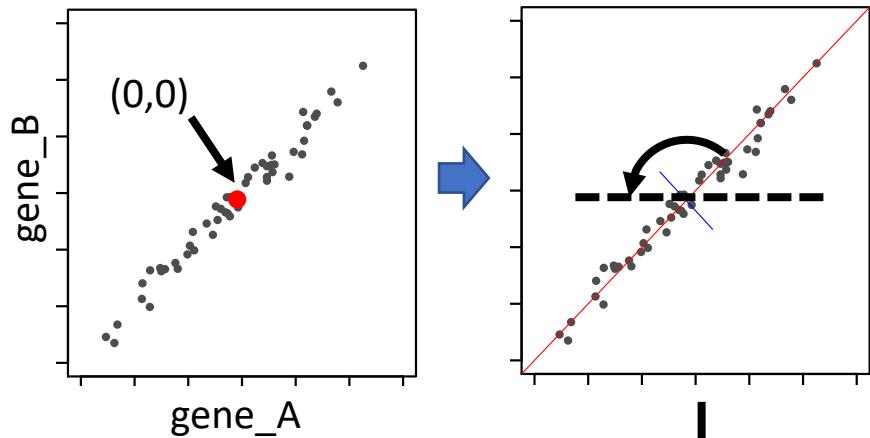
scaling

PCA on raw counts will separate genes with higher counts in the first PCs
(*higher distance to 0*)

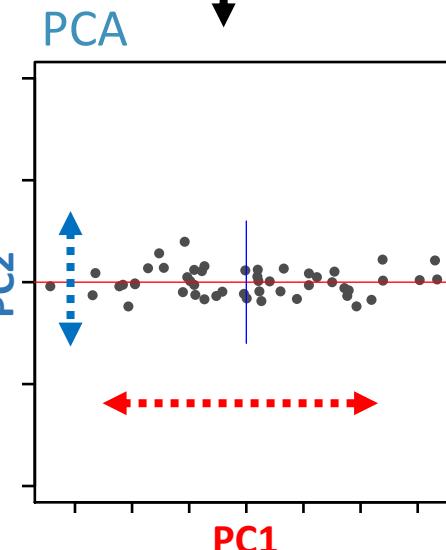
PCA on Z-score will separate genes with most common expression trends in the first PCs

How PCA works

original data (Z-score)



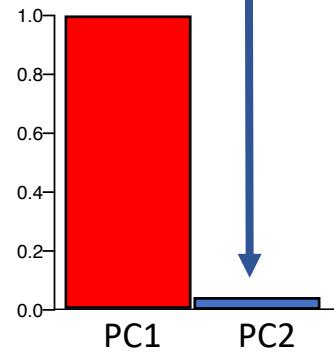
rotation to another
coordinate system



PCA

$$\begin{matrix} M_{m \times n} = & U_{m \times m} & \Sigma_{m \times n} & V_{n \times n} \\ & \text{rotation} & & \end{matrix}$$

