

Friends

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Science in Marburg

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- Infernal Rfam v.10.0 on pig: 19 cpu years

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$$1025 \cdot 110 = 112,750 \text{ files}$$

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31,728,761 blasthits

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Total 2,29 GB

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2 weeks and many weeks free time ;)

Acknowledgements

Thx 2:

Steffi, Marcus
C. germanicus

Thank You!

Introduction into the wide, complicated field of Molecular Biology:

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Feature Observation





































Biologists vs. Computer Scientists

Biologists: Favourite gene ... or hype scenario

Biologists: Favourite gene ... or hype scenario



Examples from Biology: Gene e and gene f

Examples from Biology: Gene e and gene f

Gene e



Examples from Biology: Gene e and gene f

Gene e



Gene f



Starting accurate analysis: $\Delta(e, f) = \Delta(f, e)$

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$$\forall x \in G : \Delta(e, f) < \Delta(e, x) \text{ and } \Delta(e, f) < \Delta(f, x)$$

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Sense, swapped



Sense, swapped



Sense, “Minus strand”



Antisense



Clustered with other genes



Aims

- Find conserved gene linkages throughout metazoans
- Determine time of linkage investigation
- Duplications
- Constant distances and orientations?
- Identification of divergent genes

Problem: A gene $s \in G$ jumps in: $\Delta(e, s) < \Delta(e, f)$ and $\Delta(f, s) < \Delta(e, f)$

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Solution: Compare data in different time points



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Problem: another gene j overlaps: $\Delta(f, j) = 0$

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Problem: Modified Gene or Pseudogene?

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Answered by evolution

Answered by evolution



Problem: Highly divergent genes: Fragment hit only

Problem: Highly divergent genes: Fragment hit only



Solved by the method itself



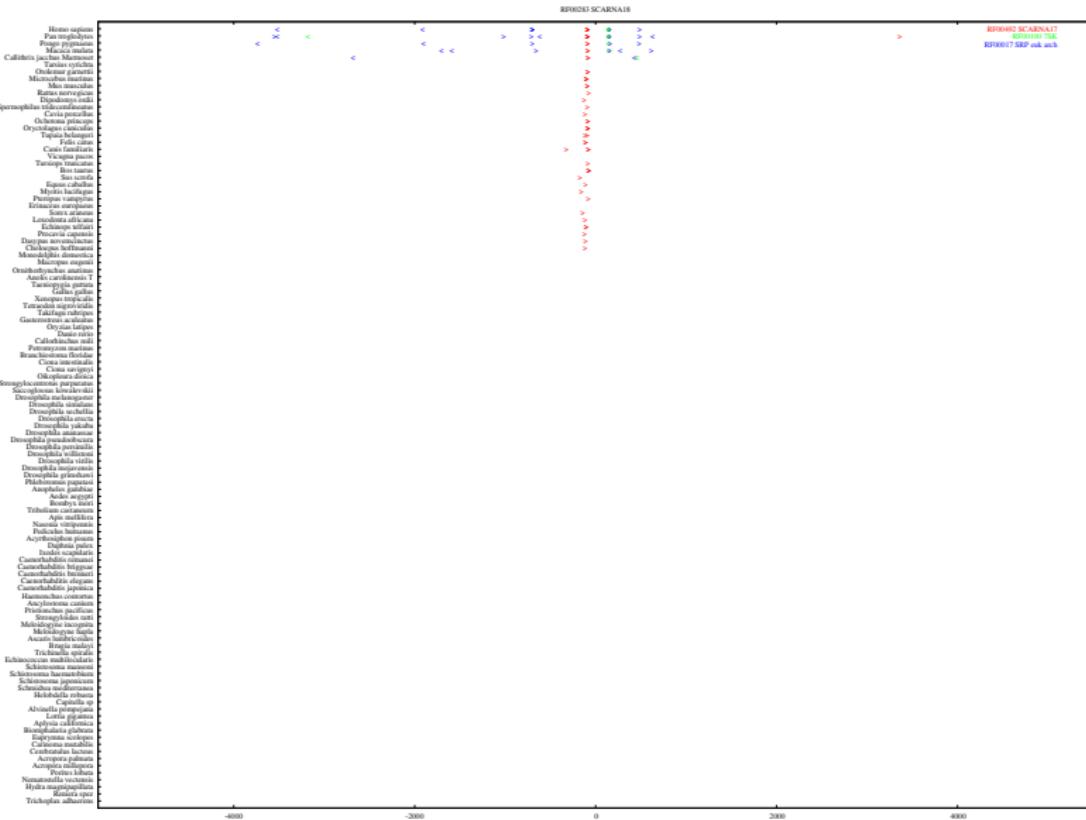
Problem: $\Delta(e, l) \ll \Delta(e, f)$

