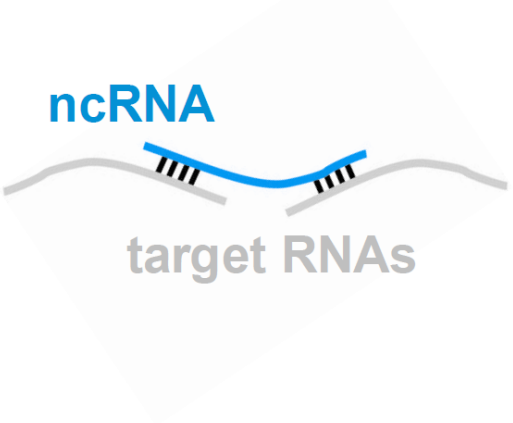
Comparison of Non-Coding RNAs in Drosophila and Human

Rebecca Kirsch

TBI Winterseminar
18/02/2015

Challenges of Experimental ncRNA Analyses

so far:
analysis of single
known ncRNA



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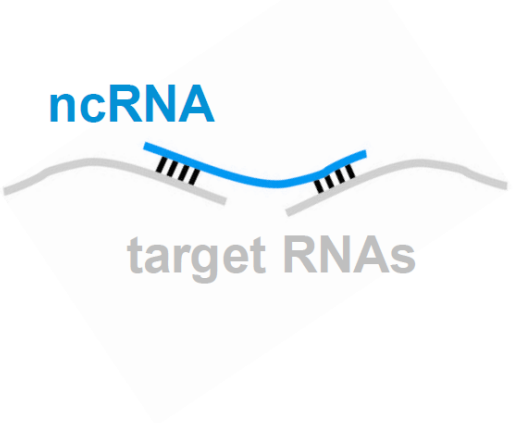

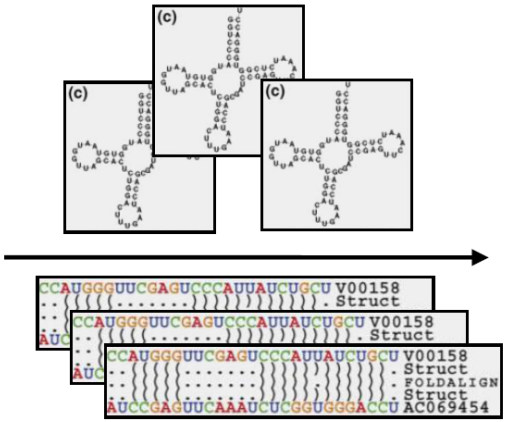

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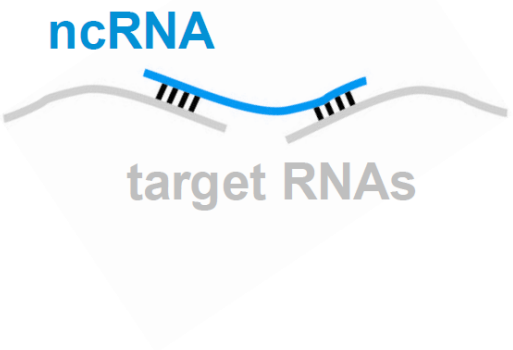
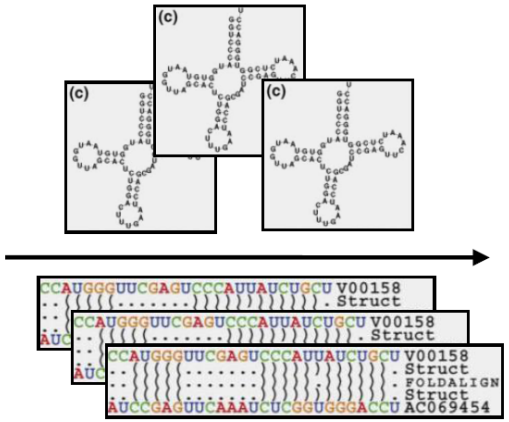
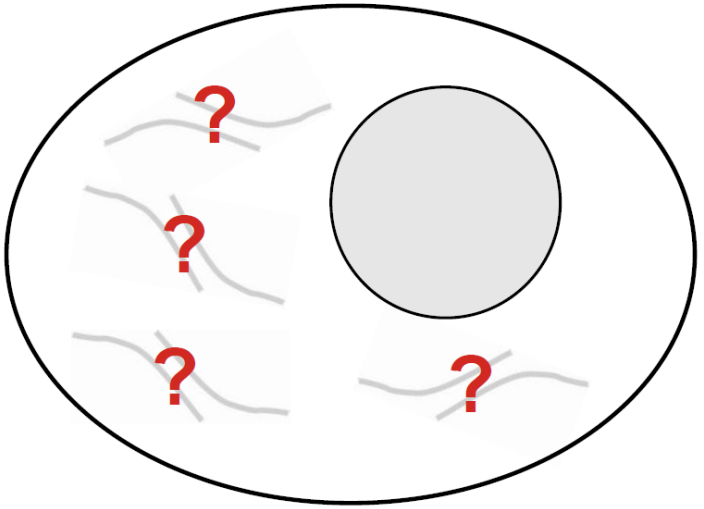




aim:
high-throughput



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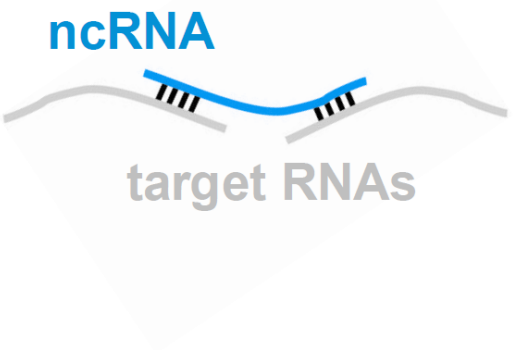

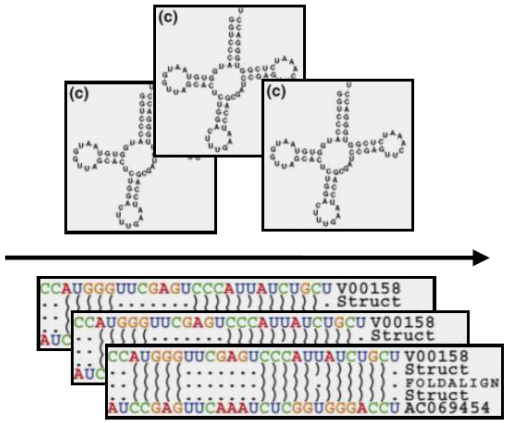

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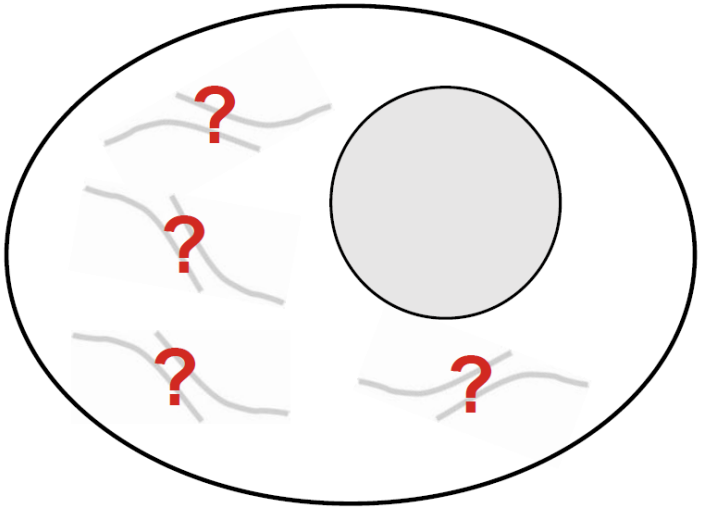

