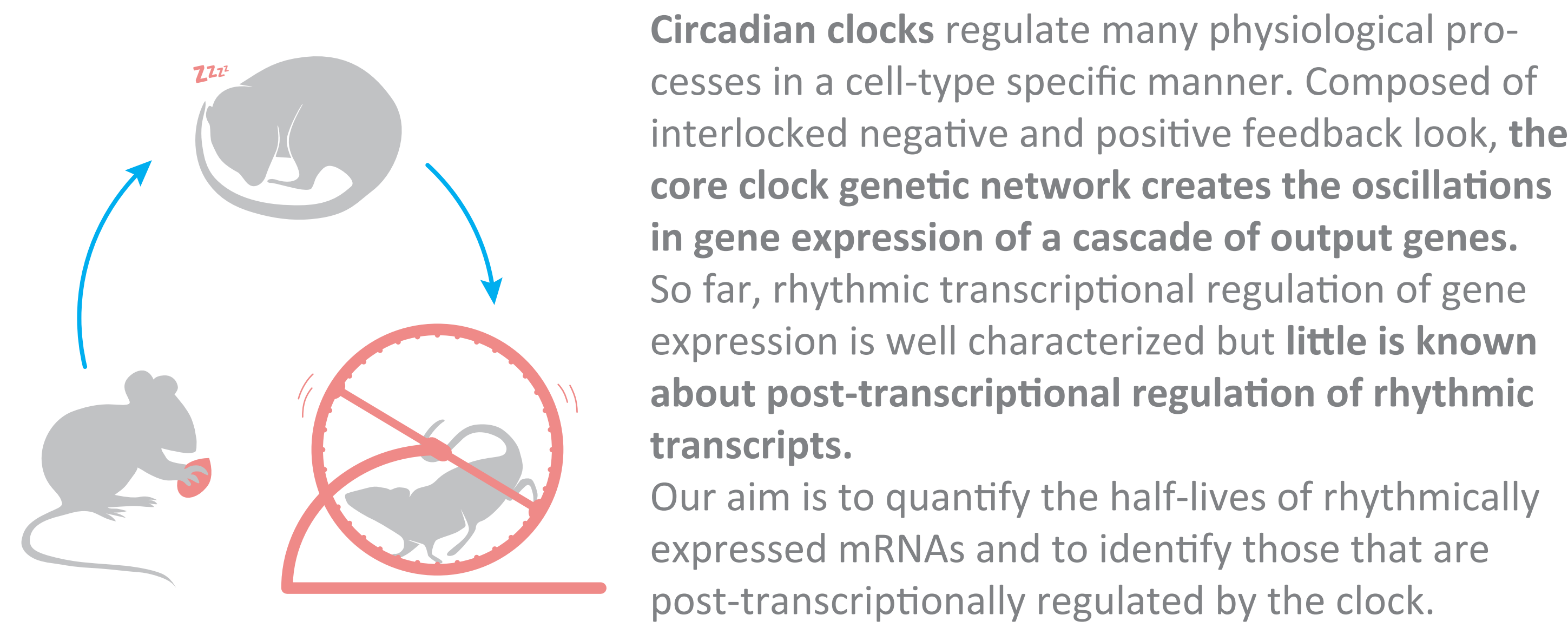


Post-transcriptional regulation : major or minor role for *circadian* expression of transcripts?