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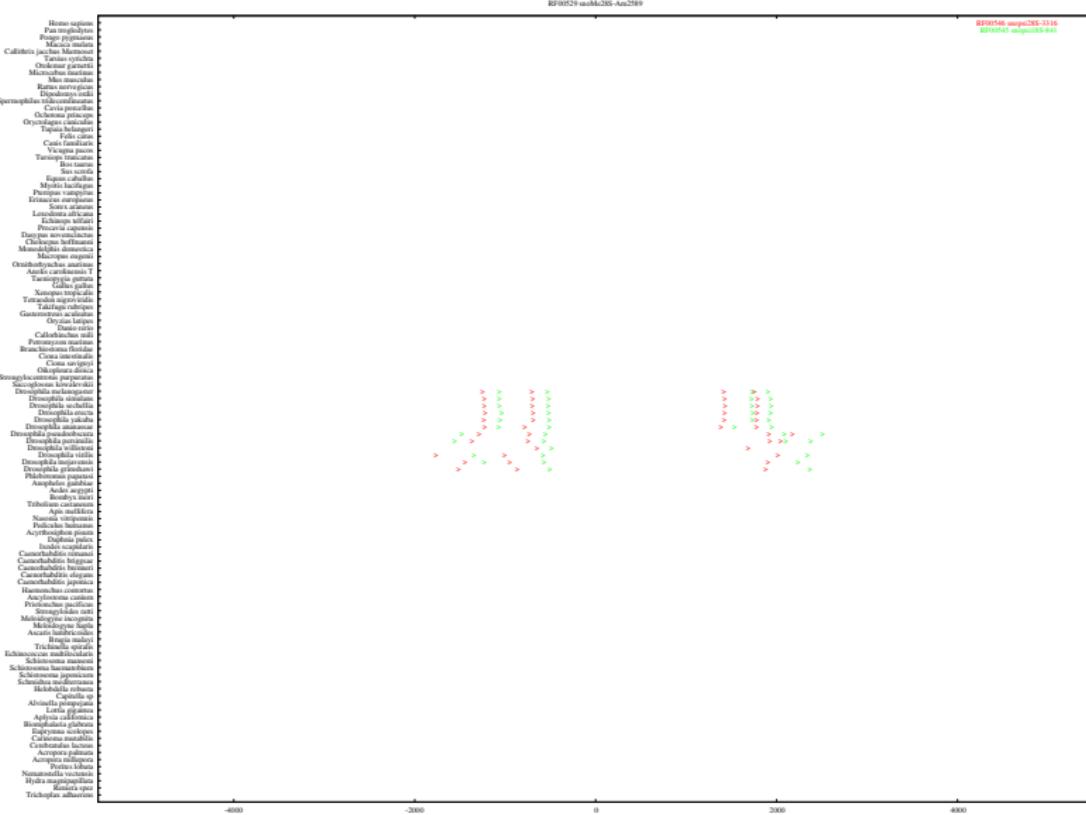


