

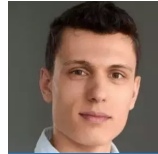
A PRACTICAL GUIDE TO DIMENSIONALITY REDUCTION

Helmholtz AI consultant team

YOUR MENTORS



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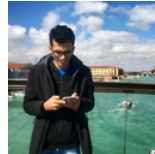
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Chandran



SCHEDULE FOR THE COURSE

- Day 1

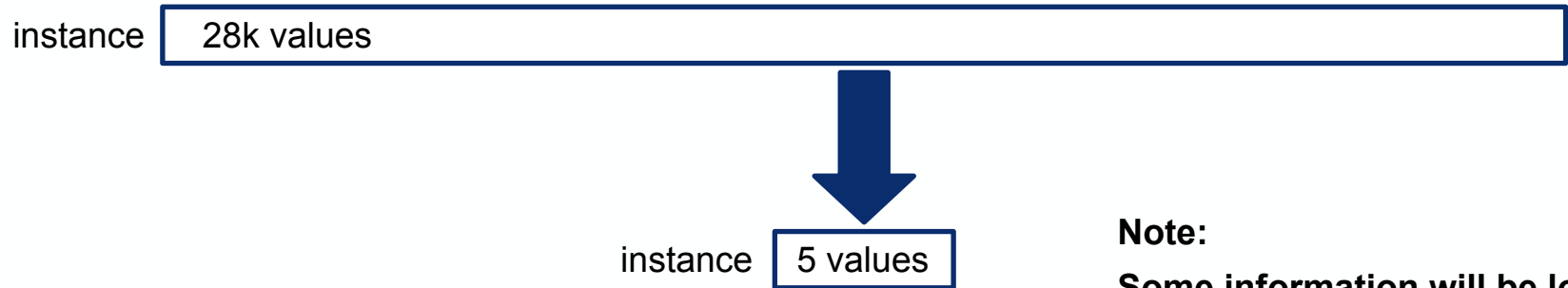
10:00 - 10:15	Main room: introduction
10:20 - 11:20	Breakout rooms: feature transformation notebook
11:20 - 11:30	Break
11:30 - 12:00	Breakout rooms: autoencoder notebook

- Day 2

10:00 - 10:20	Breakout rooms: feature aggregation notebook
10:20 - 11:20	Breakout rooms: feature selection notebook
11:30 - 11:50	Breakout rooms: stability optimization notebook
11:50 - 12:00	Main room: wrap-up and conclusions

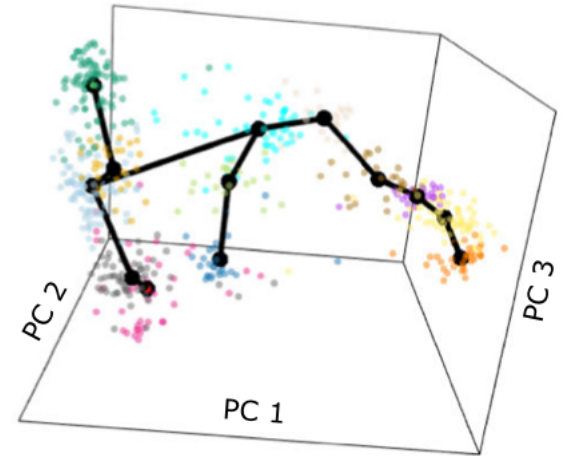
DEFINITION OF DIMENSIONALITY REDUCTION

- Given a dataset of n instances with p -dimensional measurement profiles, use a transformation to represent the n instances by l -dimensional feature profiles, with $l \ll p$
- Example: gene expression measurements
 - $n=24$ biological samples
 - $p=28k$ genes
- Can we reduce the 28k-dimensional profile of each instance to a 5-dimensional profile?



