TG9: Key topics for guiding design and analysis of high-dimensional data

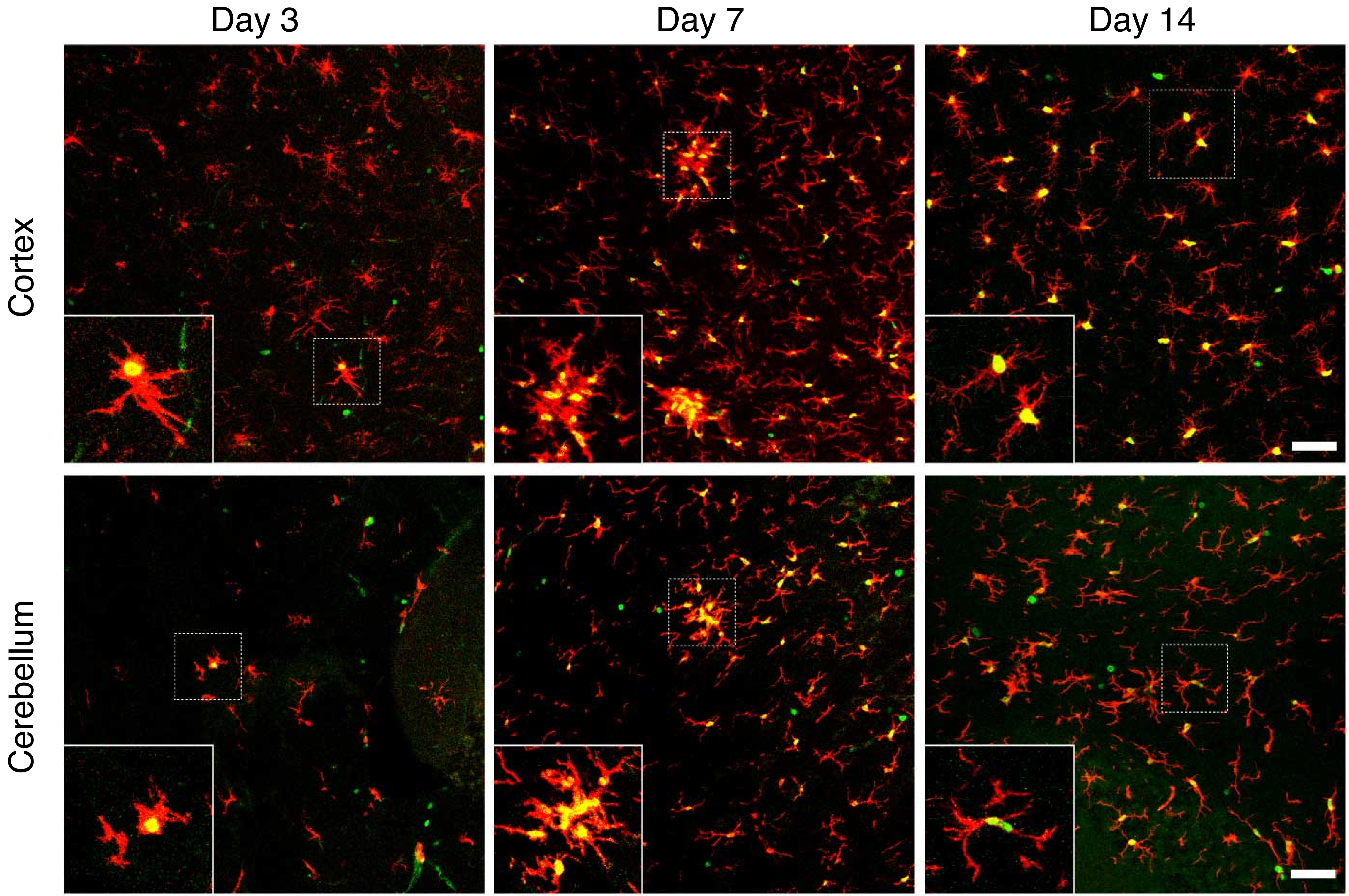
Harald Binder

Division Biostatistics and Bioinformatics
University Medical Center Mainz, Germany