Some Preliminary Results: SCARNA-17-18

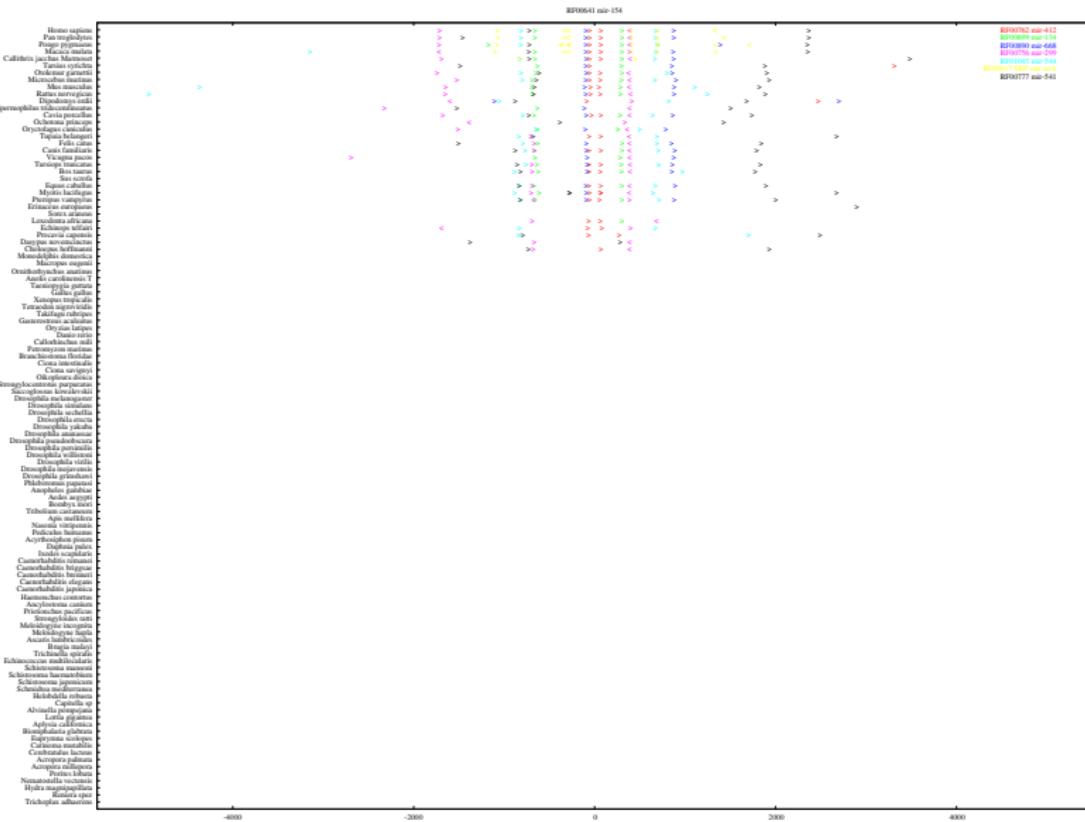
Some Preliminary Results: SCARNA-17-18



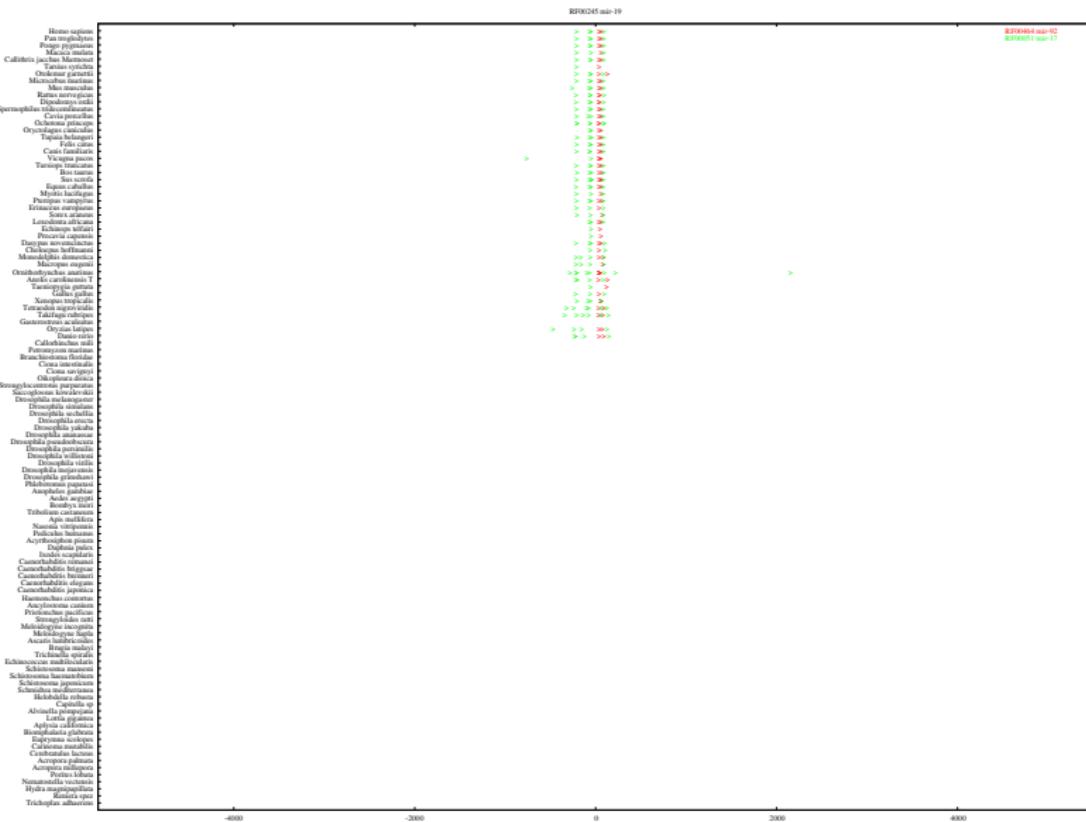
Some Preliminary Results: snoMe28S-Am2589



