Bioinformatika
Gene expression data analysis

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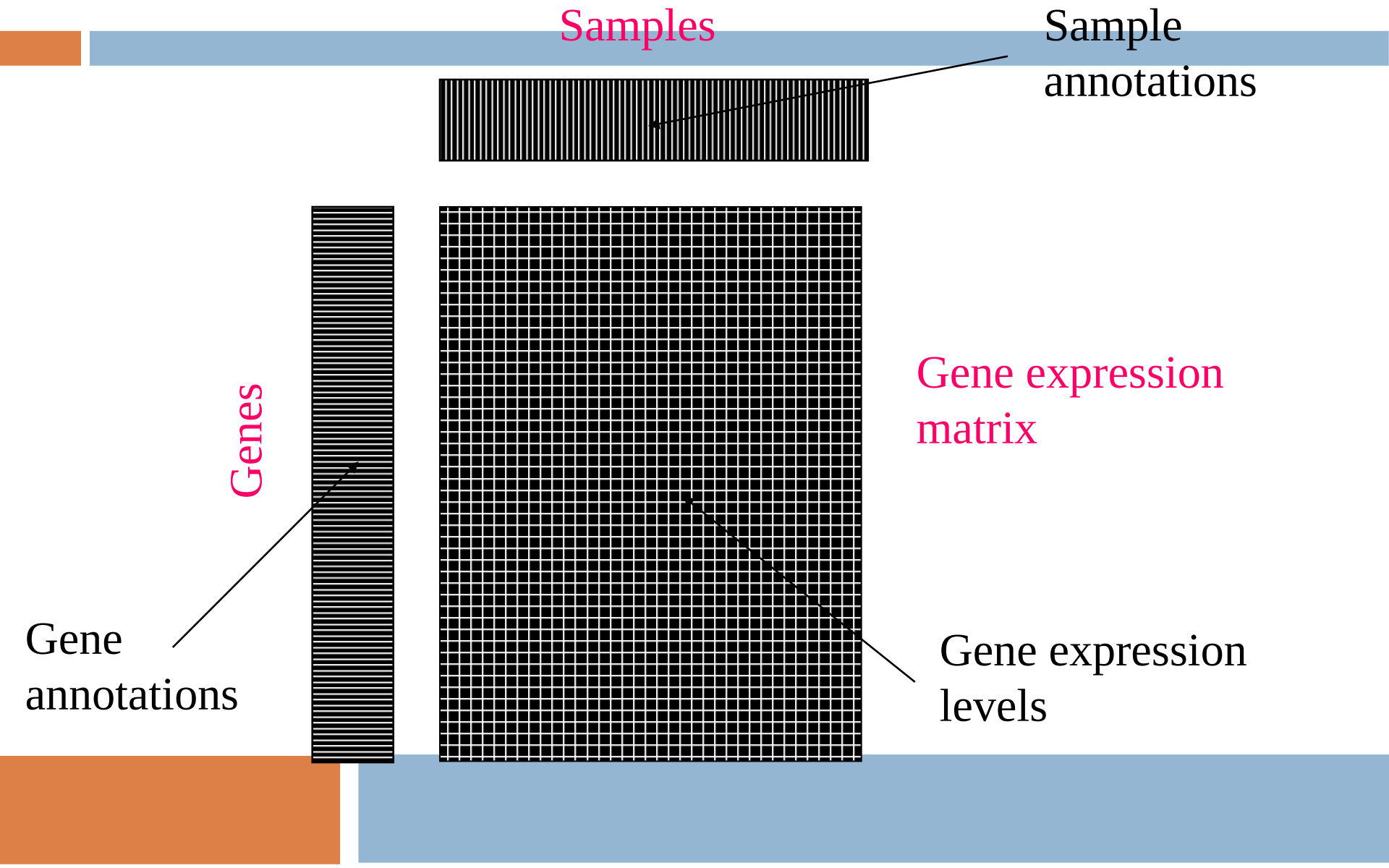
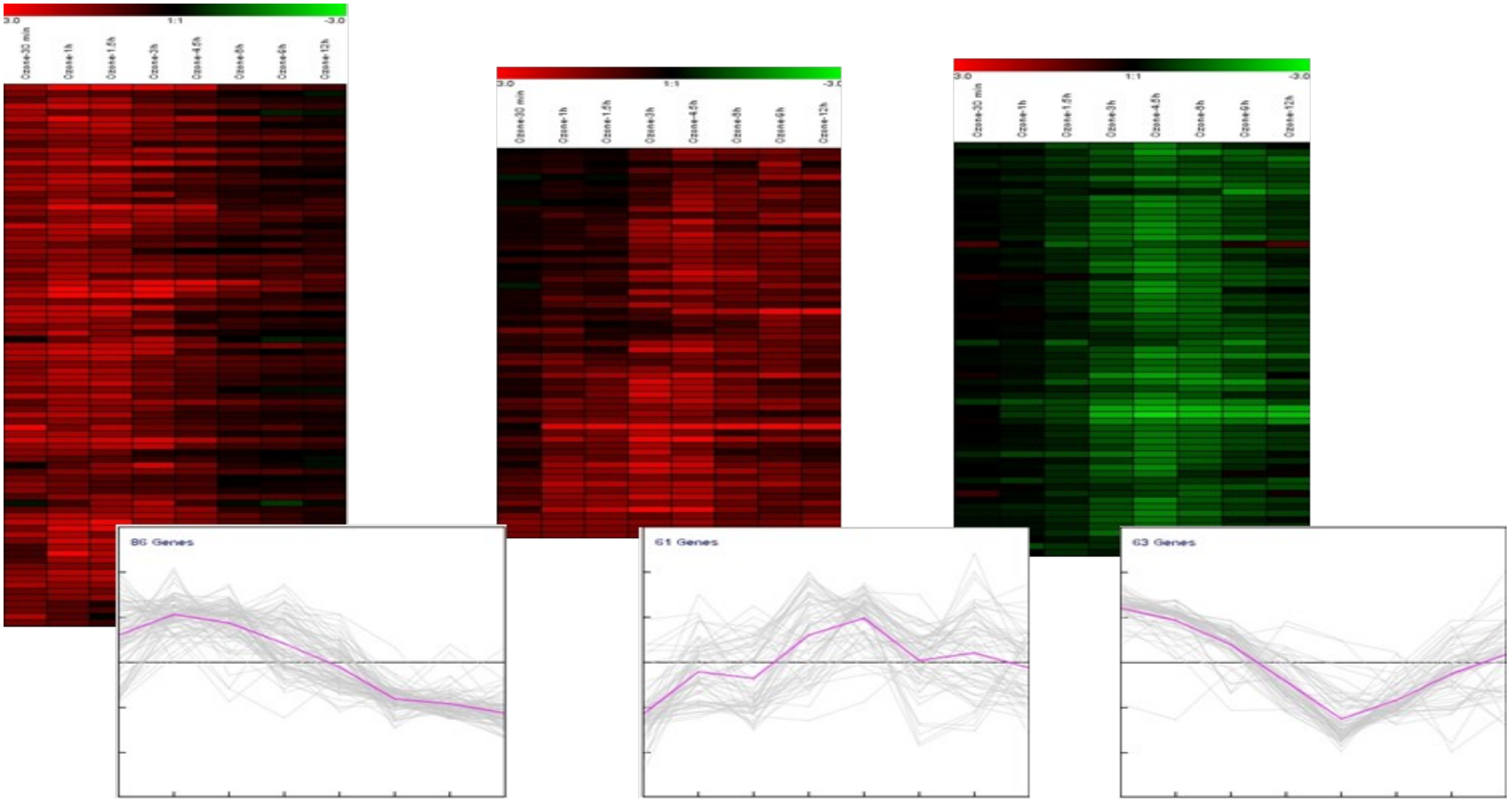
GE data – conceptual view