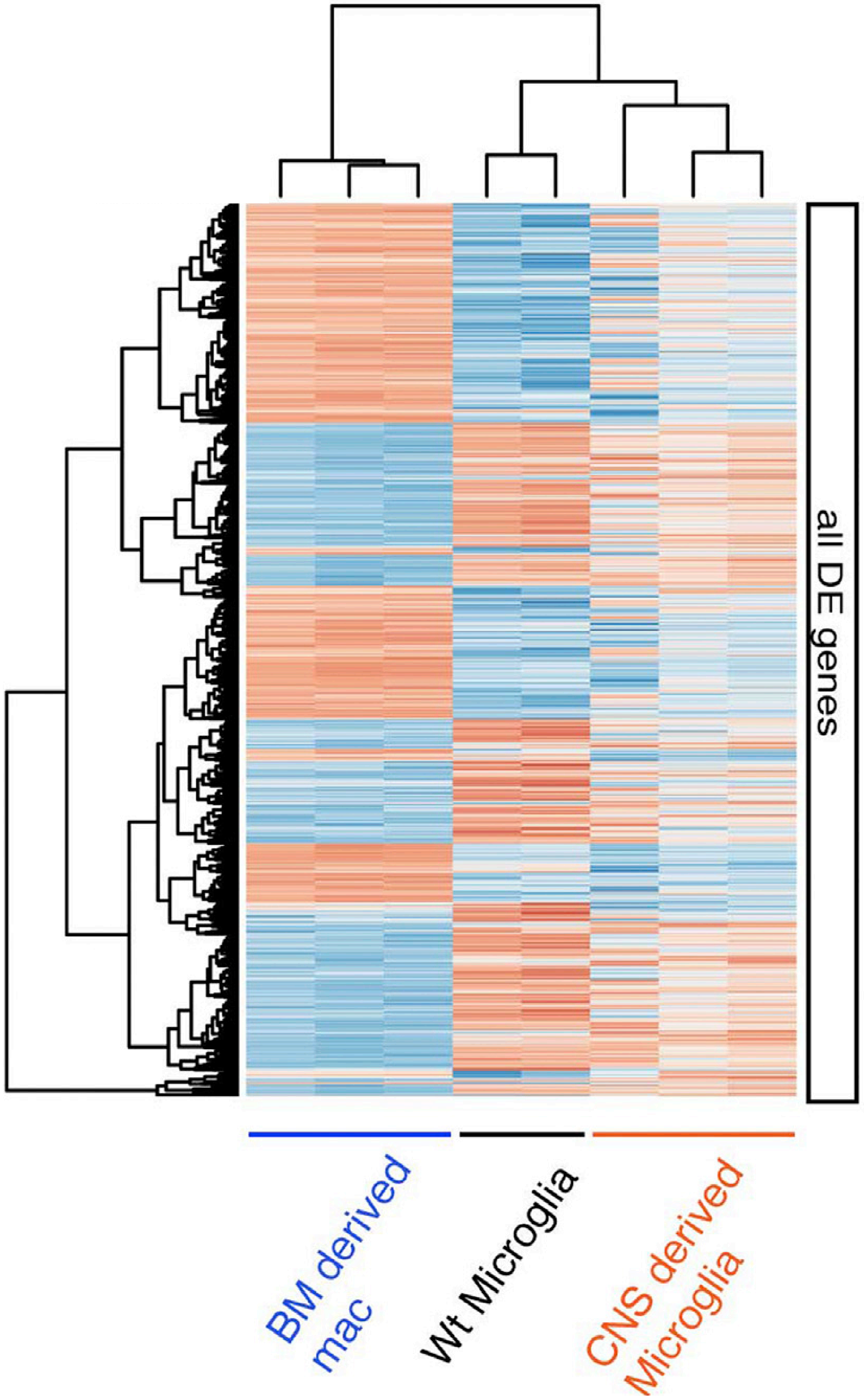
JG|U UNIVERSITÄTSmedizin.
MAINZ

Topic group 9: High-dimensional data

- Chairs: Lisa McShane (NCI, USA), Jörg Rahnenführer (TU Dortmund, Germany)
- Members:
  - Axel Benner (DKFZ Heidelberg, Germany)
  - Harald Binder (University Medical Center Mainz, Germany)
  - Anne-Laure Boulesteix (LMU Munich, Germany)
  - Tomasz Burzykowski (Hasselt University, Belgium)
  - W. Evan Johnson (Boston University, USA)
  - Lara Lusa (University of Ljubljana, Slovenia)
  - Stefan Michiels (University Paris-Sud, France)
  - Sherri Rose (Harvard Medical School, USA)



