Bioinformatika
Gene expression data analysis

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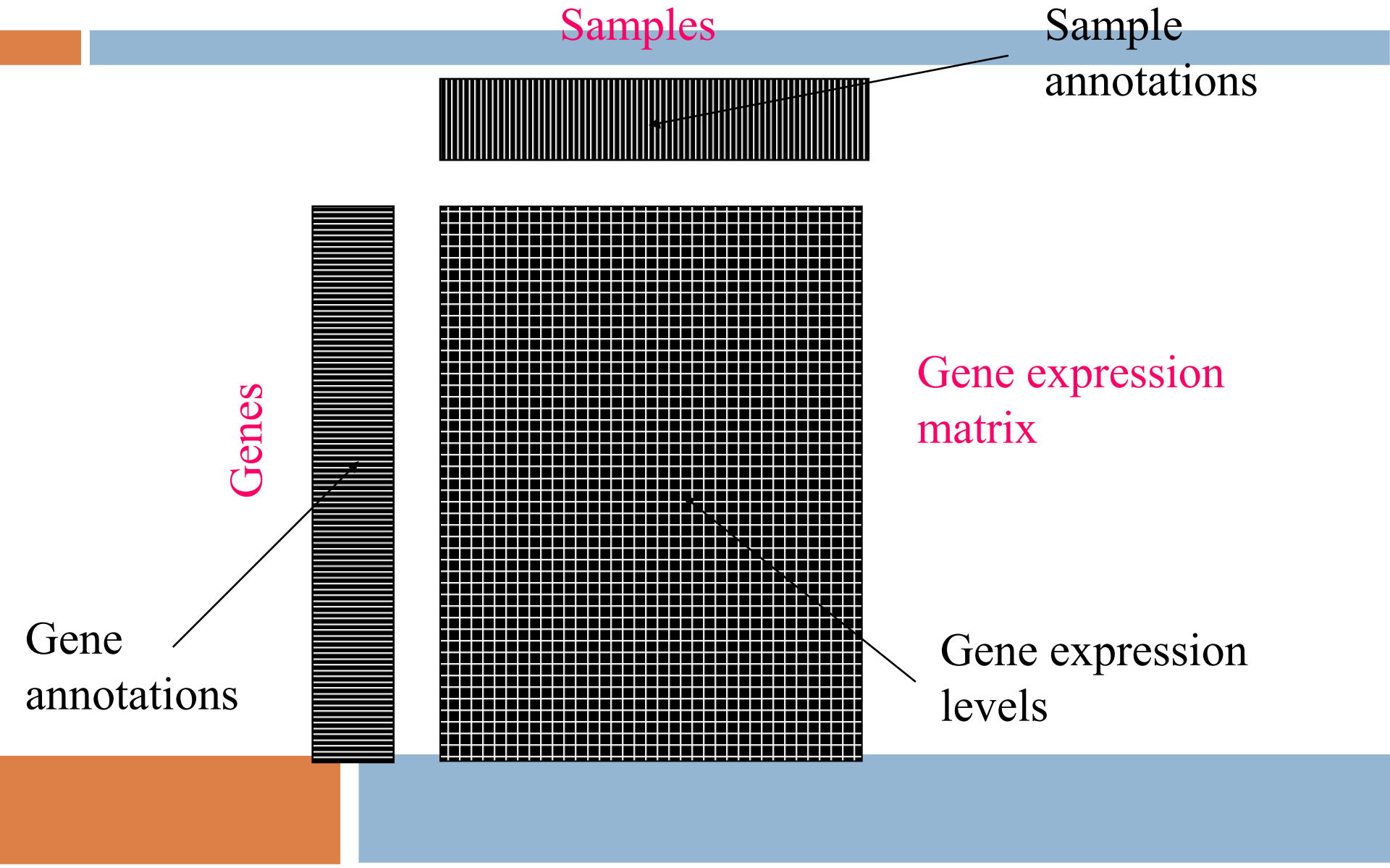