PURPOSE OF DIMENSIONALITY REDUCTION

- **Visualize the main dissimilarities between instances** (e.g. a subgroup structure)
 - Allowing humans to visually grasp the data
 - Not only useful for scatterplots of instances but also for heatmaps (number of columns)
 - Also quality control of data (e.g. batch effects)
- **Facilitate machine learning analysis of instances**
 - Clustering for detection of subgroups
 - Robust classification, e.g. healthy vs. cancer
 - Trajectory identification, e.g. cell development

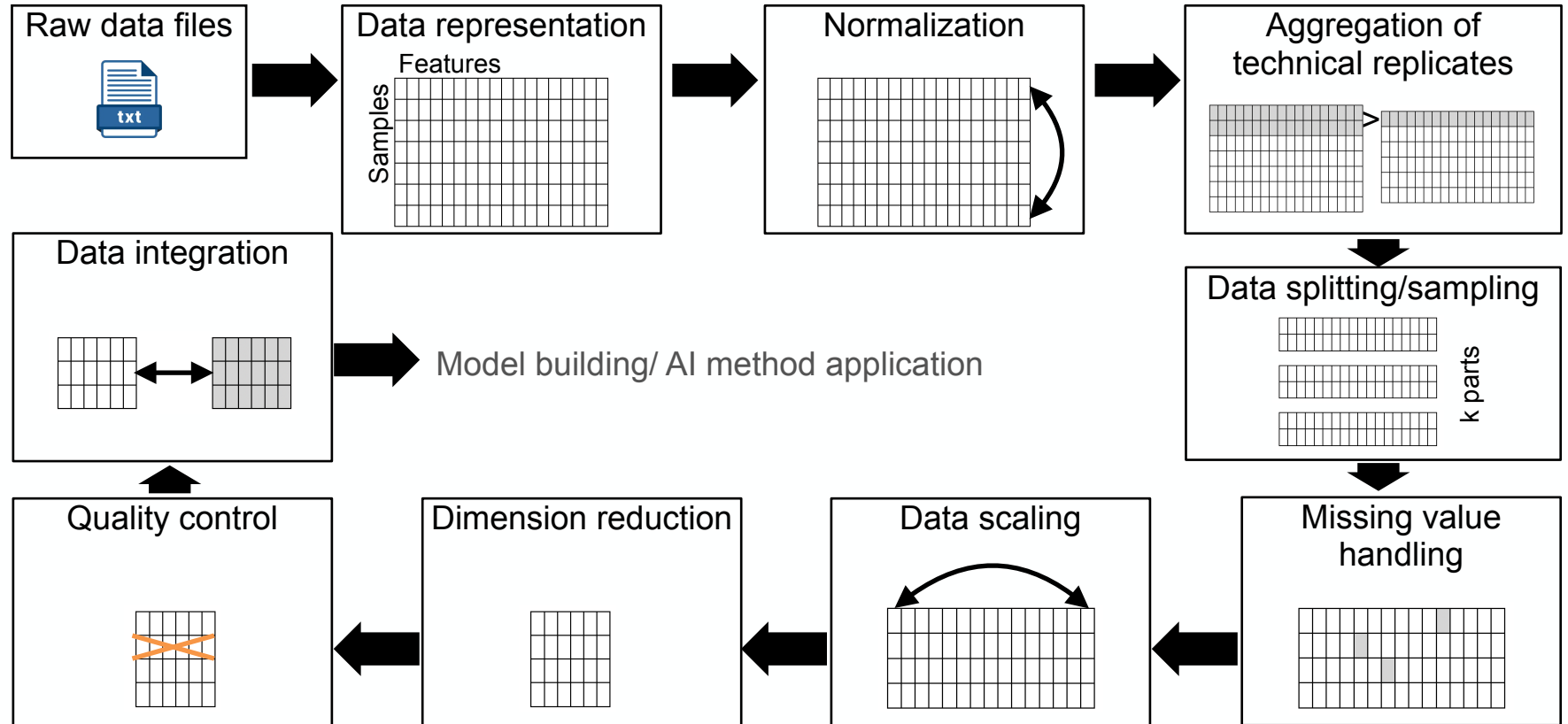


Street *et al. BMC Genomics* (2018) 19:477
<https://doi.org/10.1186/s12864-018-4772-0>