Biochemistry, Leipzig, Mario Mörl

our aim

RNA-RNA crosslinking
+
high-throughput sequencing

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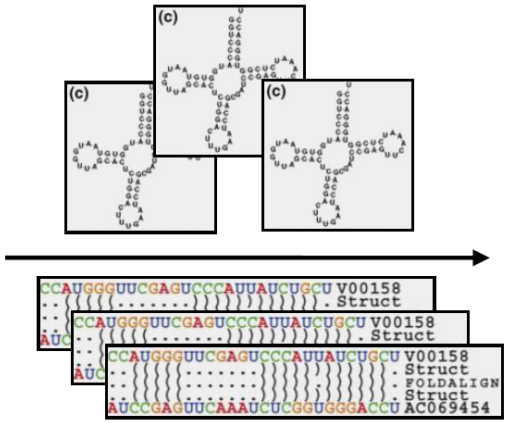

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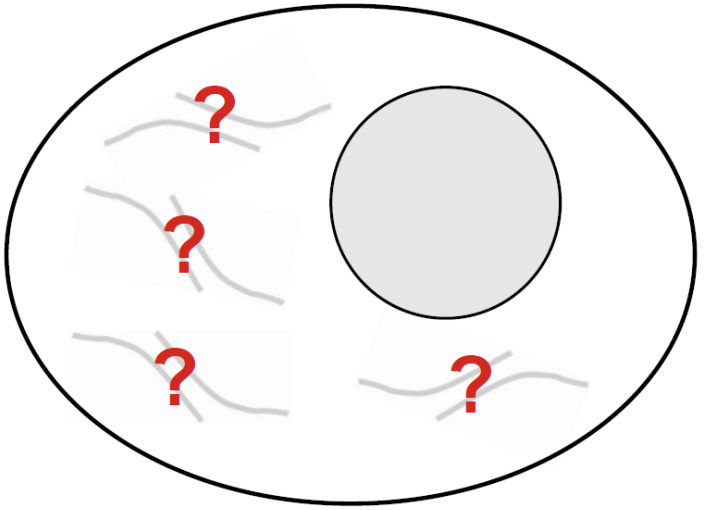

Not finished yet.
Continued by
Oskar Götze,
Institute for Biochemistry,
Leipzig

Biochemistry, Leipzig, Mario Mörl

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From RNA-RNA Interactions to Actual ncRNA Function

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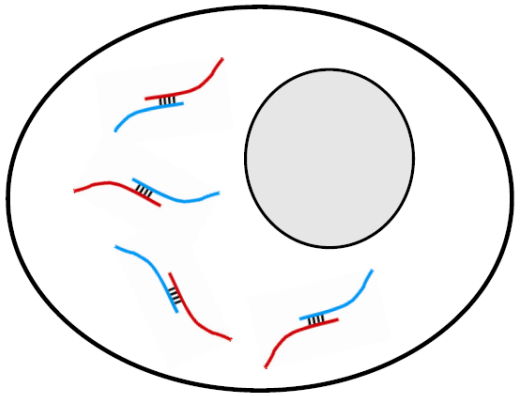

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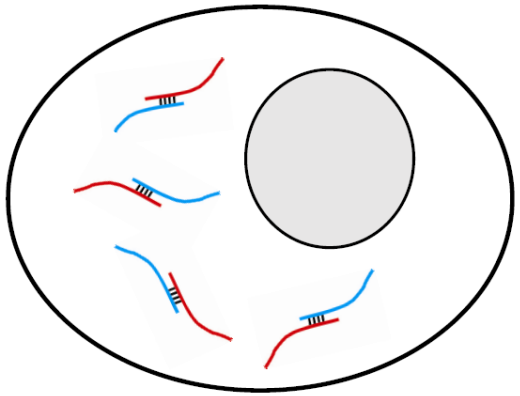

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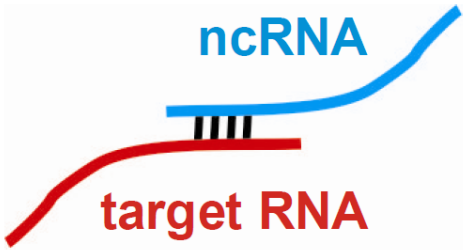
Functional Analysis:



still limited to
individual interactions!

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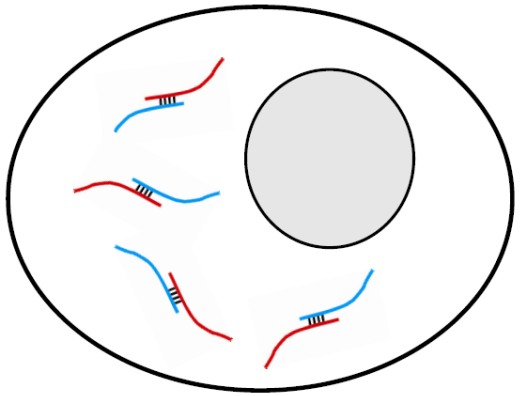

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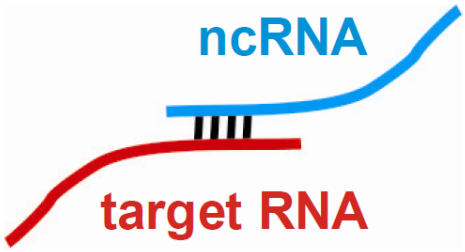

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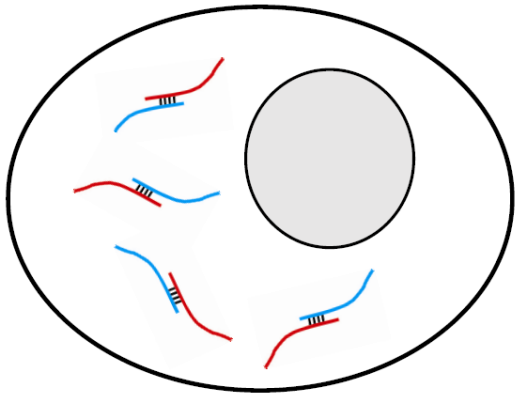

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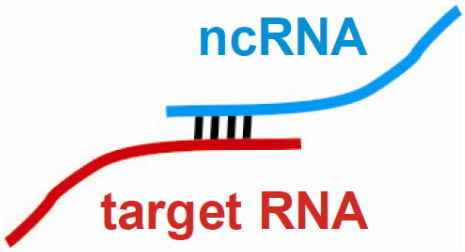

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Copenhagen:
Jan Gorodkin
• bioinformatic pipeline

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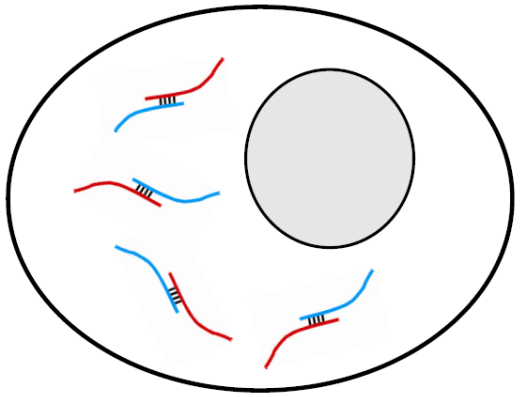