Bruttger et al. (2015) *Immunity*

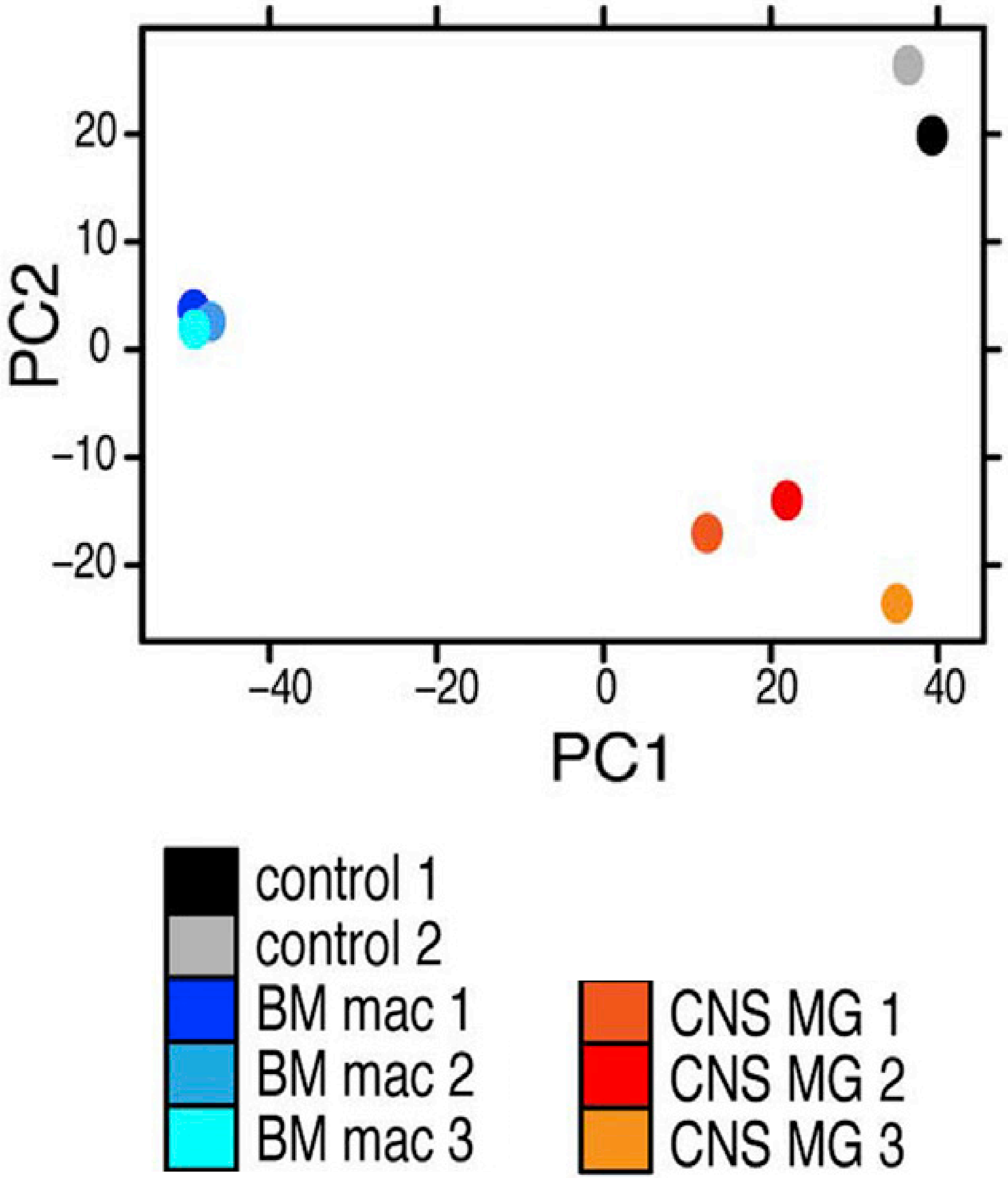


How to ...

- check for batch effects
- perform normalization
- group similar samples
- group similar genes
- select representative genes
- deal with multiple testing

Subtopics (1)

- Data preprocessing
  - normalization/calibration
  - identification of outliers/errors
- Exploratory data analysis
  - graphical displays
  - clustering approaches
  - integrative analysis of different data types
- Multiple testing
  - biomarkers differentially expressed between groups
  - common set of explanatory variables on a large set of outcomes