PURPOSE OF DIMENSIONALITY REDUCTION: DETAILS

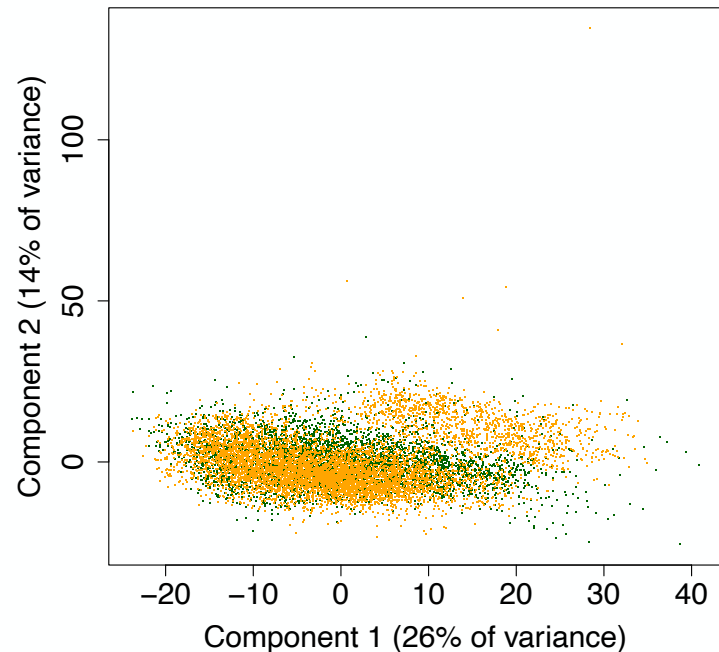
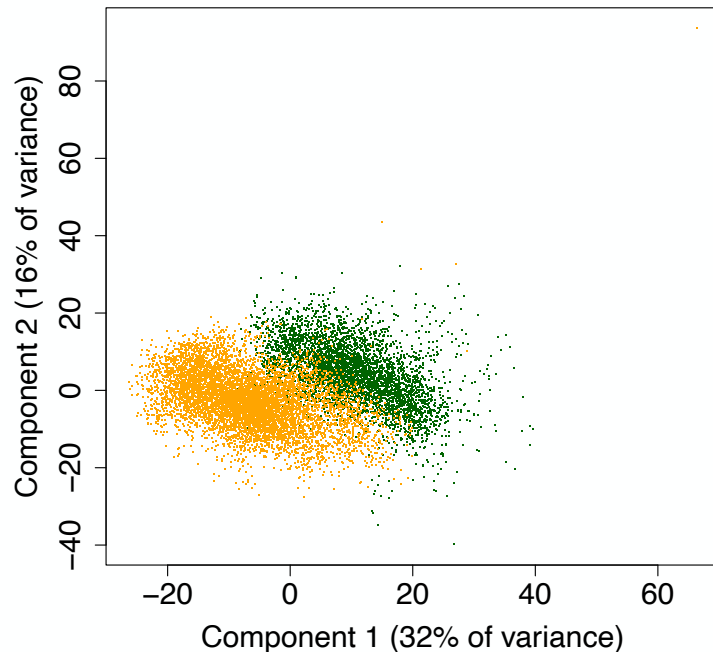
- Dimensionality reduction **facilitates data visualization** but not necessarily scientific interpretation: its purpose is **different from explainable AI** (XAI, see other course)
 - E.g. transformed features are composed of contributions from all original variables and transformations might even be nonlinear, so the influence of single variables may not be easy to trace
- Dimensionality reduction **counteracts the curse of dimensionality** in machine learning
 - With increasing number of dimensions, the available data become sparser in the space and instance similarities and groupings get harder and harder to detect
- Dimensionality reduction **leads to computational advantages**: less storage space, more efficient training of models

PART OF DATA PREPROCESSING



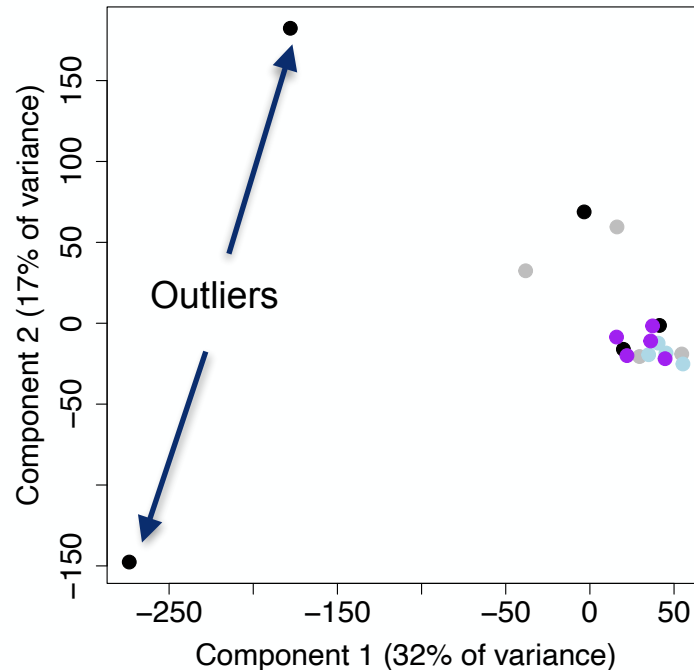
QUALITY CONTROL

- Dimension reduction assists in revealing batch effects (left)
- Dimension reduction assists in checking success of batch effect correction (right)