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candidate selection

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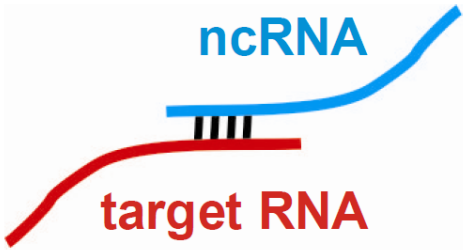

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Copenhagen:
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- RNAi knock-down
  → in cell culture
  → tissue-specific (GAL4)

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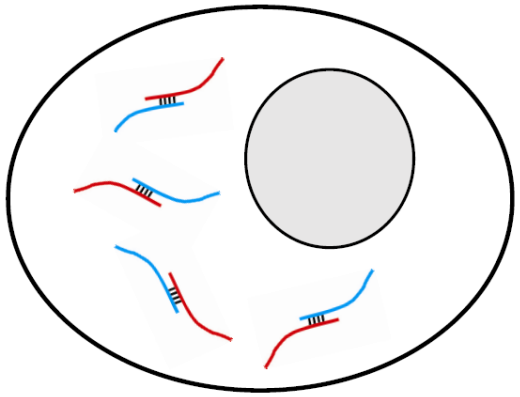


identified in high-throughput

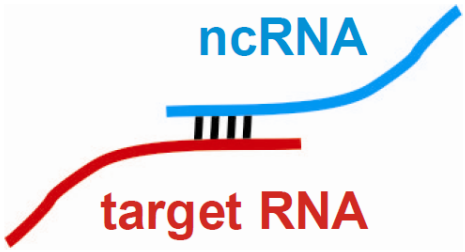
no list of interactions out of experiment yet

CMfinder: ~ 700,000 RNA Structures (Mammals)

Stefan Seemann

candidate selection

Functional Analysis:



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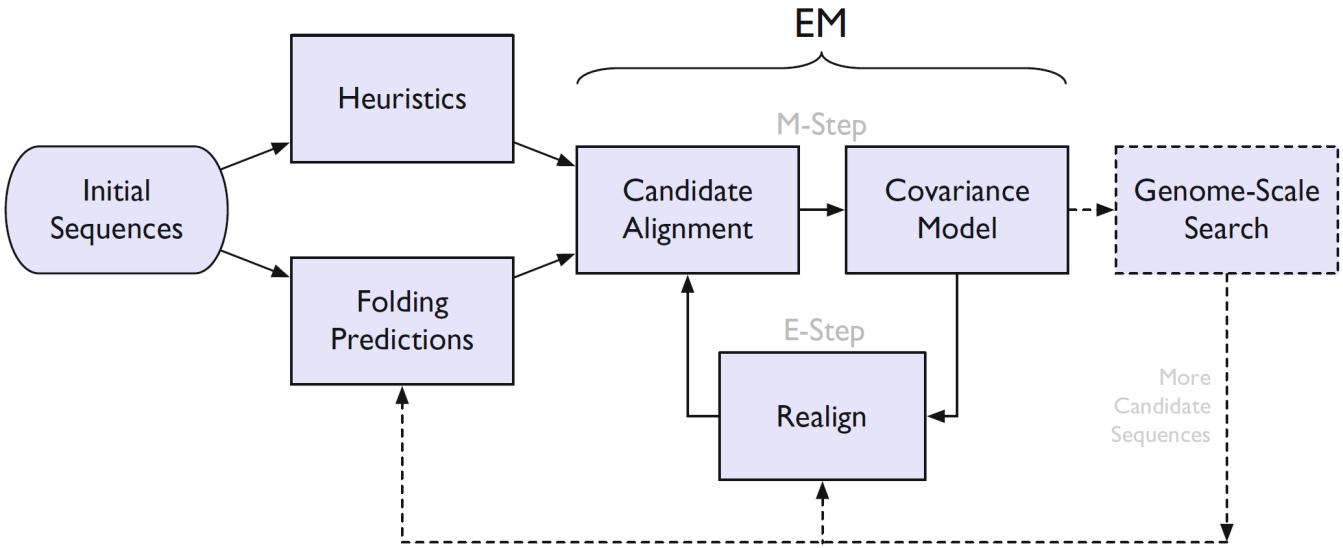
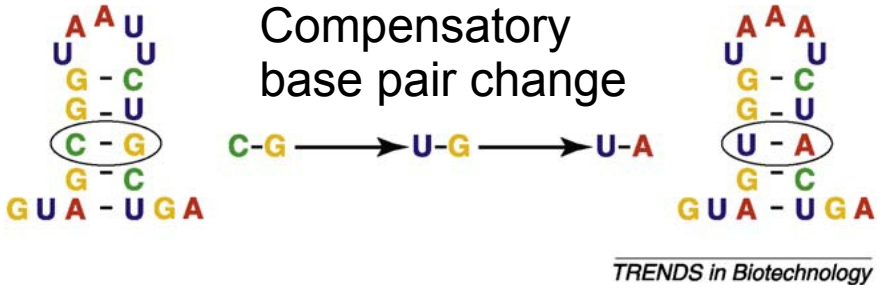
Prediction of Structured RNAs in Mammals

CMfinder (Yao, 2006)



Ruzzo, 2014

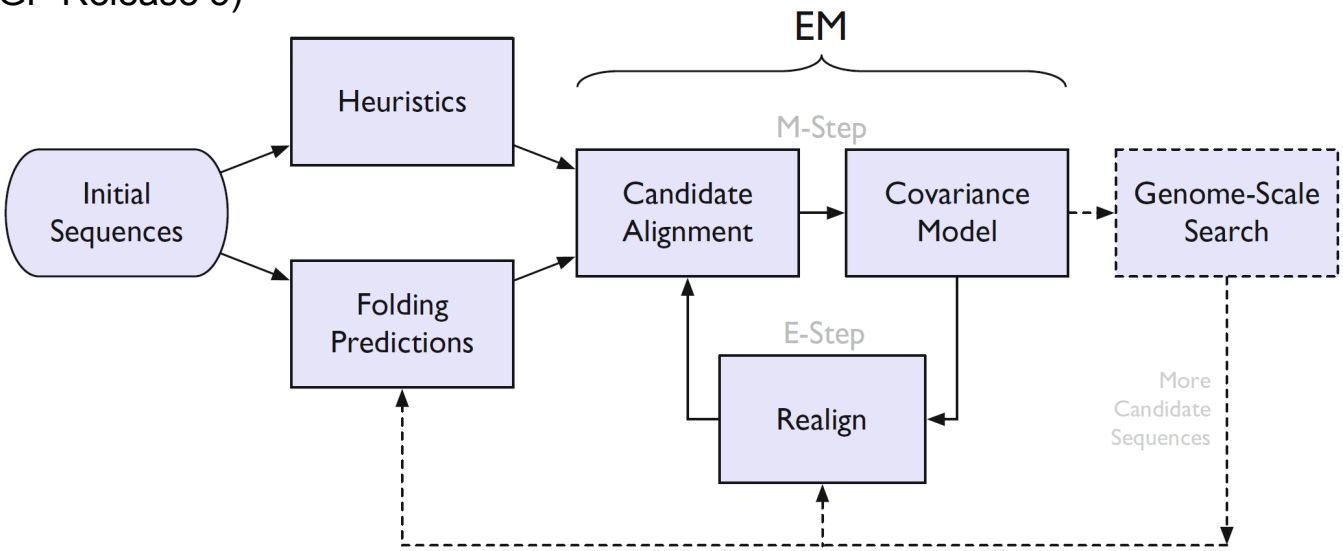


Gorodkin, 2010

Prediction of Structured RNAs in Drosophilids

Multiple alignment of 15 insect species → CMfinder (Yao, 2006)