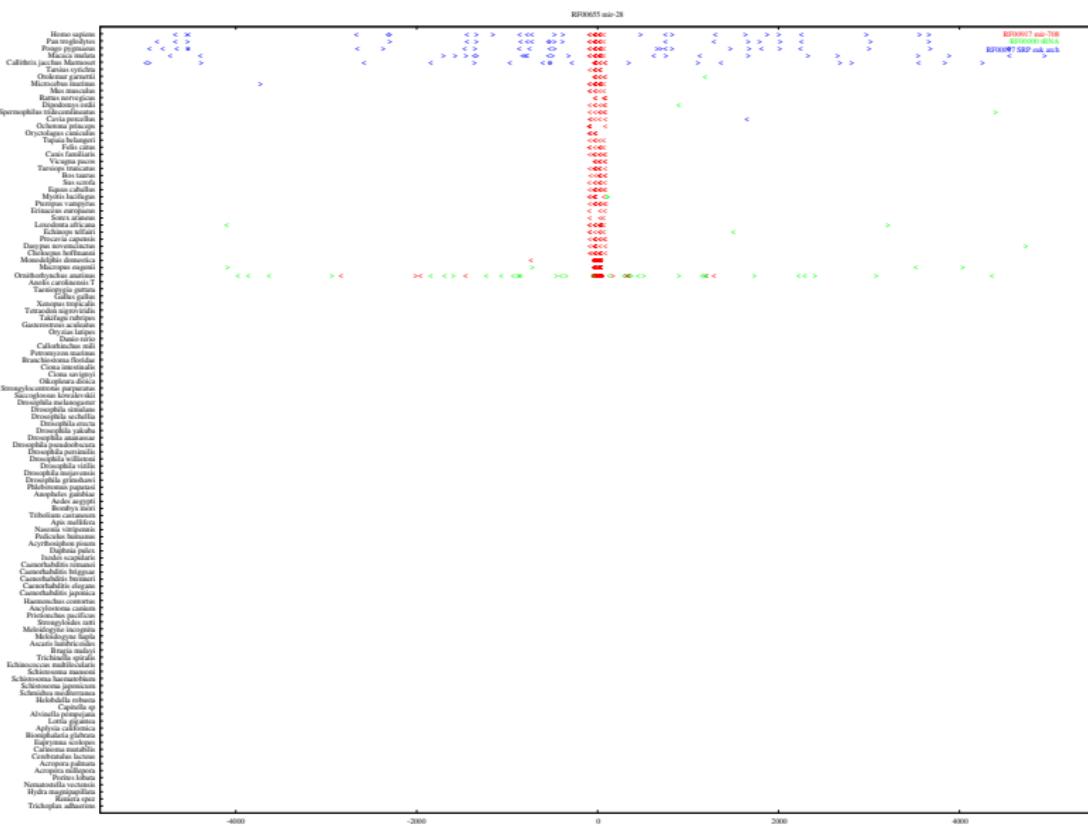
Some Preliminary Results: miRNA-154 cluster