Laura Symul^a, N. Molina^a, A. Zeisel^b & F. Naef^a

^aUPNAE-IBI-SV, EPFL, Lausanne
^bWeizmann Institute of Science, Israel

Introduction & Questions



- How can we measure/infer post-transcriptional regulation?
(see Material & Methods panel)
- What fraction of rhythmic genes have a circadian regulation after transcription?
(see Results panel)
- Can we characterize this post-transcriptional regulation?
(see Results panel)
- What are the potential regulators? When do they act?
(see Conclusion & further work panel)

Conclusions & further work

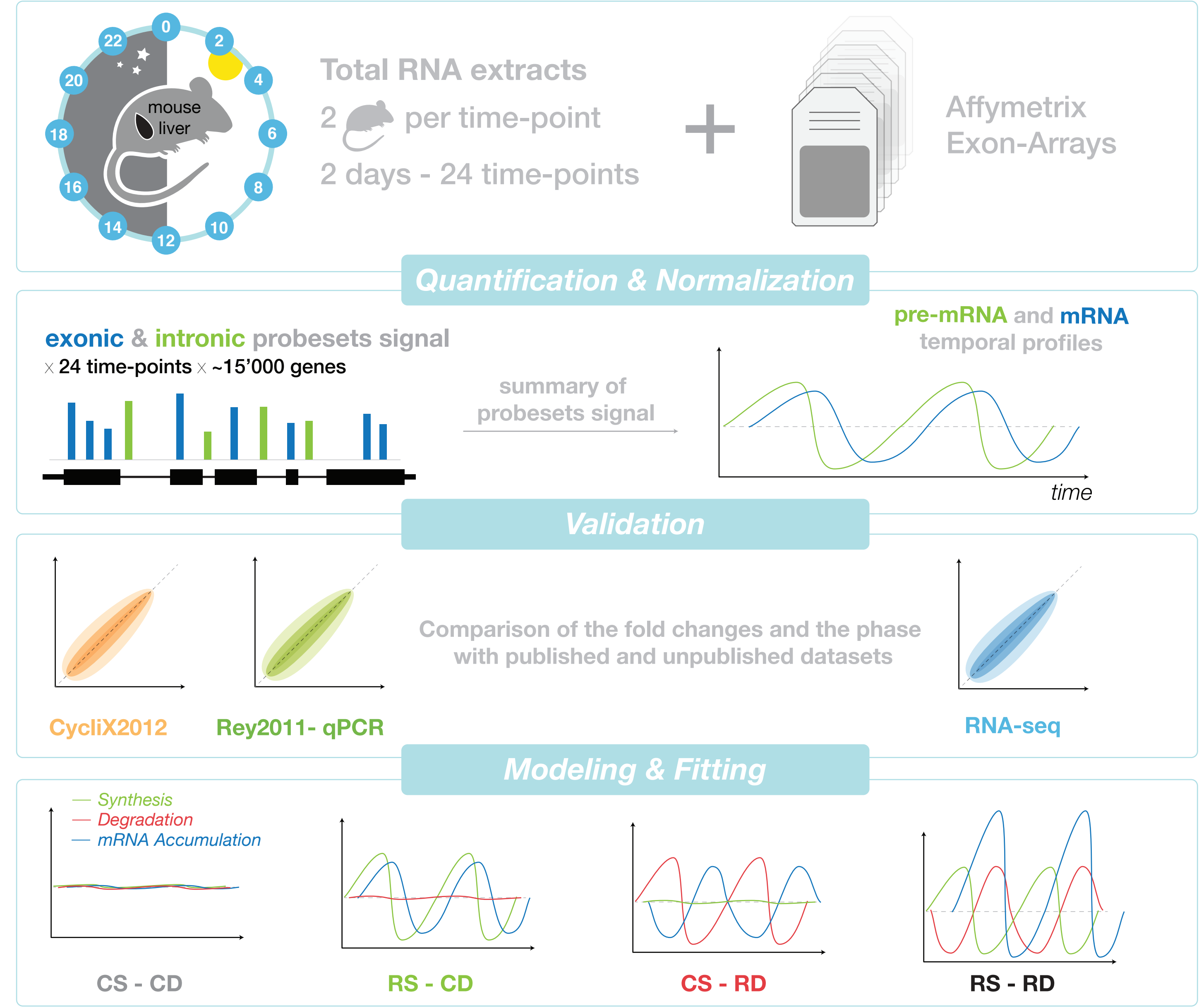
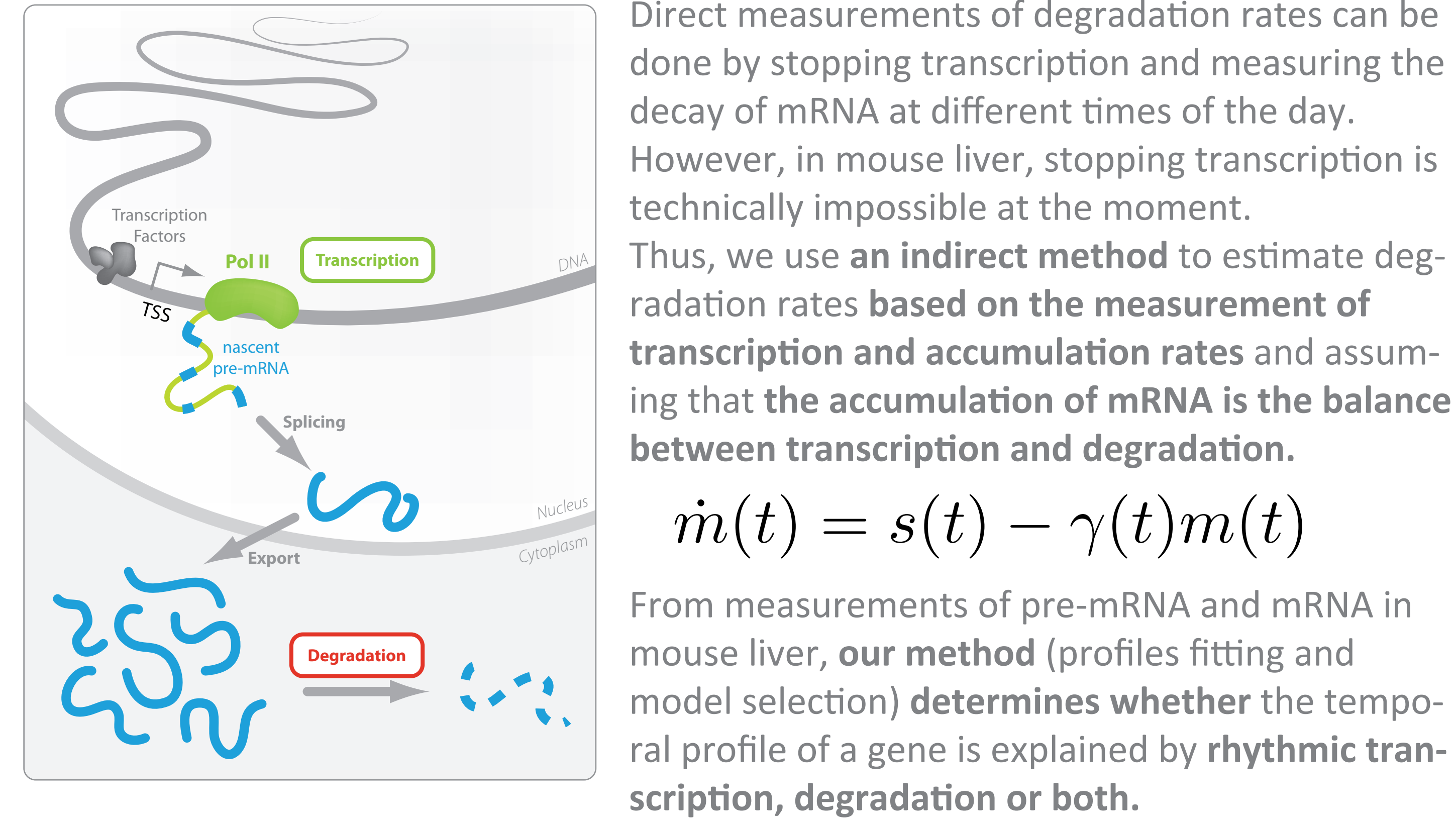
Thanks to a **model-based approach**, we were able to indirectly predict the post-transcriptional regulation of mRNA. We provide estimation of the half-lives for rhythmic transcripts in mouse liver and we found that a small fraction (about 20% of rhythmic transcripts) is characterized by half-lives shorter at given time of the day.