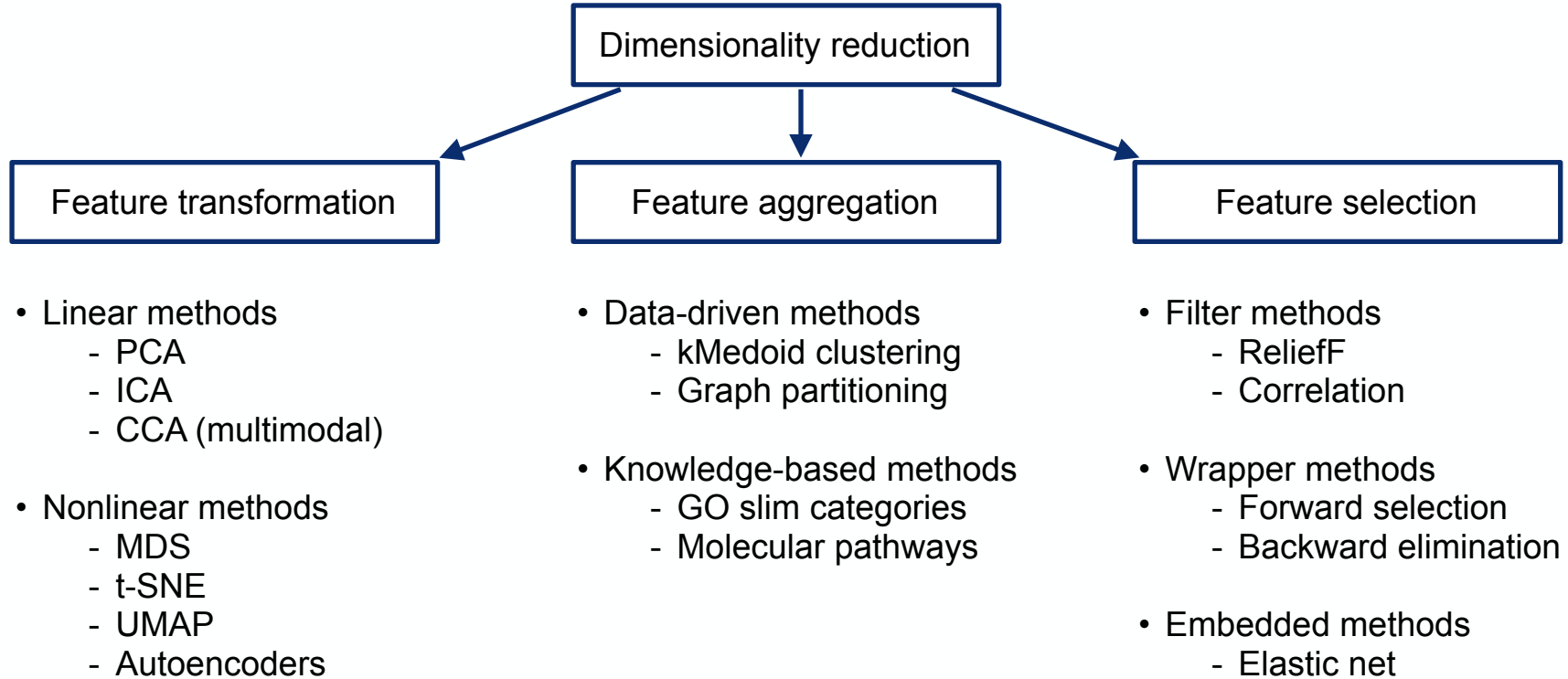
QUALITY CONTROL

- Dimension reduction assists in revealing outlier samples
- Removing outliers might be beneficial for downstream AI analysis