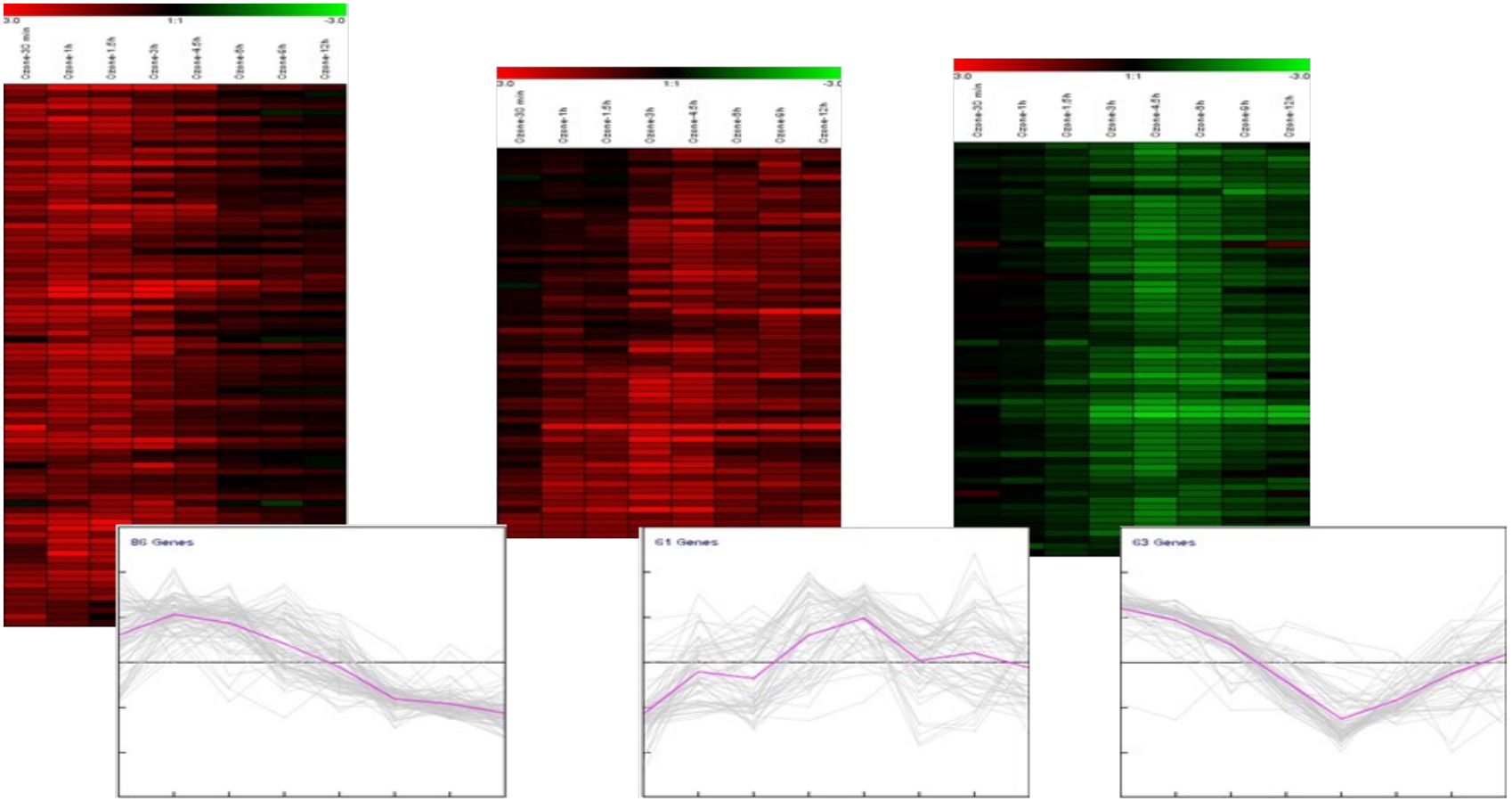
(some slides are courtesy of Mark Craven, U. of Wisconsin)