D. melanogaster (dm3, Apr. 2006, BDGP Release 5)
D. simulans (droSim1, Apr. 2005)
D. sechellia (droSec1, Oct. 2005)
D. yakuba (droYak2, Nov. 2005)
D. erecta (droEre2, Feb. 2006)
D. ananassae (droAna3, Feb. 2006)
D. pseudoobscura (dp4, Feb. 2006)
D. persimilis (droPer1, Oct. 2005)
D. willistoni (droWil1, Feb. 2006)
D. virilis (droVir3, Feb. 2006)
D. mojavensis (droMoj3, Feb. 2006)
D. grimshawi (droGri2, Feb. 2006)
A. gambiae (anoGam1, Feb. 2003)
A. mellifera (apiMel3, May 2005)
T. castaneum (triCas2, Sep. 2005)



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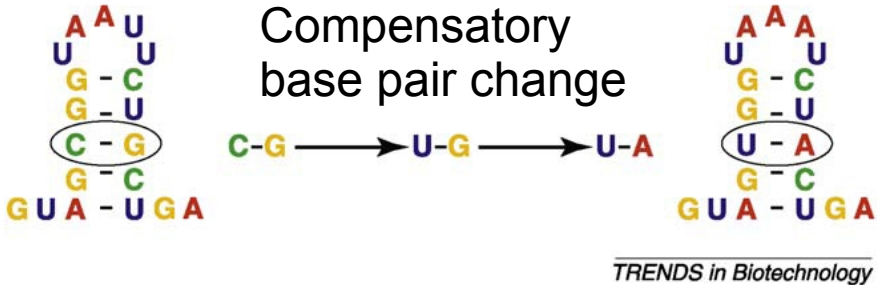

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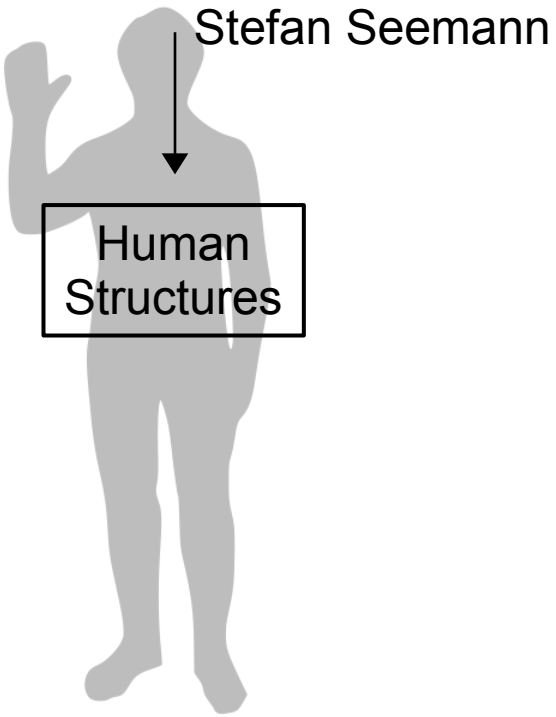
Prediction of Structured RNAs in Human

CMfinder: ~ 700,000 RNA Structures (Mammals)

Stefan Seemann



CMfinder Comparison in Drosophila and Human

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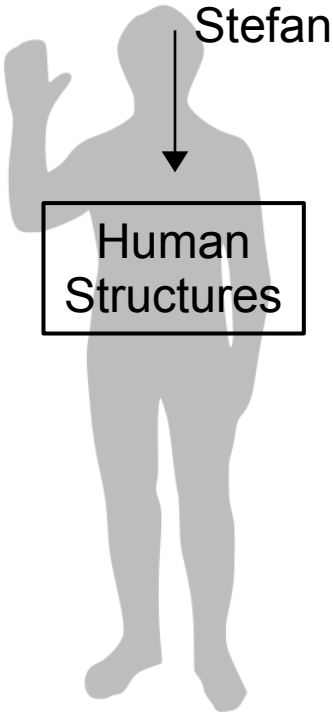
Human Structures



CMfinder Screen on Drosophilids

Drosophila Structures

CMfinder Comparison in Drosophila and Human

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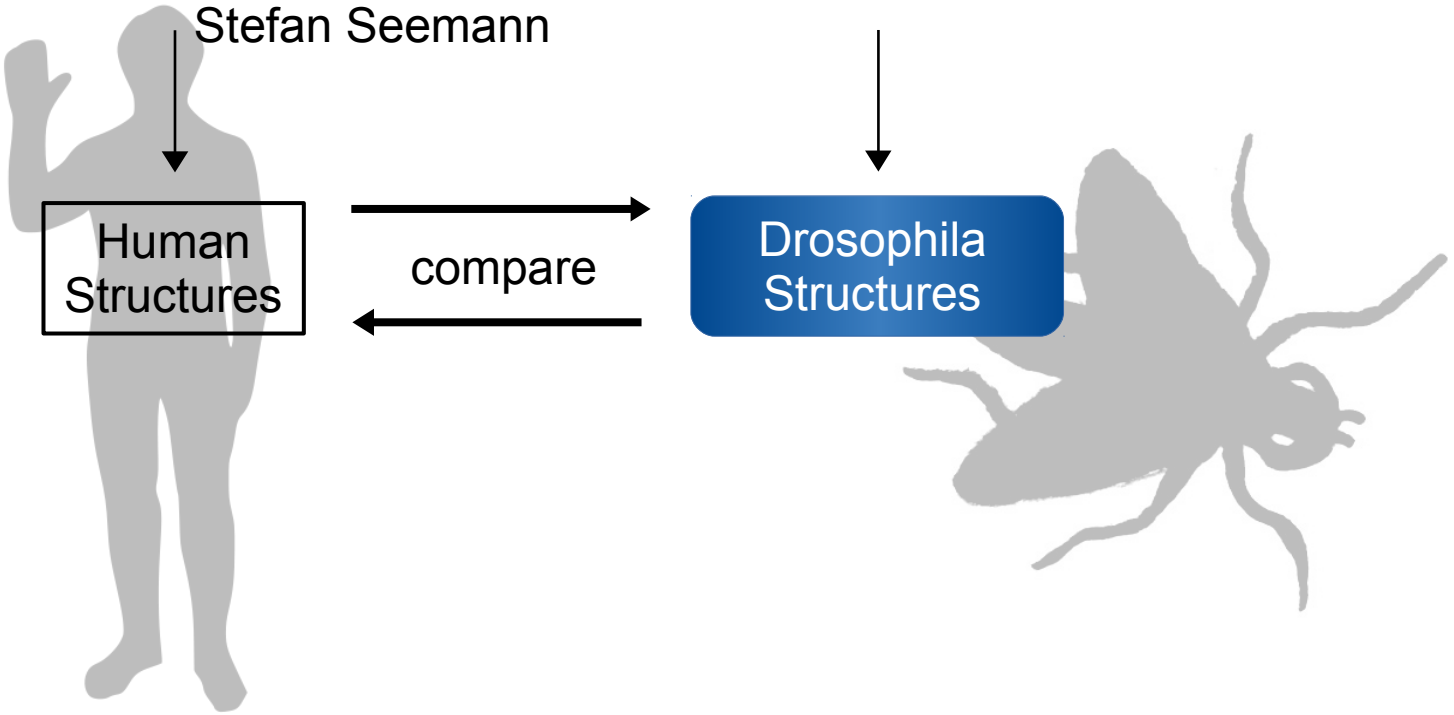
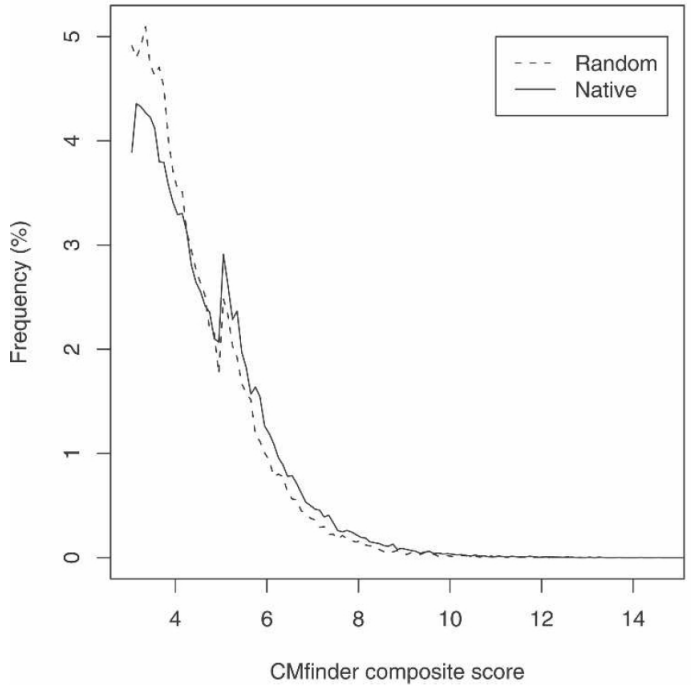
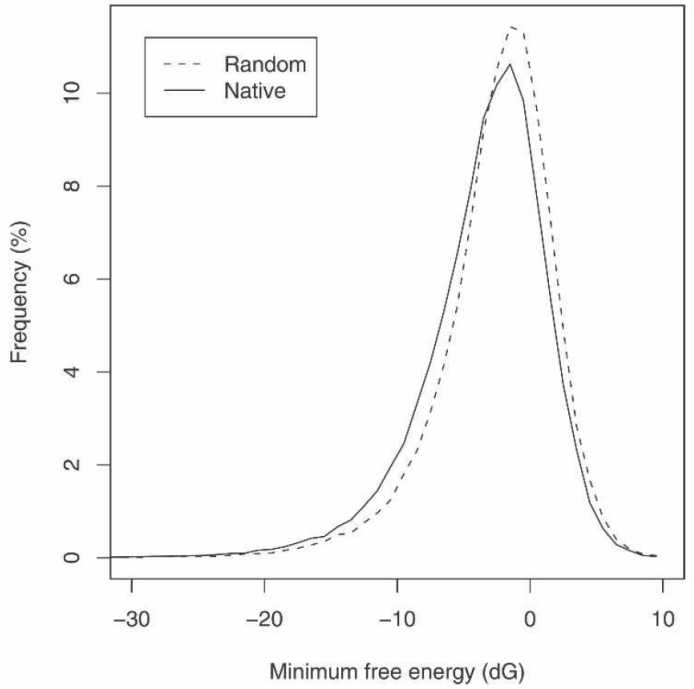
CMfinder Screen on Drosophilids