Our results suggest that the mRNA that undergo rhythmic degradation are **less stable during the day** (when the mouse is sleeping). We also observe that rhythmic degradation is used either to create oscillations of transcripts that are transcribed constitutively, either to adjust the time and the amplitude of transcripts that are rhythmically transcribed.

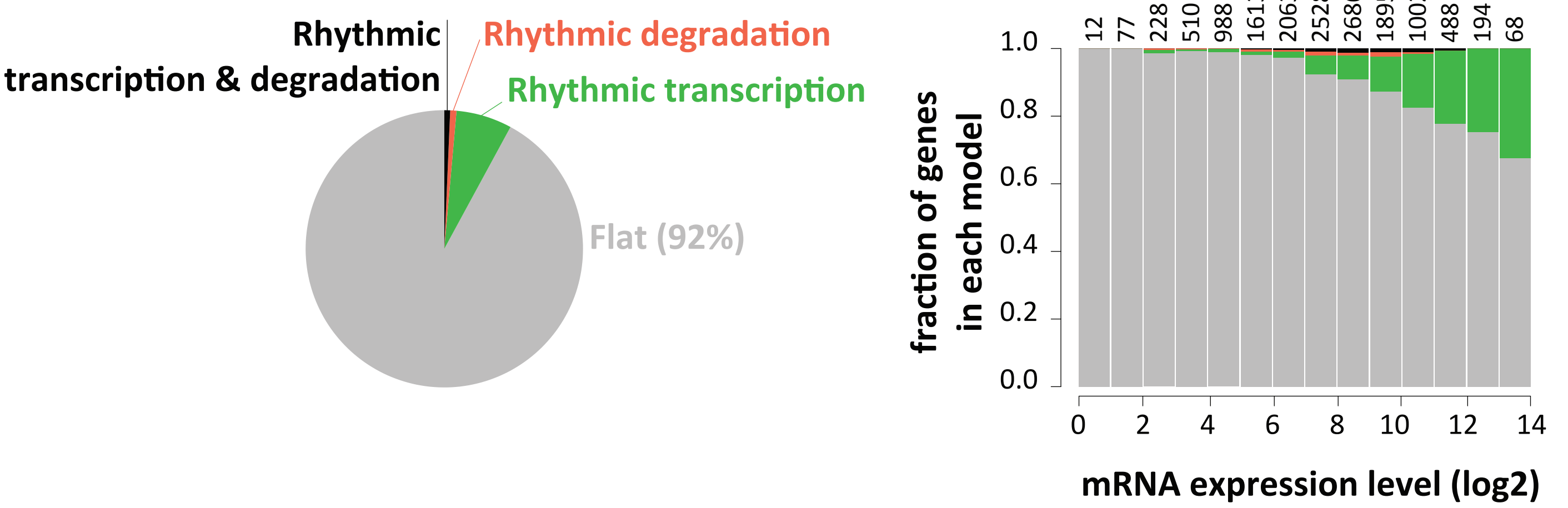
These results lead to other questions about this post-transcriptional regulation:
What are the regulators?
miRNA? RNA Binding Proteins (RBPs)?
It has also been observed that some deadenylases (that trigger the degradation of mRNA) or associated proteins are rhythmically expressed.

The next step of this project is to first use bioinformatics tools to find whether some of the regulators can explain the specific post-transcriptional regulation of some transcripts. We then plan to experimentally validate this regulation.