percentage
of variance
explained

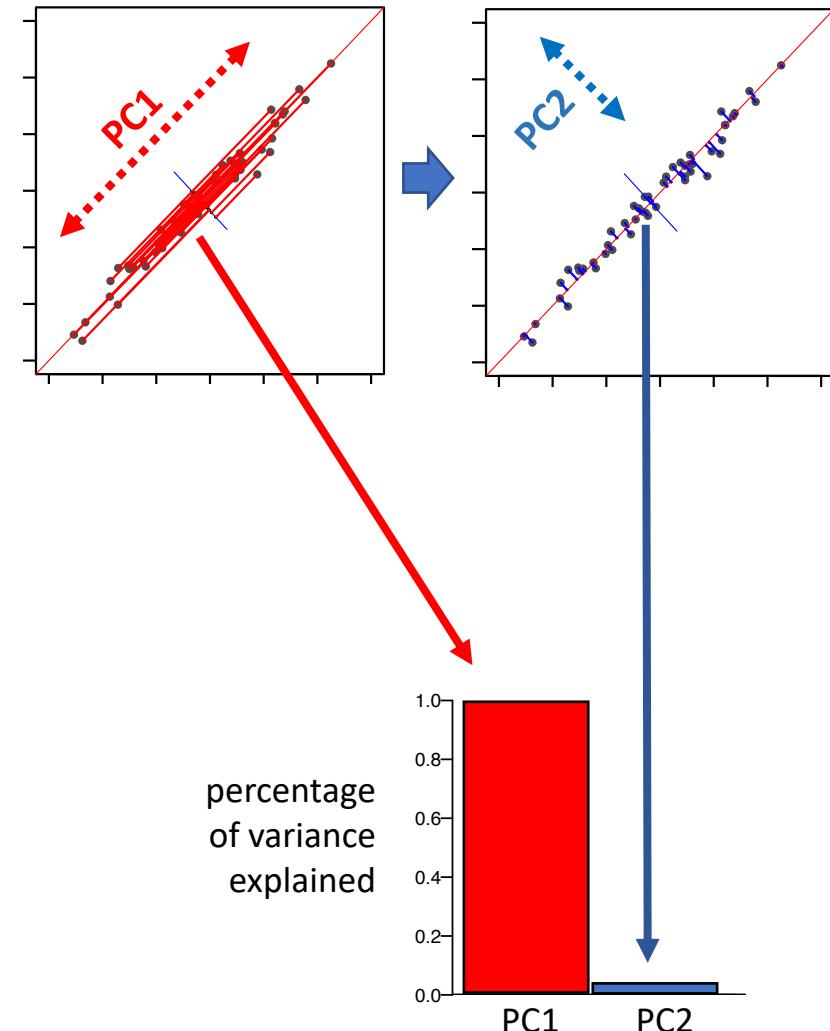
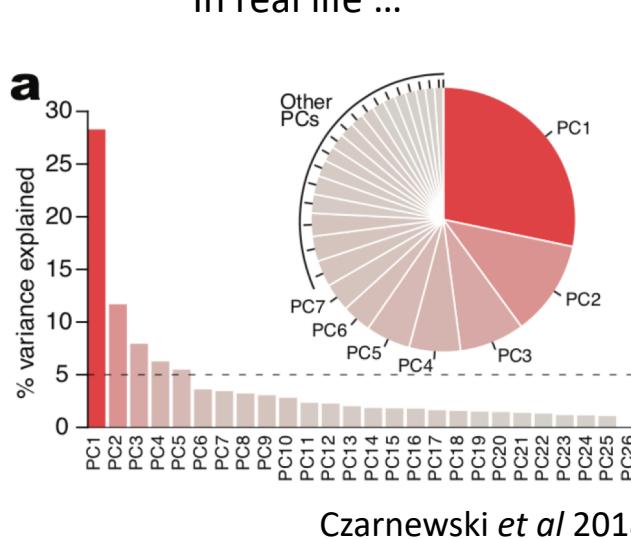


How PCA works

