

Correlation between the fission yeast transcriptome and proteome

Project description

Goal

- Compare mRNA levels with protein levels through the time course of meiosis in the fission yeast *S.pombe*.
- Extract and cluster uncorrelated samples.

Context

- The mRNA is the precursor of the protein.
- Synchronous meiosis occurs within a time window of 10 hours: meiotic nuclear divisions occur at 5 and 6 hours.
- Studies show that correlation between mRNA and proteins levels are often weak.. Indeed, mRNA and protein synthesis and stability are regulated by different pathways to allow a rapid adaptation to the cell's need.

Data

- Dataset of relative protein concentrations *Simanis-lab, EPFL* – 2978 proteins
- Dataset of relative mRNA concentrations *Bählerlab, ULC* – 5121 mRNAs

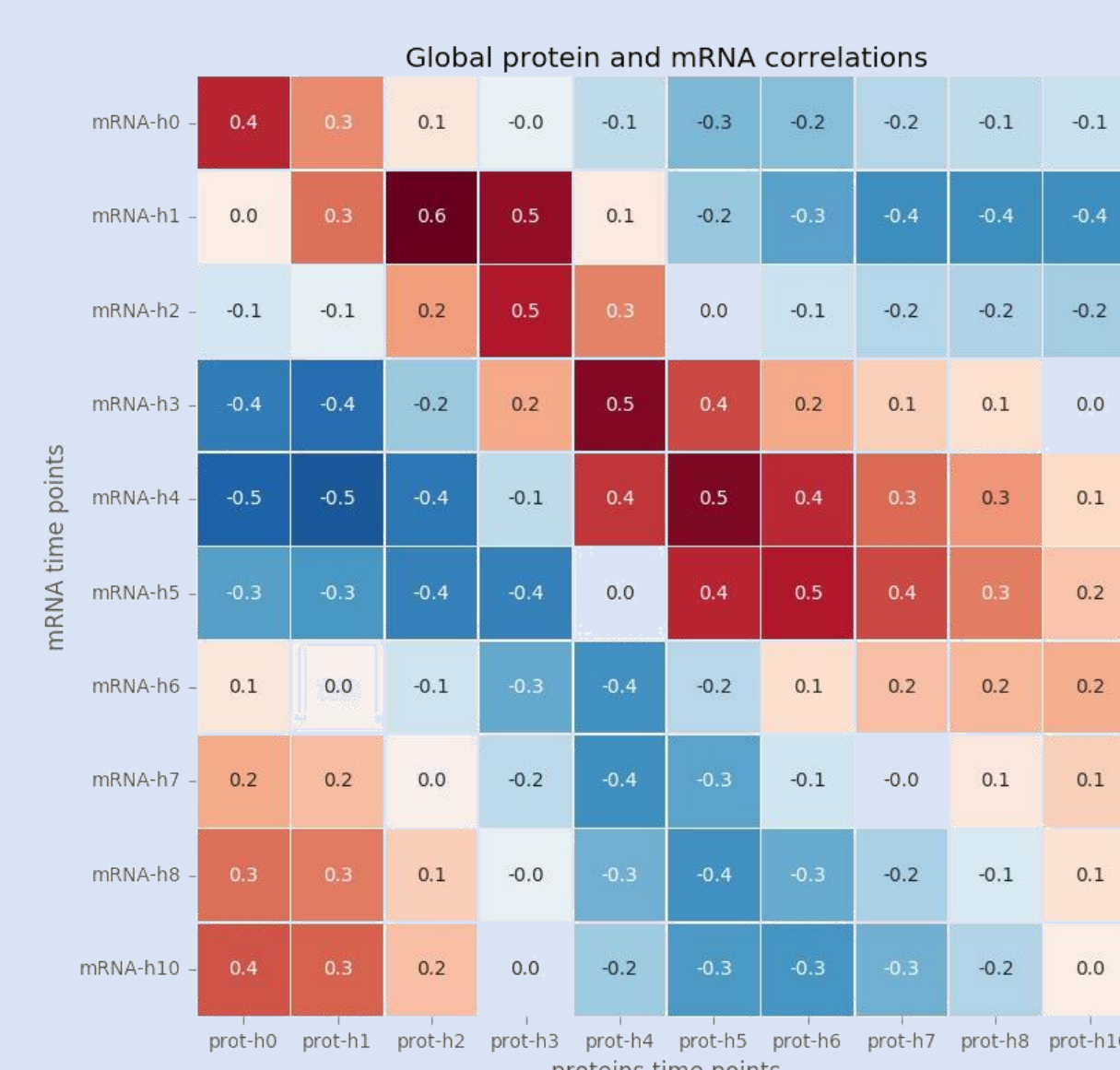
Data preprocessing

- Correspondence in time points
- Matching mRNA and protein entries
- Data standardization