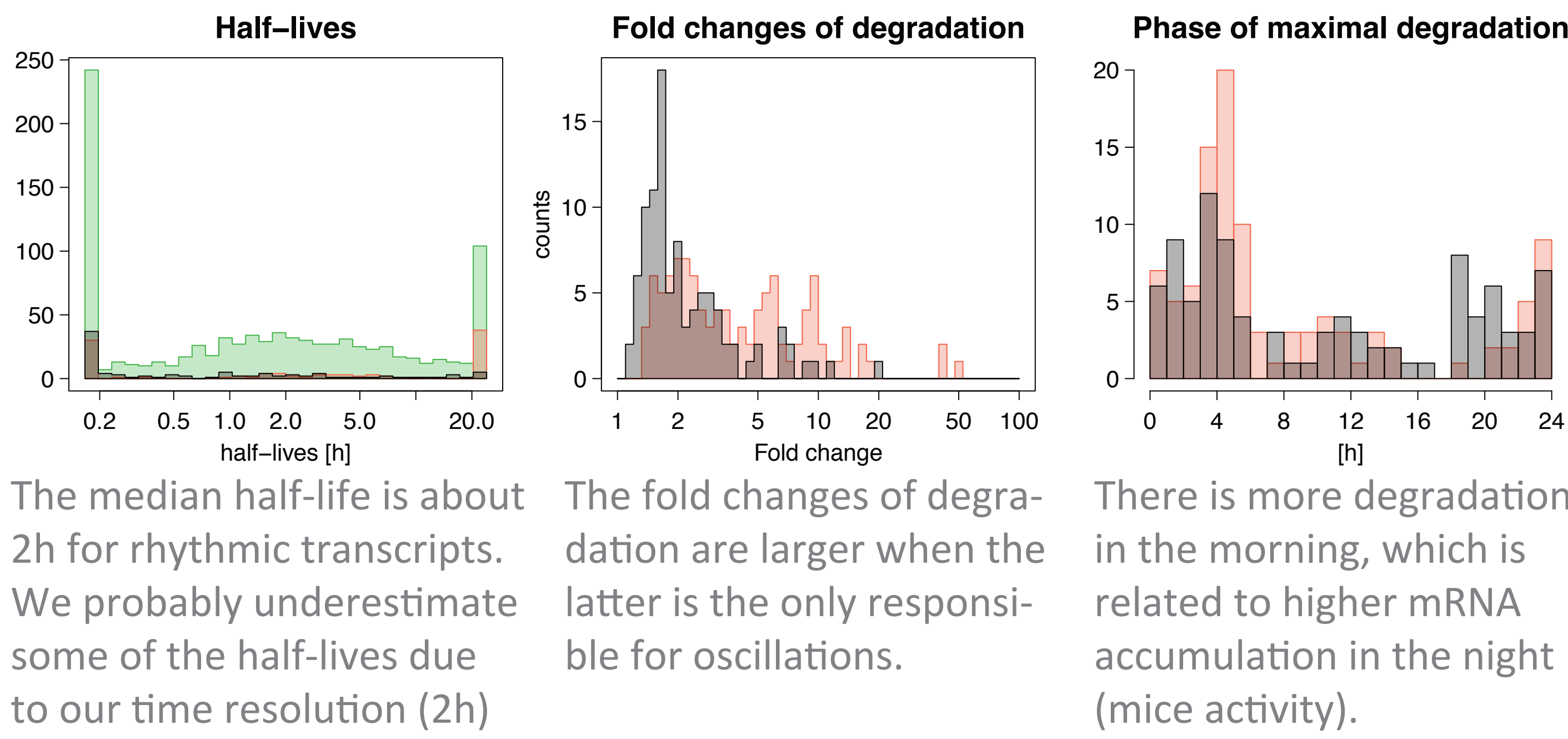
Material & Methods



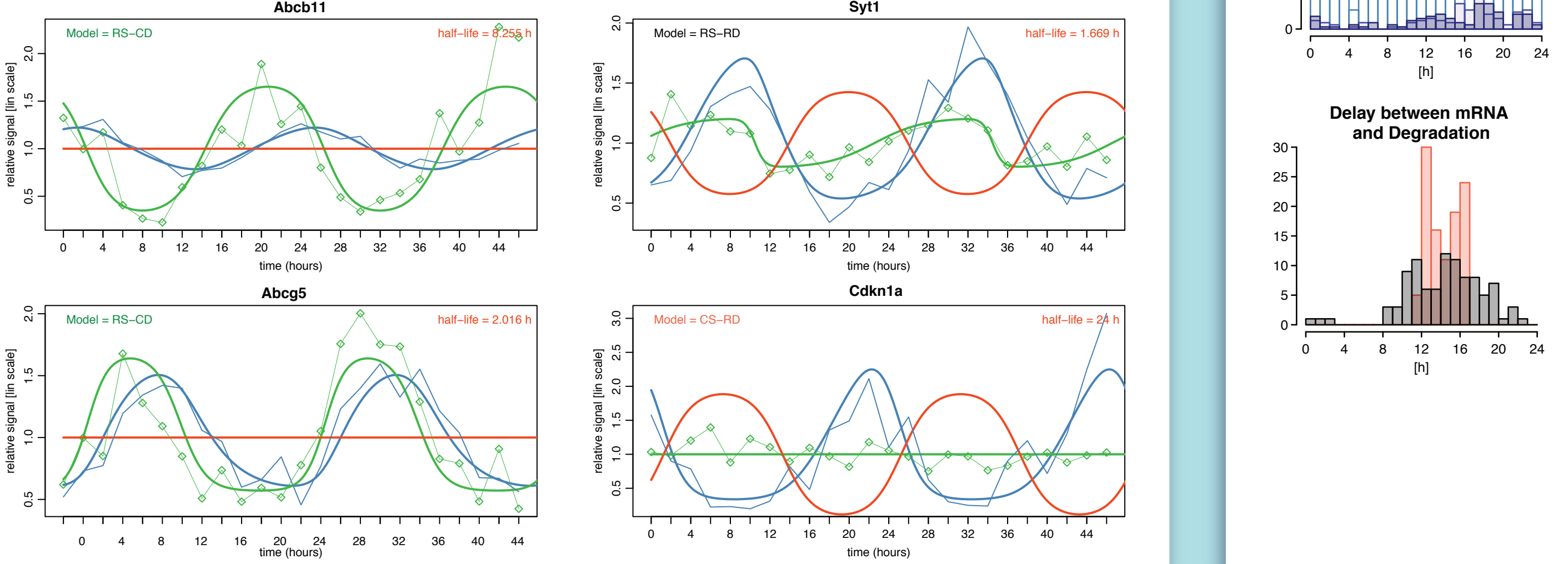
(Preliminary) Results



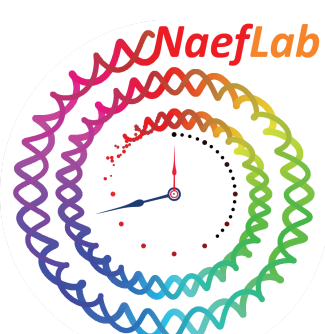
Most genes are not expressed rhythmically but that fraction increases with the level of expression. Among the rhythmic transcripts, only 20% of them have rhythmic degradation.



Examples



Aknowledgements & Ressources



Félix Naef Nacho Molina
Rosamaria Cannavo
Jingkui Wang & others

Frederic Gachon
UNIL | Université de Lausanne
for the biological samples

Amit Zeisel & E. Domany
מכון ויצמן למדע
WEIZMANN INSTITUTE OF SCIENCE
for their help on the analysis of exonarrays

cyclix.ch
The CycliX Consortium

High Performance
Computing Center
for their clusters/servers