GE data – image view



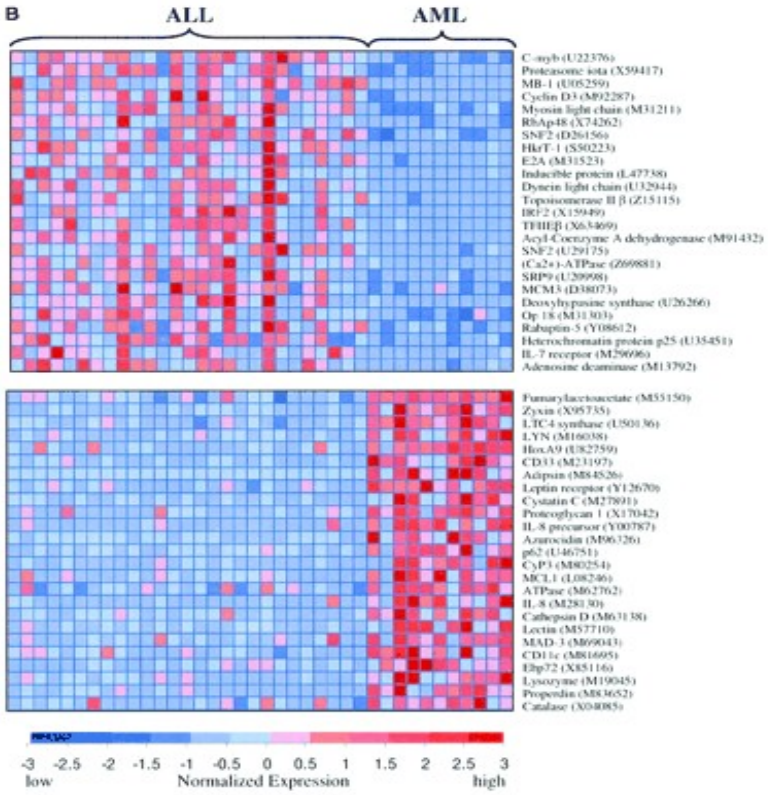
Classification task

Challenge:

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

What to do?