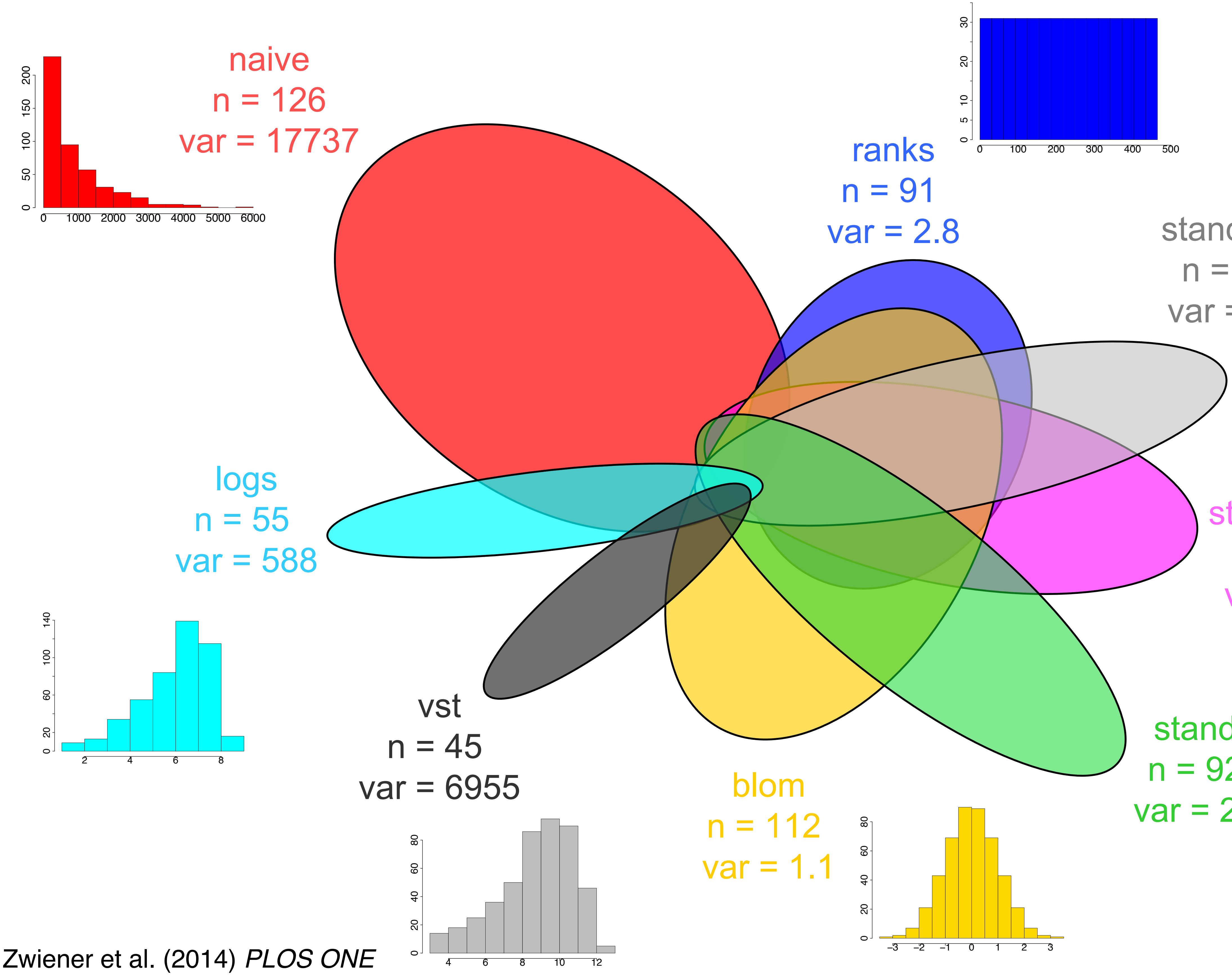


How to ...

- find a low-dimensional representation
- perform inference there
- perform simulations for checking properties

Subtopics (2)

- Data reduction
  - Tasks: visualization of samples or variables, building/finding prototypical samples, building new features
  - Traditional approaches: principal components, multidimensional scaling, correspondence analysis, cluster analysis
  - Current research: representation learning, deep learning
- Simulation
  - Distributions (RNA-seq, methylation microarrays, ...)
  - Simulation using extracted parameters
  - Simulation approaches
  - Simulation based on real data