Example visualization
of RNA-seq samples

DIMENSIONALITY REDUCTION APPROACHES



Mostly unsupervised: no target variable taken into account

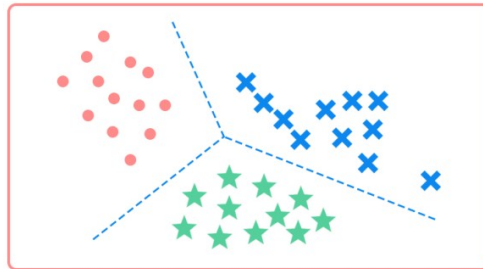
Mostly supervised prediction

SUPERVISED VS. UNSUPERVISED APPROACHES

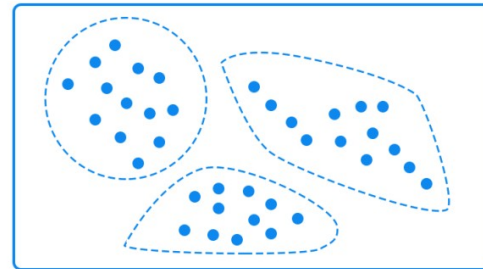
- Most often, *feature transformation and feature aggregation* are performed in an *unsupervised* manner, i.e. no target variable for the instances (e.g. class label, continuous output) is taken into account during dimensionality reduction
- However, *there also exist supervised feature transformation methods*, e.g. linear discriminant analysis, and feature aggregation may be targeted toward supervised tasks
- *Feature selection methods are typically supervised, but there are also unsupervised methods*, e.g. variance-based filters

X ₁	X ₂	X _p	Y

Target



Supervised learning



Unsupervised learning

X ₁	X ₂	X _p	Y

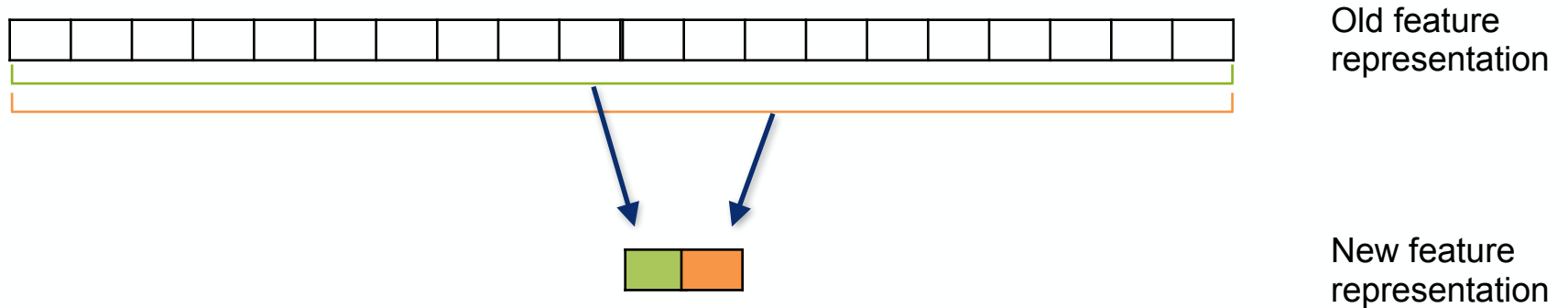
No
Target

<https://www.linkedin.com/pulse/supervised-vs-unsupervised-learning-whats-difference-smriti-saini/>