GE data – conceptual view



GE data – image view



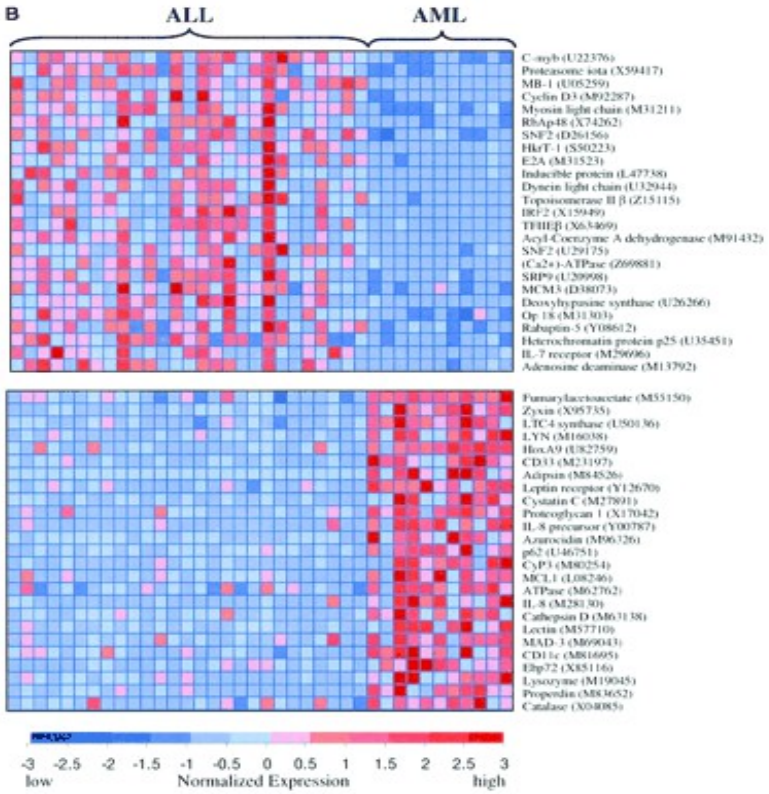
Classification task

Challenge:

- samples (10^1) x features (10^3)
- False hypotheses, overfitting
- Interpretability:
  are the expressed genes the causal ones?

What to do?

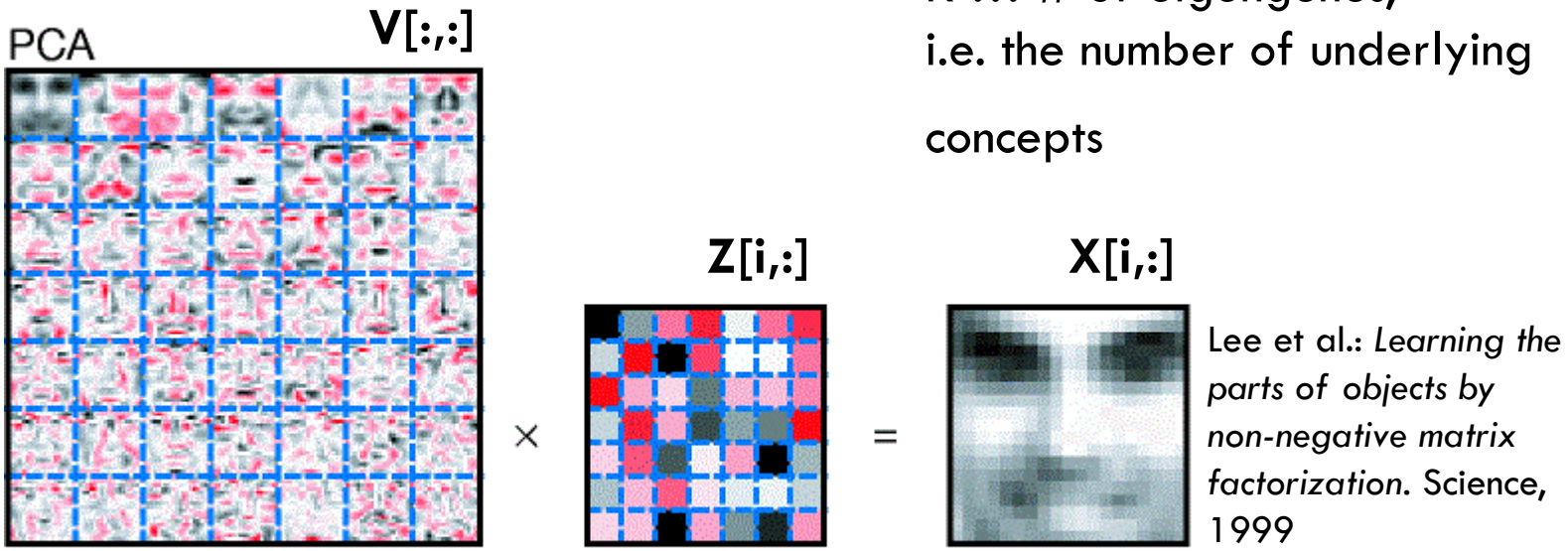
- Decrease number of hypotheses
- Analyze more abstract entities than genes, eg. principal components