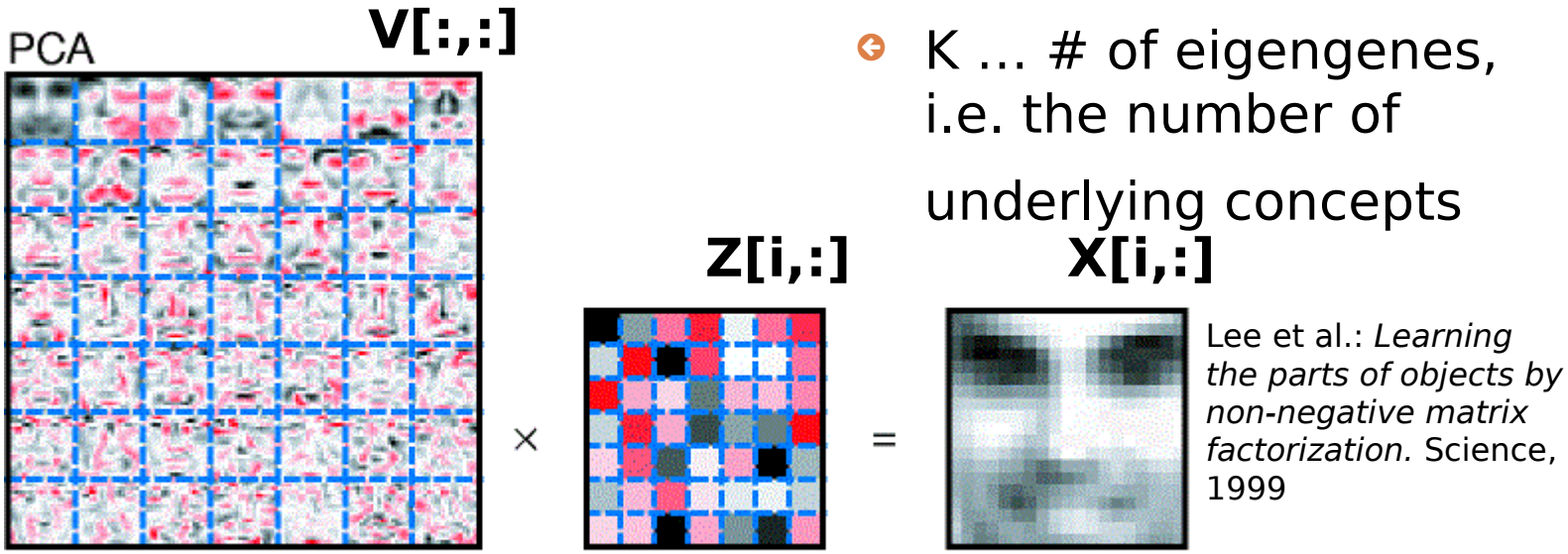
- Decrease number of hypotheses
- Analyze more abstract entities than genes, eg. principal components



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

Assignment

Data:

- 7,129 GE profiles of 72 patients
- 25 samples: acute myeloid leucaemia (AML)
- 47 samples: acute lymphoblastic leucaemia (ALL)

Golub, T., et al. *Molecular classification of cancer: class discovery and class prediction by gene expression monitoring*. Science 286.5439 (1999): 531-537.

Task:

- Construct decision model to differentiate these types of tumours.

Assignment

Workflow I:

1. Learn a decision tree on subjected data. Use Matlab class `ClassificationTree` and its method `fit`.
2. Show the tree (method `view`) and enumerate its *training* accuracy. How would you interpret this model? Which gene is crucial for decision? Compare it with the original article. Have this gene been previously reported as Leucaemia associated? Use e.g. phenopedia.
3. Estimate its *real* accuracy by the means of crossvalidation. Compare the two accuracies. Why are they so different?

Assignment

Workflow II:

1. Learn a basis matrix *V* of the data. Use attached function `pca.m`.
2. For $K = \{5, 10, 20, 50\}$, project the original data *X* to the top *K* components *V*. The result is reduced data $Z = XV^T_{1:K,:}$
3. On these 4 transformations, learn decision trees, show them and enumerate their *training* accuracy.
4. Choose optimal decomposition and corresponding tree-model (use training accuracy and Occam razor). Estimate *real* accuracy of the optimal model by crossvalidation.

Assignment

Understanding the model:

1. Use attached function `mineGenes` to extract the genes, frequnetly appearing in the components presented in your tree-model
2. Resulting gene-sets, related to each component in the tree, interpret in overrepresented GO terms. Use e.g. amigo.
3. Create a story!