Correlation analysis

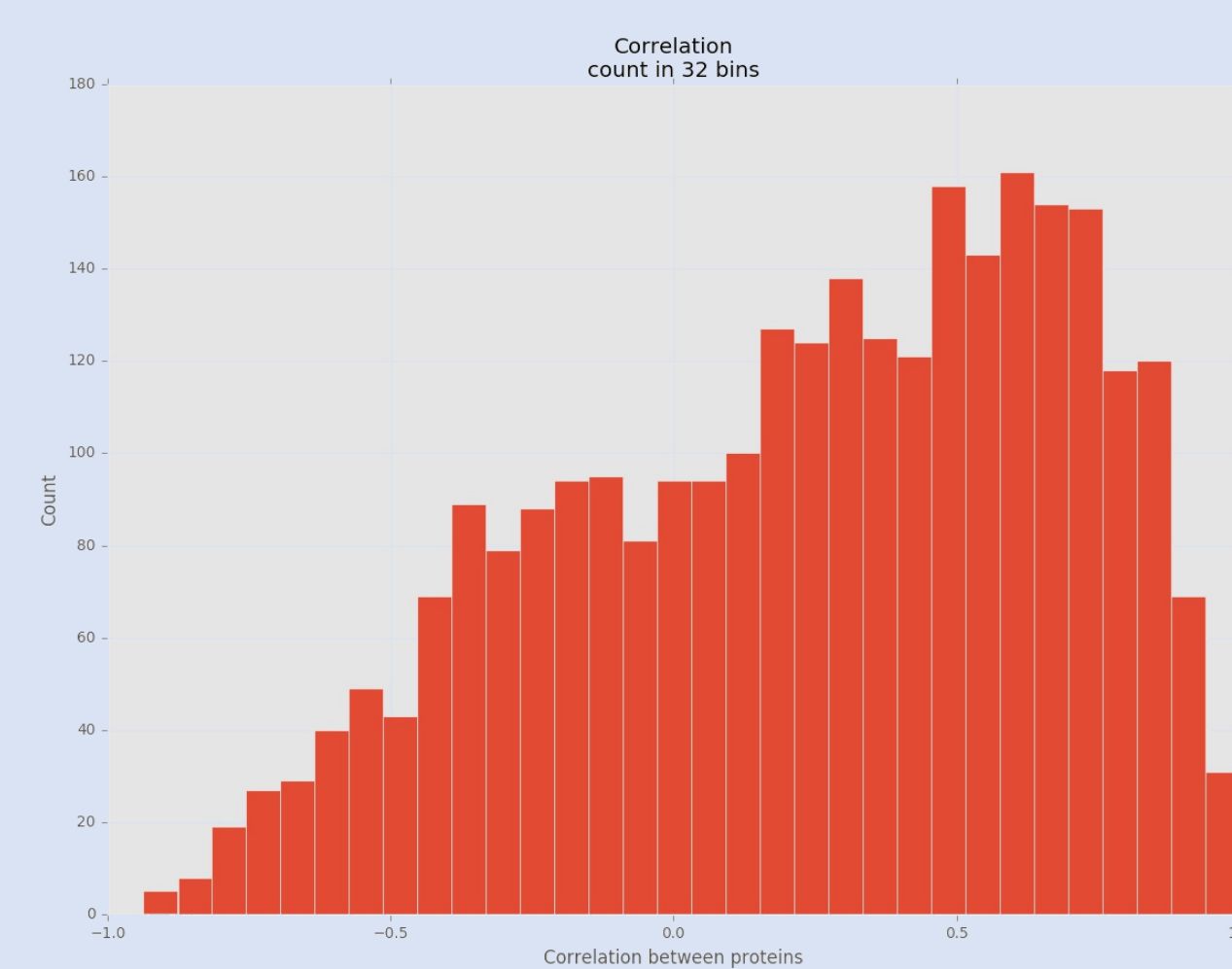
Heatmap:

- mRNA levels at t correlate to protein levels $t+1h$ (reflecting the delay in protein synthesis) until mRNA at 5h



Pearson's correlation:

- Few entries are anti-correlated,
- Global correlation (with varying strength)
- Significant number of weakly correlated/uncorrelated levels



Plotting individual entries:

Uncorrelated and anti-correlated entries are of special interest, since they hint towards regulatory processes aimed to adapt the levels to the development of the spores.