CMfinder on ENCODE Regions





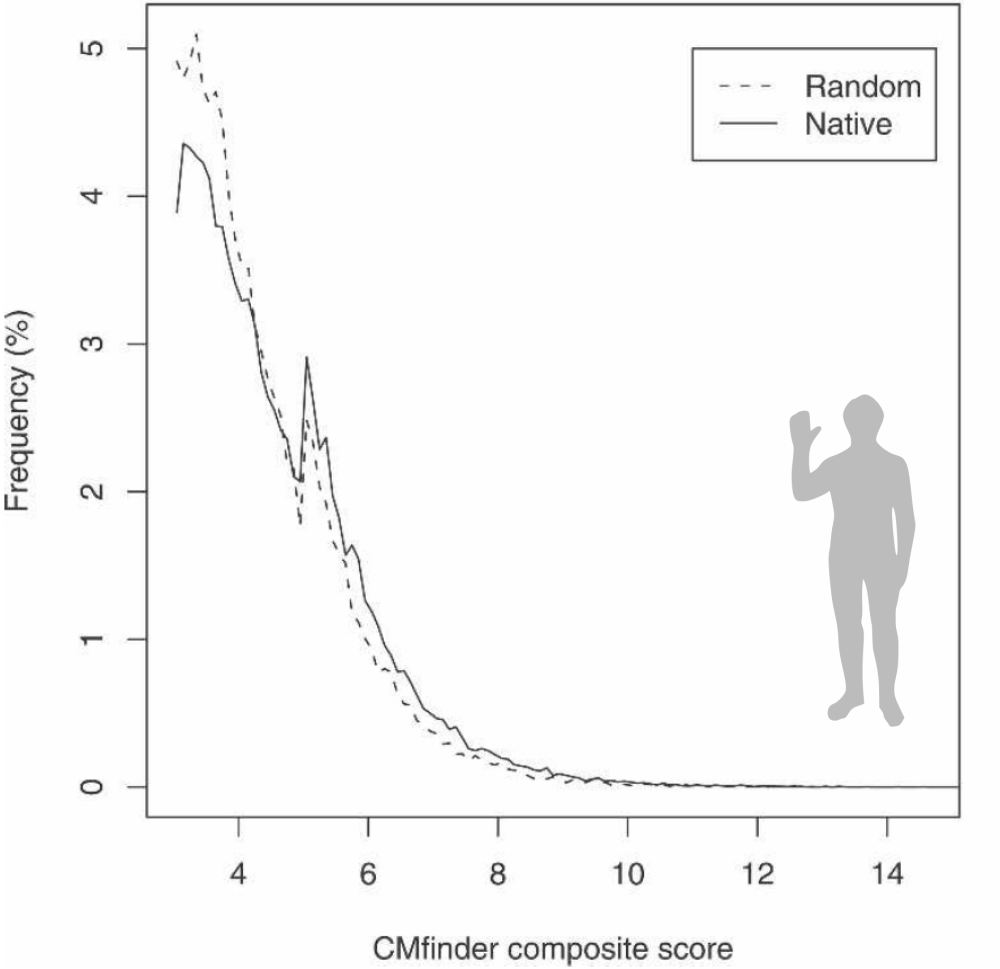
Torarinsson et al. 2008 **Cut-off criteria**

