Patterns of tRNA Modifications

Peter F. Stadler

Bioinformatics Group, Dept. of Computer Science & Interdisciplinary Center for Bioinformatics, **University of Leipzig**

Max Planck Institute for Mathematics in the Sciences,Leipzig
RNomics Group, Fraunhofer Institute for Cell Therapy and Immunology, Leipzig
Institute for Theoretical Chemistry, Univ. of Vienna (external faculty)
The Santa Fe Institute (external faculty)

Joint work with
Anne Hoffmann, Jörg Fallmann, Fabian Amman, and the Mörl Lab

Benasque, Jul 17 2018

## Conservation of Modification Patterns

- How conserved are chemical modifications of RNAs
  - between different species
  - between different tissues
- Can this be studied with widely available data?
  tRNAs (or at least fragments) appear in high coverage in
  most small-RNA-seq datasets.
  Can this information be mined?

The answer is a partial yes: Many but not all chemical
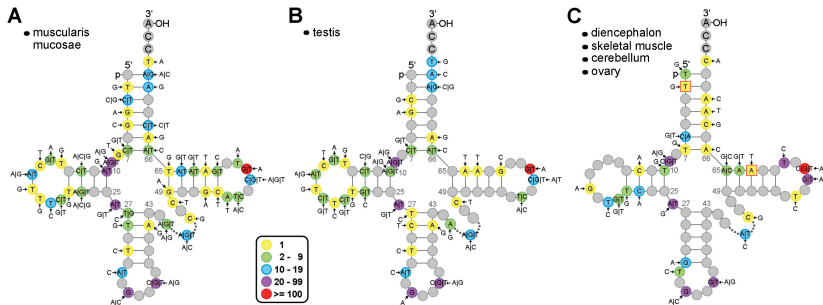modification leave detectable traces in normal RNA-seq data
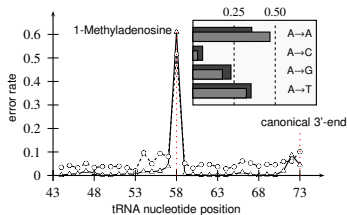
mismatches
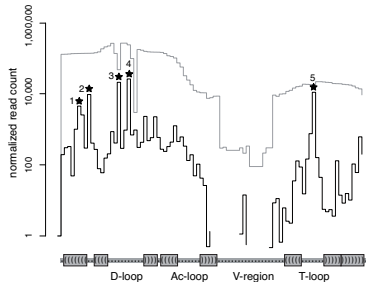
RT stops

- Many very similar tRNA paralog
- tRNAs with introns

Specialized mapping pipeline

- remove pre-tRNA reads that map across the boundaries of mature tRNAs (and everyhing that maps well outside tRNAs)
- mask out tRNA genes from genome
- cluster very similar mature tRNAs and use a consensus
- add these "tRNA prototypes" as artificial chromosomes
- disregard positions with variations between paralogs in the same cluster
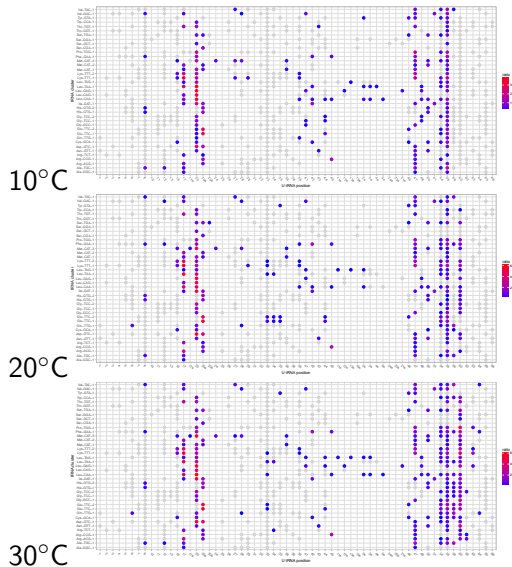
Variations between tissues

A
- muscularis mucosae

B
- testis

C
- diencephalon
- skeletal muscle
- cerebellum
- ovary

Legend:
- 1
- 2 – 9
- 10 – 19
- 20 – 99
- >= 100

- Very similar results for rat tissues
- Evidence for a few modifications in miRNAs
- the method also picks up A-I editing in miRNAs (and other small RNAs)
- modifications seem to be common also in snoRNAs

S. cerevisiae tRNA^Trp
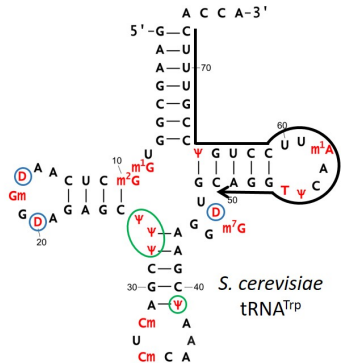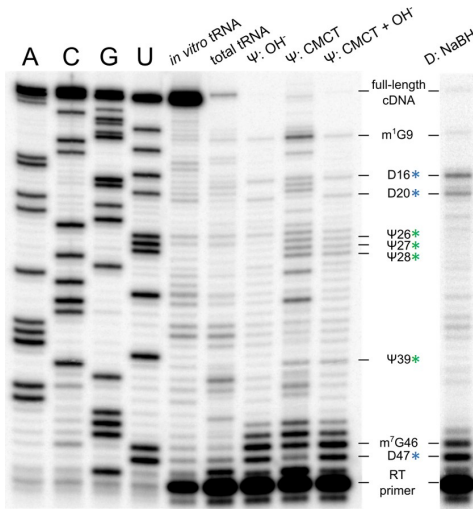
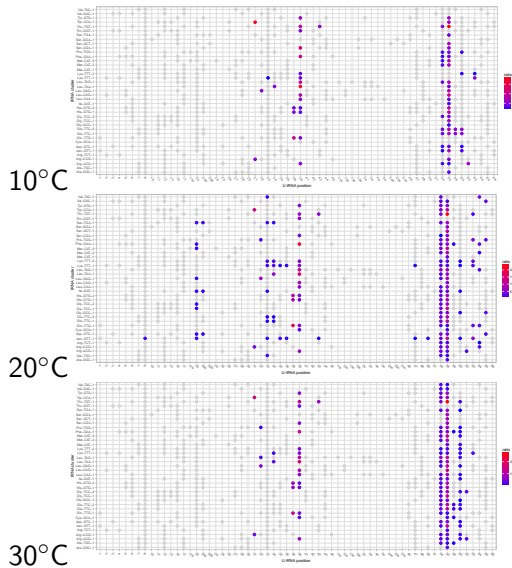# Temperature dependence of Dihydrouridine

10°C

20°C

30°C

Exiguobacterium sibiricum

- 3 biological replicates
- simple model to determine a *p*-value for the over-representation of RT-stops at each position
- Benjamini-Hochberg correction with 5% FDR
- cutoff for minimum fold change

10°C

20°C

Exiguobacterium sibiricum

30°C