PC1 explains >98% of the variance

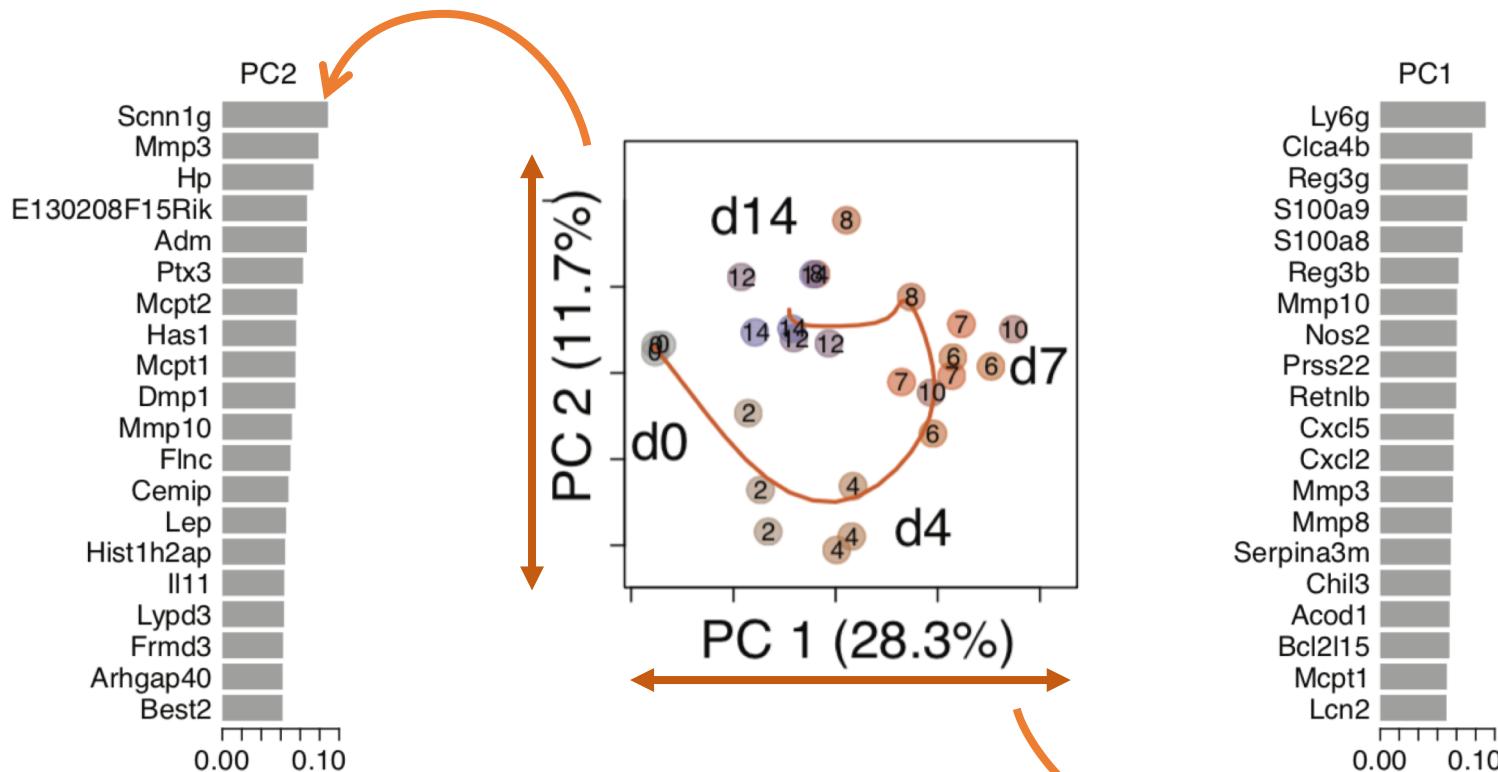
1 PC thus represents 2 genes very well
“Removing” redundancy