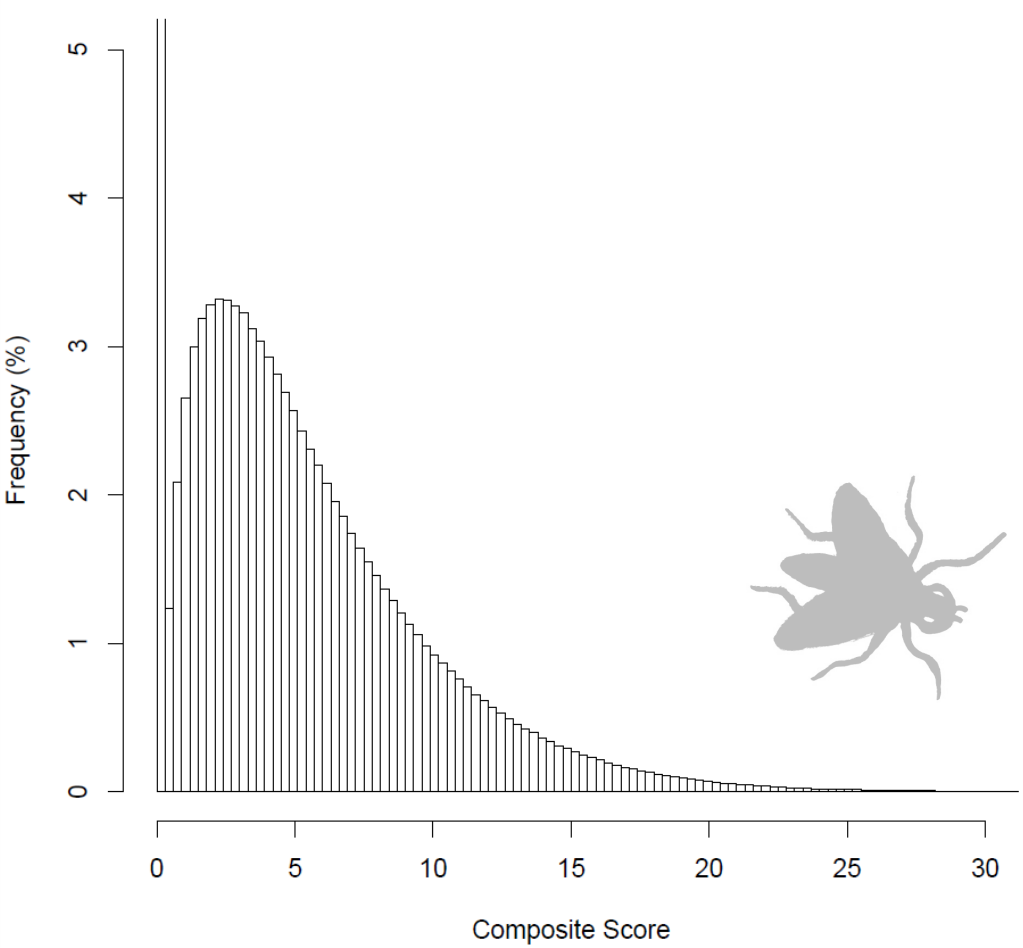
Composite Score:
> 5

takes motif and sequence conservation, sequence identity, number of base pairs and alignment length into account

Minimum Free Energy
< -5

Prediction of Structured RNAs in Drosophilids





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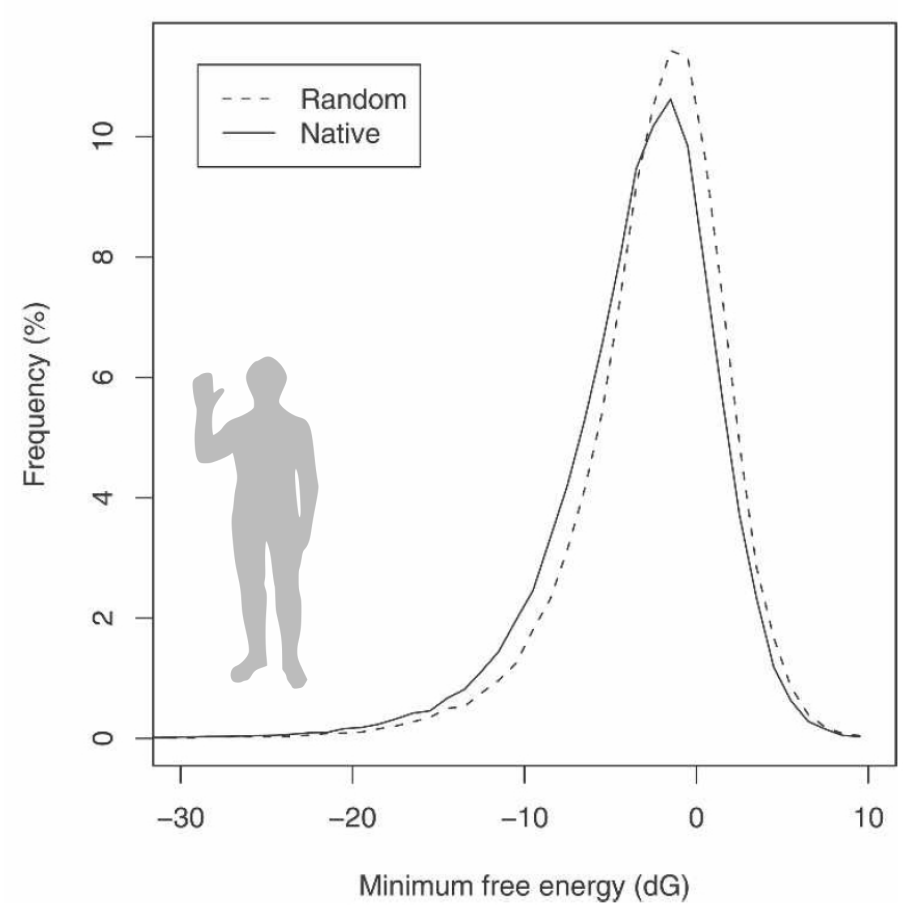