Golub et al.: *Molecular classification of cancer: Class discovery and class prediction by gene expression monitoring.* Science, 1999

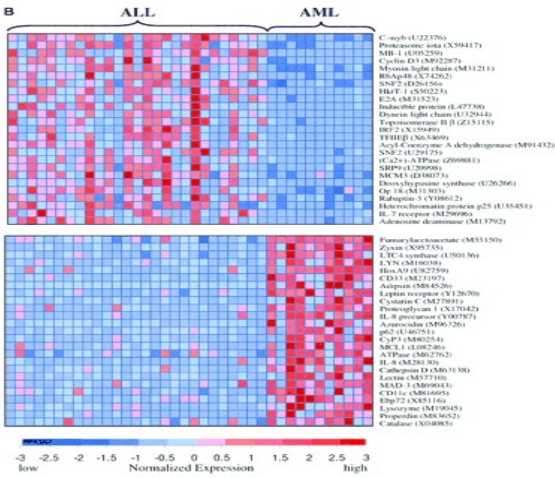
PCA – motivation

- M … # genes
- N … # samples
- **X** (N x M) … GE data in the space of *genes*
- **V** (M x K) … transformation basis, eigengenes
- **Z** (N x K) … transformed GE data in the space of eigengenes
- K … # of eigengenes, i.e. the number of underlying concepts



Lee et al.: *Learning the parts of objects by non-negative matrix factorization.* Science, 1999

Assignement



Golub et al.: *Molecular classification of cancer: Class discovery and class predi-ction by gene expression monitoring*. Science, 1999

Data

- 7,129 GE profiles of 72 patients
- 25 samples … acute myeloid leukemia (AML)
- *47* samples … acute lymphoblastic leukemia (ALL)

Task

- Construct decision tree model to differentiate these types of tumours.

Assignement

Workflow

1) Learn a decision tree on subjected data. Use Matlab class **ClassificationTree**, for learning use method **fit()**.
2) Visualize resulting model (function **view()**) and enumerate the training error (function **predict()**)
3) Estimate the real error of the model by the means of crossvalidation. Use script **cv11.m**.
4) Compare the training error and real error estimation. Why are so different?

Assignement

Analyzing in terms of PCAs

Transform the data to the reduced space of eigengenes. Use attatched functio **pca.m:**

1) Do the transformation for the number of cmponents K=5:5:64, i.e. **Z** = **X** **V**(1:K,:).
2) For each of these transformed data **Z** learn the decision tree.
3) Choose an appropriate model according to its training error and model complexity.
4) Evaluate the chosen model by the crossvalidation
5) Compare the error estimation with the one of simple tree.

Assignement

Interpreting the results

1) Use web tool Phenopedia HuGE Navigator
2) Try to find some gene from most important PCAs of the tree under the disease terms 'Leukemia, Myelocytic, Acute' and 'Leukemia, Lymphocytic, Acute'
3) To mine the genes from the important components of the tree use attached function **mineGenes.m** and **geneNames.mat**
4) Simmilarly find some genes from the **component tree**