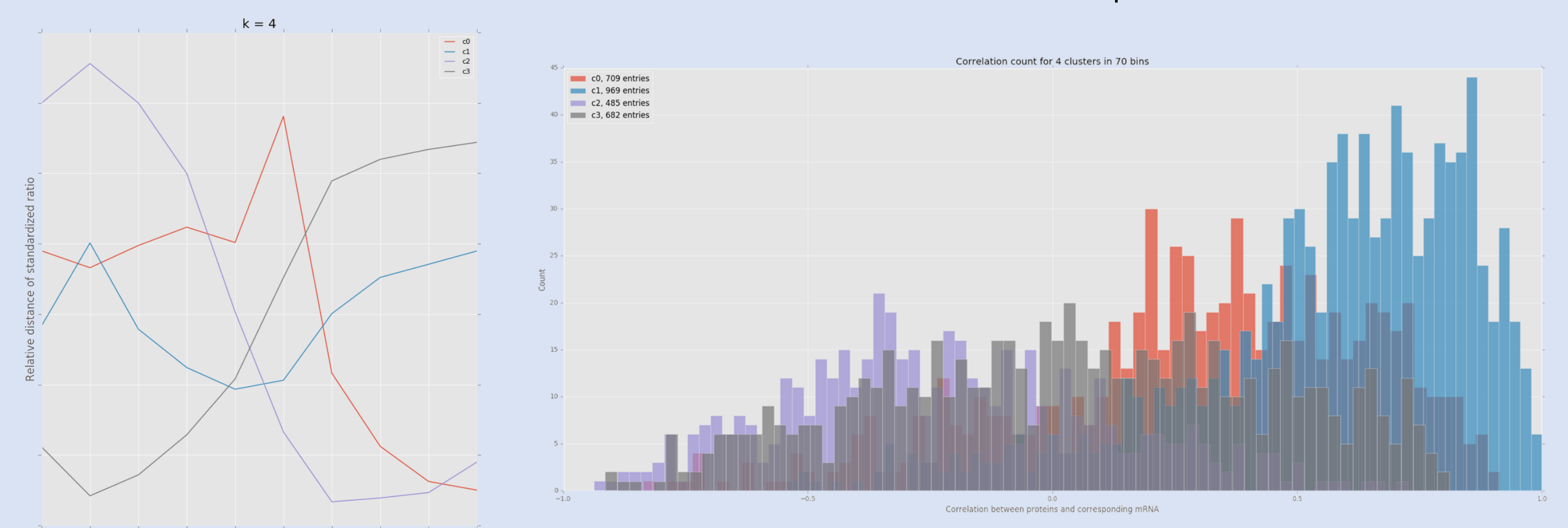
Problem : choice of a threshold to extract uncorrelated entries

Clustering the whole dataset

Goal : define clusters of uncorrelated entries

Clustering methods : k-means, ward

Data : relative distance between mRNA and protein levels



Results :

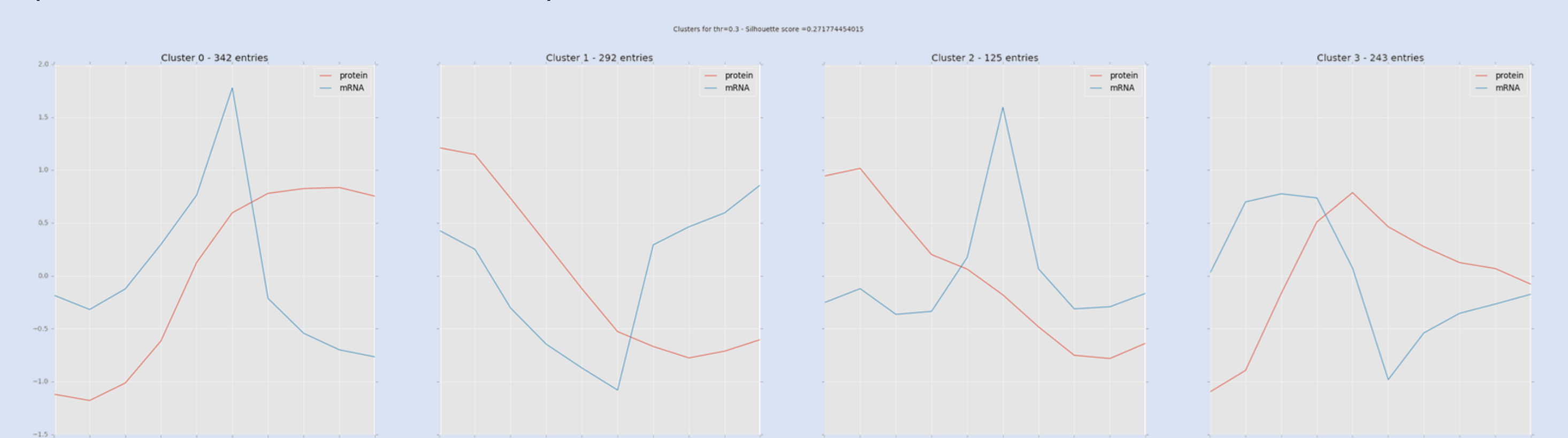
- Similar results for different clustering methods
- Definition of two clusters of uncorrelated proteins: 1. protein levels are higher than mRNA levels, indicating stable proteins; and 2. protein levels are lower than mRNA levels, indicative of fast protein degradation

Clustering uncorrelated levels

Goal : Find patterns in uncorrelated entries

Clustering methods : k-means, ward

Data : Extraction of uncorrelated data for several thresholds (between 0.3 and 0.01)



Results :

- Similar results for different clustering methods.
- Overlapping clusters (clusters for k contained in $k+1$)
- For all thresholds, we obtain similar clusters
- Major variation at 5h (corresponding to the time point where major biological transitions take place – meiotic divisions).

Conclusion

- Loss of correlation at 5h reflection biological transitions
- Correlation between t , $t+1h$ reflecting delay in protein synthesis
- Difficult to extract uncorrelated entries (clustering or thresholds)
- Clusters defining different regulatory processes (stability versus degradation)