naive
n = 126
var = 17737

ranks
n = 91
var = 2.8

stand. vst
n = 83
var = 1.9

logs
n = 55
var = 588

stand. logs
n = 78
var = 2.0

vst
n = 45
var = 6955

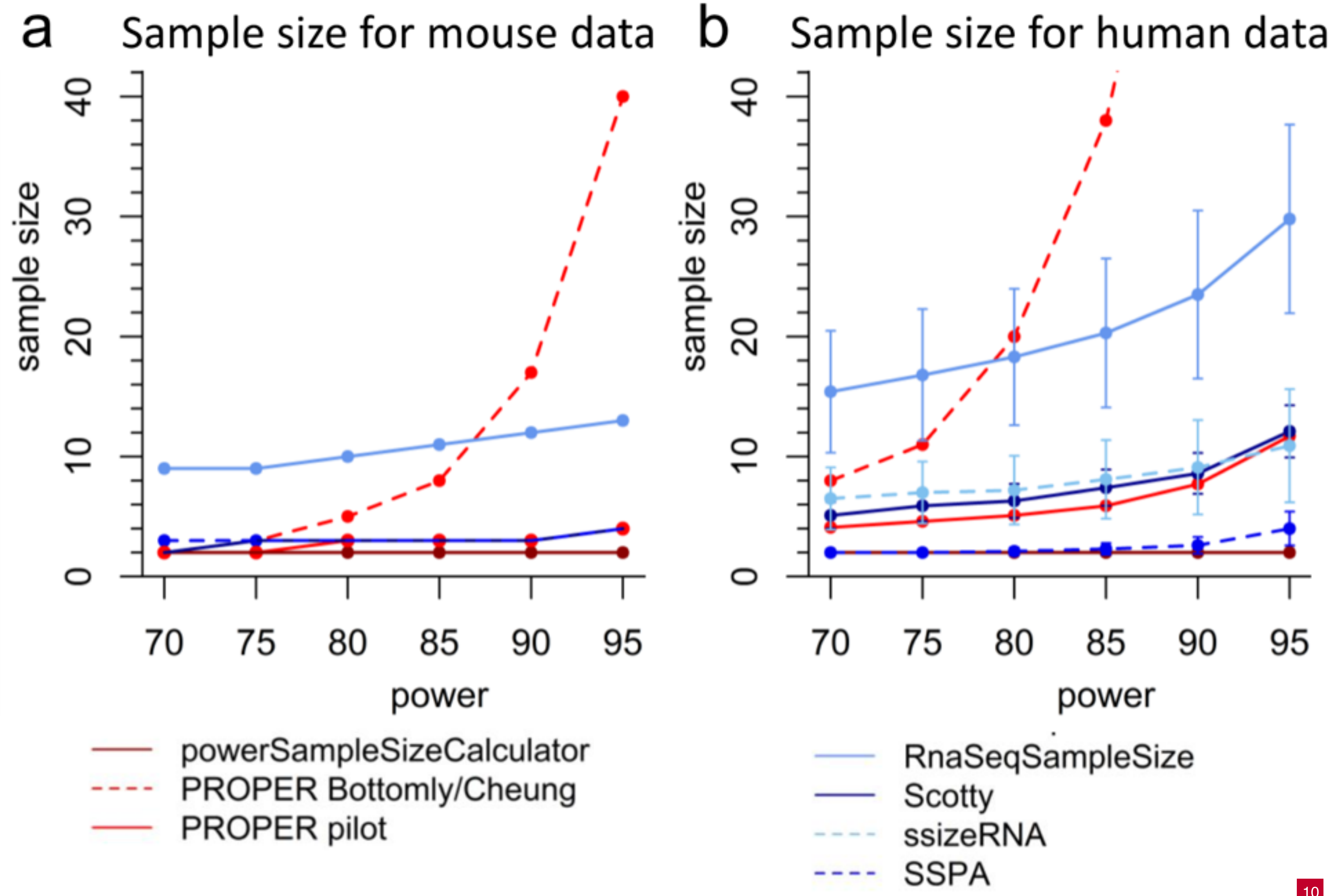
blom
n = 112
var = 1.1

stand.
n = 92
var = 2.6

Zwiener et al. (2014) *PLOS ONE*

Subtopics (3)

- Prediction models
  - Machine learning methods
  - Penalized regression
  - Evaluation
- Categorical and ordinal data
- Comparative effectiveness and causal inference
- Design considerations
  - Sample size planning and power calculation
  - Experimental design for observational studies
- Publicly available data sets



a Sample size for mouse data

b Sample size for human data

Outlook

- Large topic with links to Bioinformatics and Systems Biology
- But: high-dimensional challenges also in non-omics settings
- Overlap with many other topic groups, but always with high-dimensional flavor
- Subtopics make progress feasible
- First drafts of papers by end of 2016