PC2 is nearly insignificant in this example
Could be disregarded



How PCA works

Each PC has a meaning



rotation

$$M_{m \times n} = U_{m \times m} \Sigma_{m \times n} V^*_{n \times n}$$

A visual intuition of PCA

The top principal components store more important Shakira information

Original

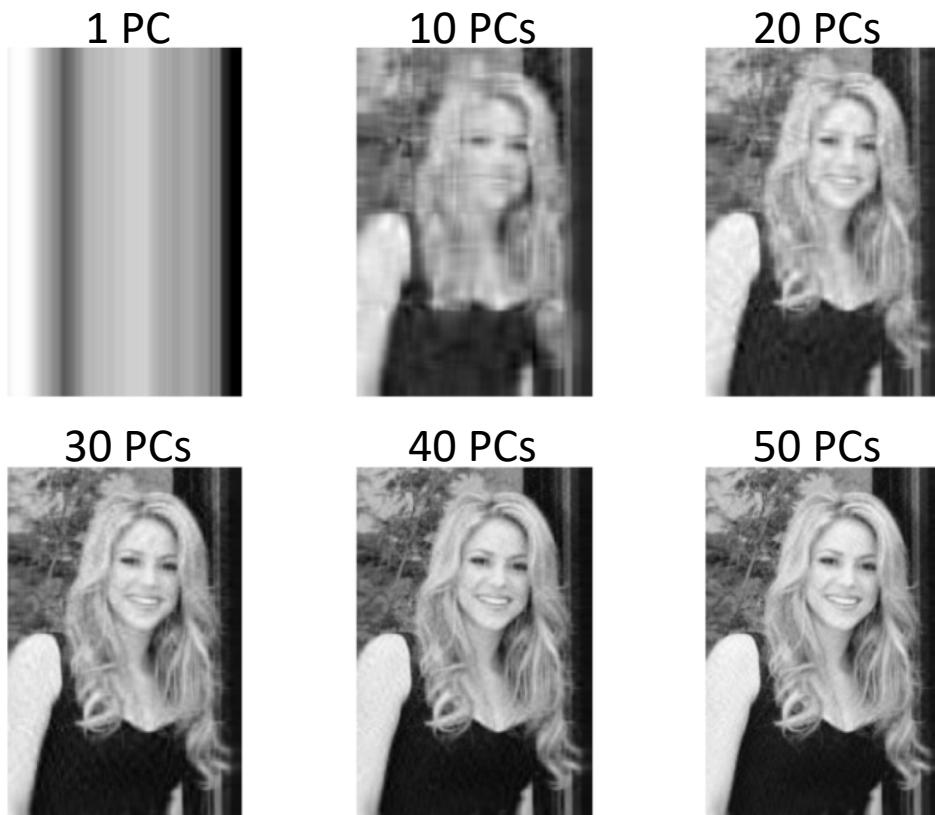


PCA

$$\begin{matrix} \textcolor{blue}{V}^* \\ n \times n \end{matrix}$$

Use only

PCs



It is a LINEAR method of dimensionality reduction

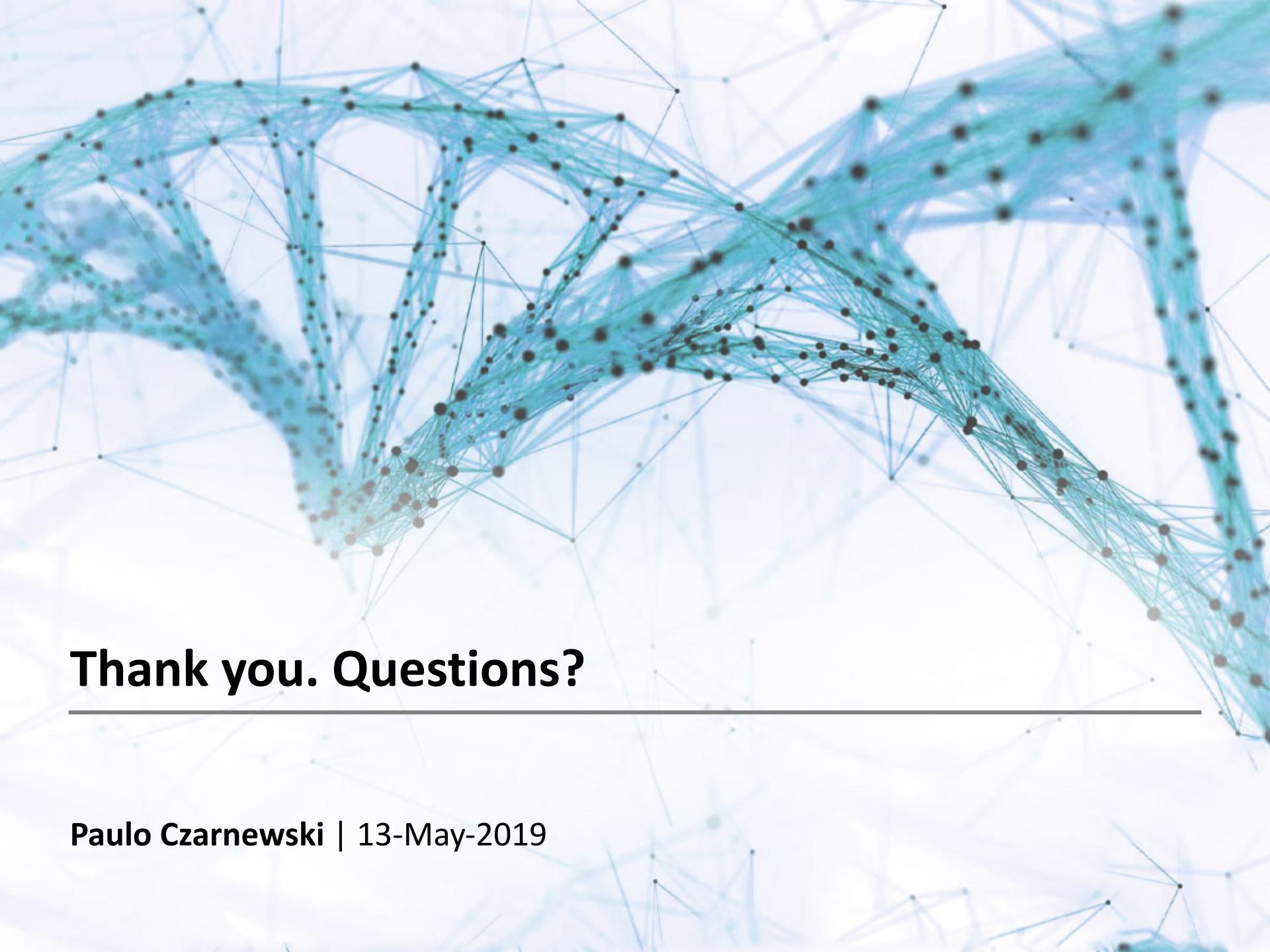
The data is usually SCALED (i.e. Z-score) and TRANSFORMED (i.e. log) prior to PCA

It is an interpretable dimensionality reduction

The top principal components contain higher variance from the data

Can be used as FILTERING, by selecting only the top significant PCs

- PCs that explain at least 1% of variance
- The first 5-10 PCs

The background of the slide features a complex, abstract network graph. It consists of numerous small, dark brown dots representing nodes, connected by a dense web of thin, translucent blue lines representing edges. The graph is highly interconnected, with many cycles and dead ends, creating a sense of organic complexity.

Thank you. Questions?

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