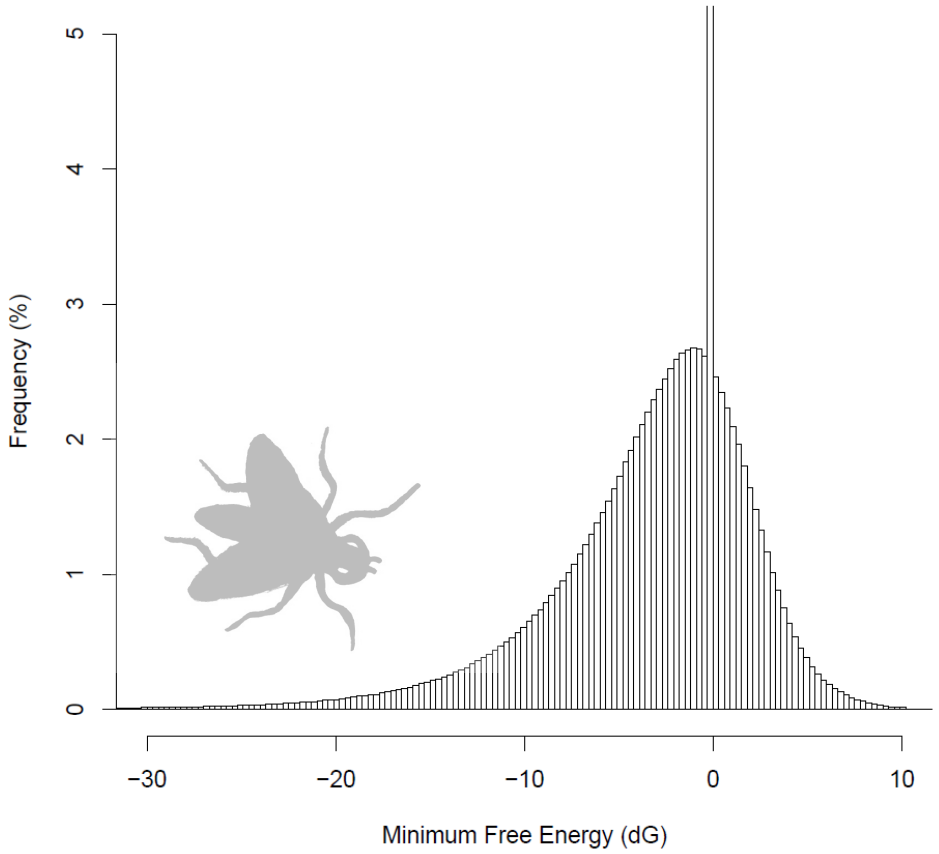

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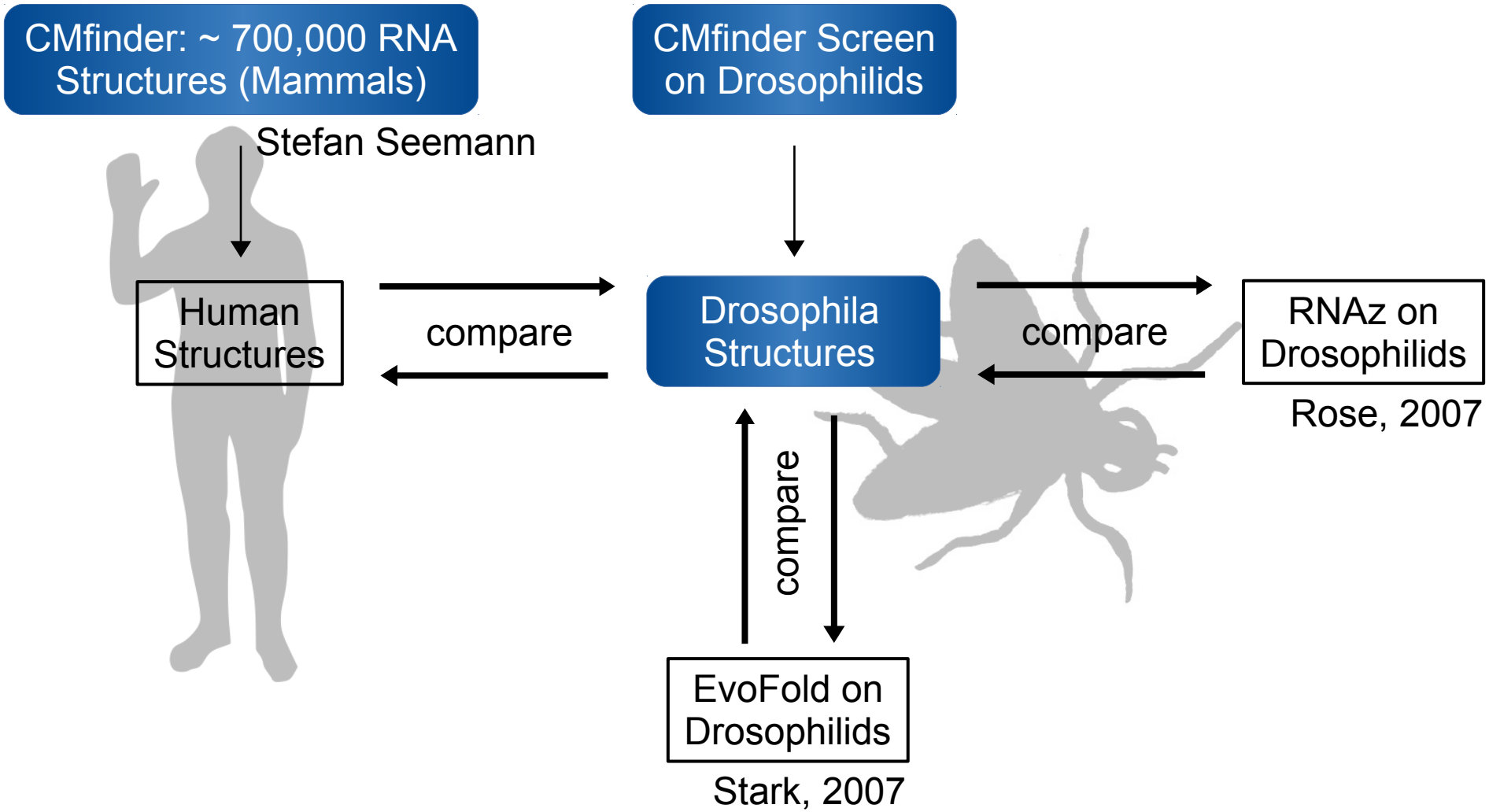
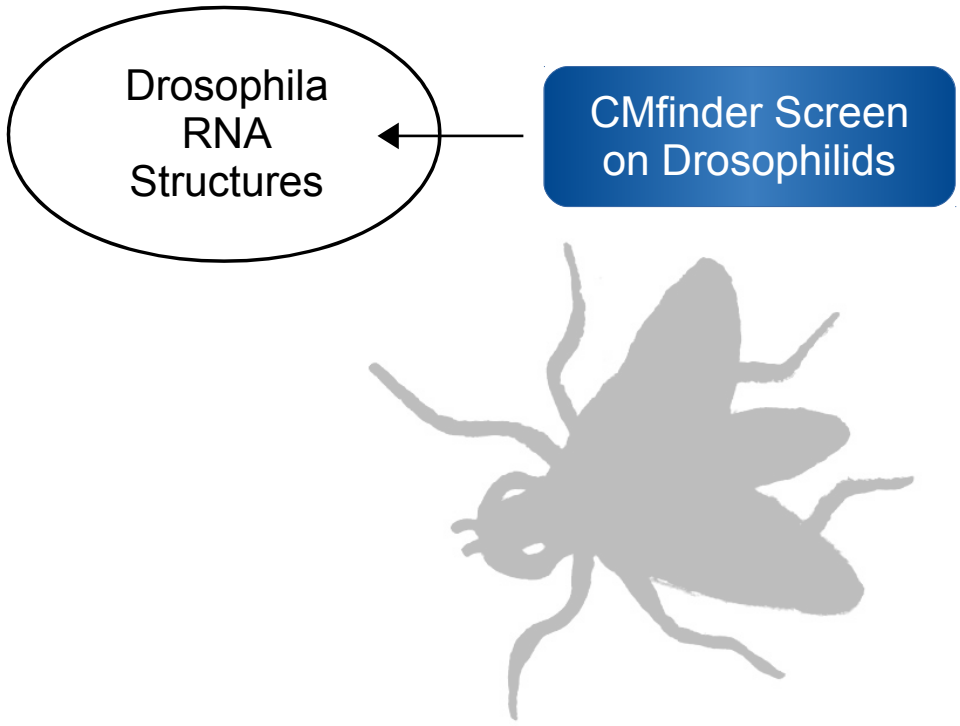


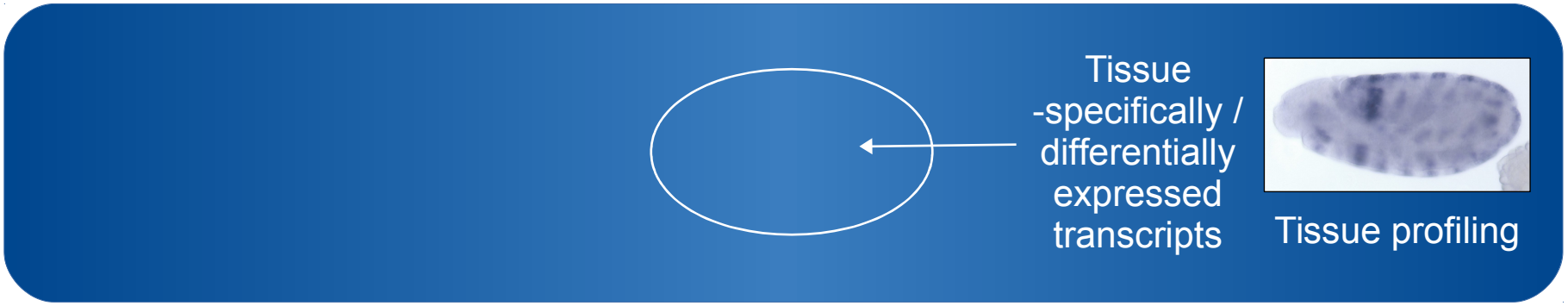
Identification of RNA Candidates for Functional Studies