<https://www.sharpsightlabs.com/blog/supervised-vs-unsupervised-learning/>

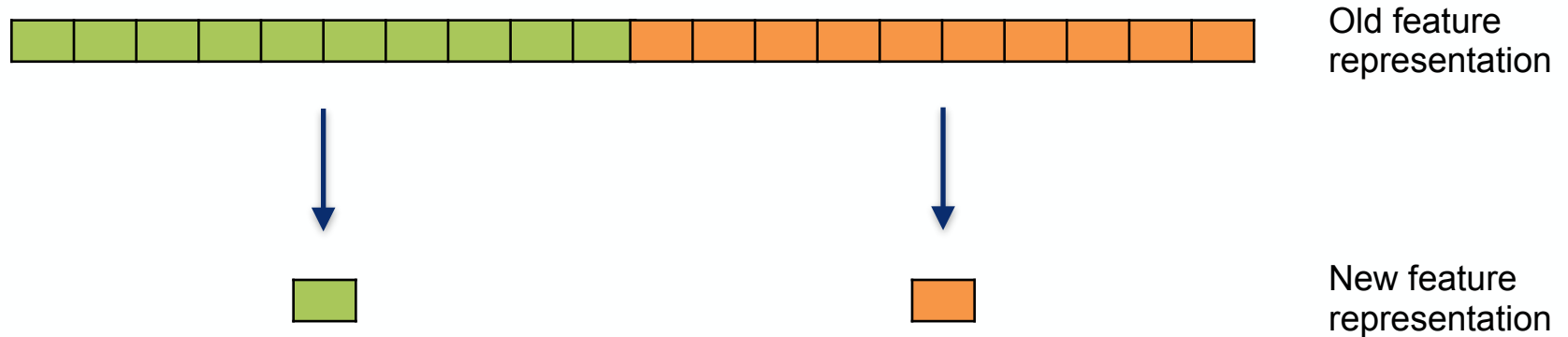
FEATURE TRANSFORMATION

- **Idea:** reduce dimensionality by computing new features based on all original features to condense the most relevant information
- **Linear methods:** new features are linear combinations of original features
- **Nonlinear methods:** new features are nonlinear transformations of original features



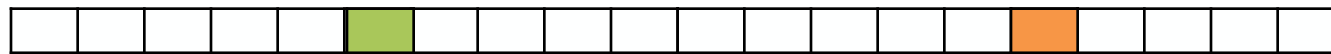
FEATURE AGGREGATION

- **Idea:** reduce dimensionality by summarizing each group of original features into one aggregated feature
- **Data-driven methods:** use the dataset at hand to group similar features
- **Knowledge-based methods:** use annotation databases to define feature groups



FEATURE SELECTION

- **Idea:** reduce dimensionality by picking a subset of original features
- **Filter methods:** score each individual feature
- **Wrapper methods:** test different sets of features
- **Embedded methods:** learn the importance of features



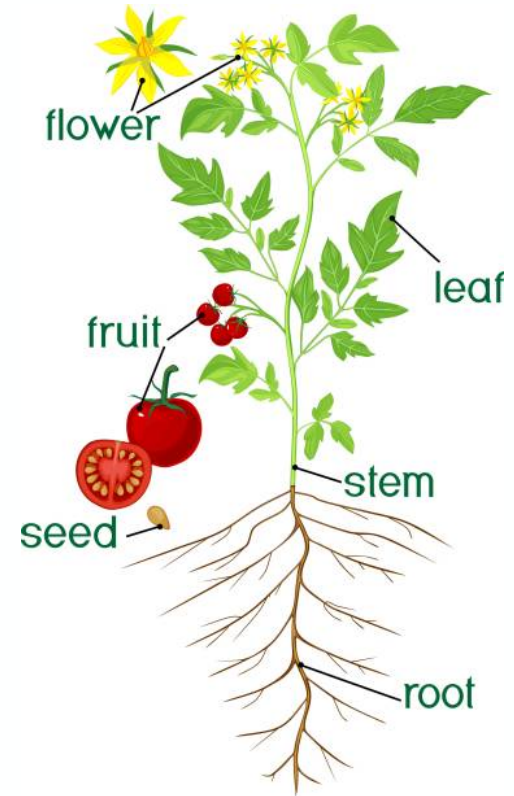
Old feature representation



New feature representation

EXAMPLE DATASET

- Gene expression dataset (RNA-seq) of tomato plants
- For each plant sample, there are expression measurements for more than 28k genes ([Koenig et al., PNAS](#))
- There are 24 samples, which cover all combinations of three experimental factors:
 - Plant tissue: floral tissue, leaf, root, seedling, stem, vegetative tissue
 - Tomato species: *Solanum lycopersicum* M82 (domesticated), *Solanum pennellii* (wild, desert-adapted)
 - Growing location: sun, shade



REPO

<https://github.com/HelmholtzAI-Consultants-Munich/DimRed-Course>



How to get started:

- Go to the notebooks folder
- Open 1_feature_transformation.ipynb
- Use Google colab (recommended, Google account needed)

Alternative:

- Clone or download the repo
- Run the following commands in a terminal

```
conda create -n dimred python=3.10
conda activate dimred
pip install -r requirements.txt
```
- Open 1_feature_transformation.ipynb from the notebooks folder and select dimred as kernel

BREAKOUT ROOMS: 0, F, 9

Please distribute now evenly among these 3 rooms, you are allowed to freely choose one of the rooms. The following is a rough suggestion to get started.

Last name A-G	Room 0
Last name H-R	Room F
Last name S-Z	Room 9