PREDIC-TIONS



Identification of RNA Candidates for Functional Studies

EXPERIMEN-TAL DATA



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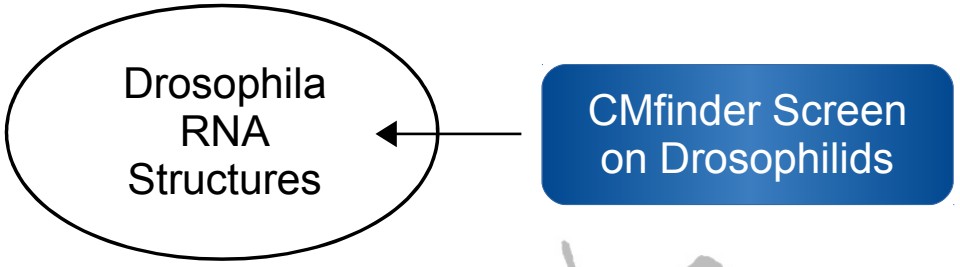

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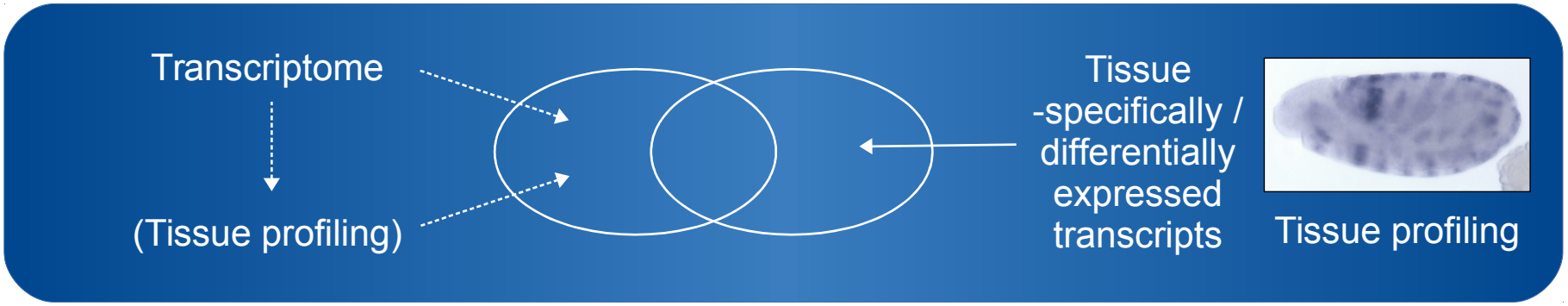


PREDIC-TIONS

Drosophila RNA Structures

CMfinder Screen on Drosophilids

Identification of RNA Candidates for Functional Studies

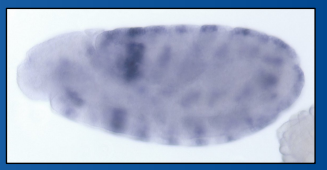
EXPERIMEN-TAL DATA

PREDIC-TIONS

Transcriptome

(Tissue profiling)

Tissue -specifically / differentially expressed transcripts



Tissue profiling

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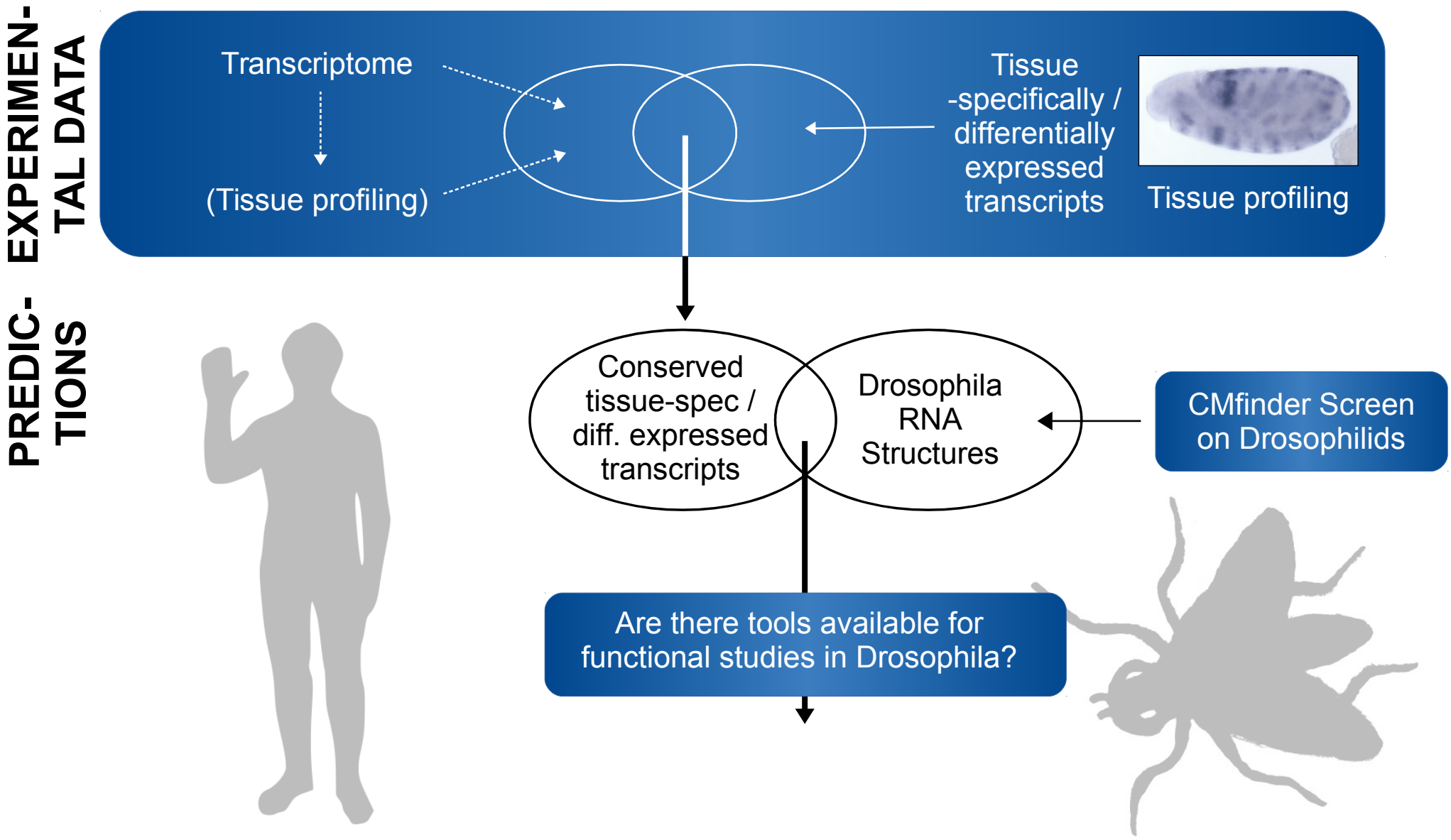

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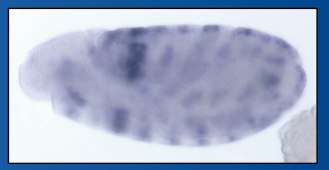

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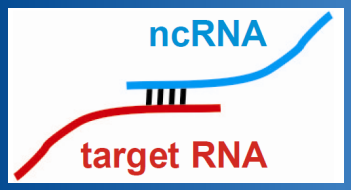
Are there tools available for functional studies in Drosophila?



Final ncRNA Candidates for Functional Studies in Fly

Thanks to...

Leipzig

Oskar Götze
Heike Betat

Mario Mörl
Peter Stadler

Copenhagen

Stefan Seemann
Jakob Hull Havgaard
Jan Gorodkin

all other RTH members

Stephen Cohen