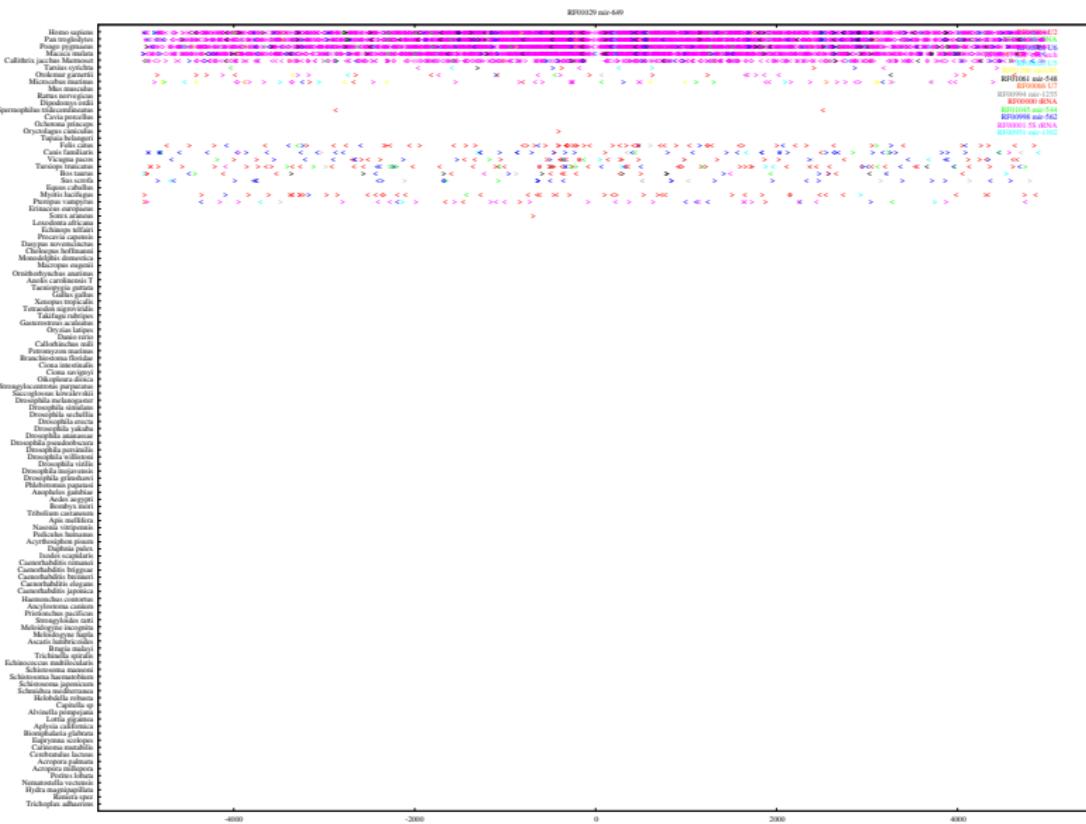
Some Preliminary Results: miRNA-17-92 cluster



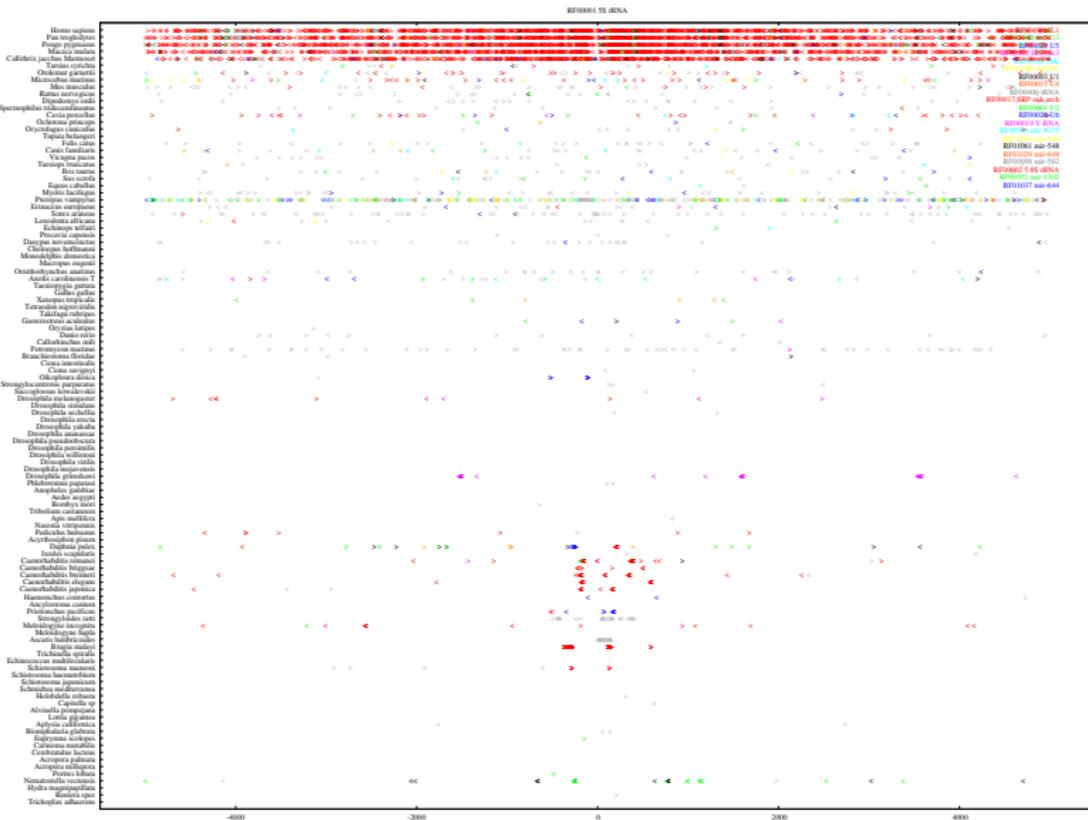
Some Preliminary Results: miRNA-28 cluster



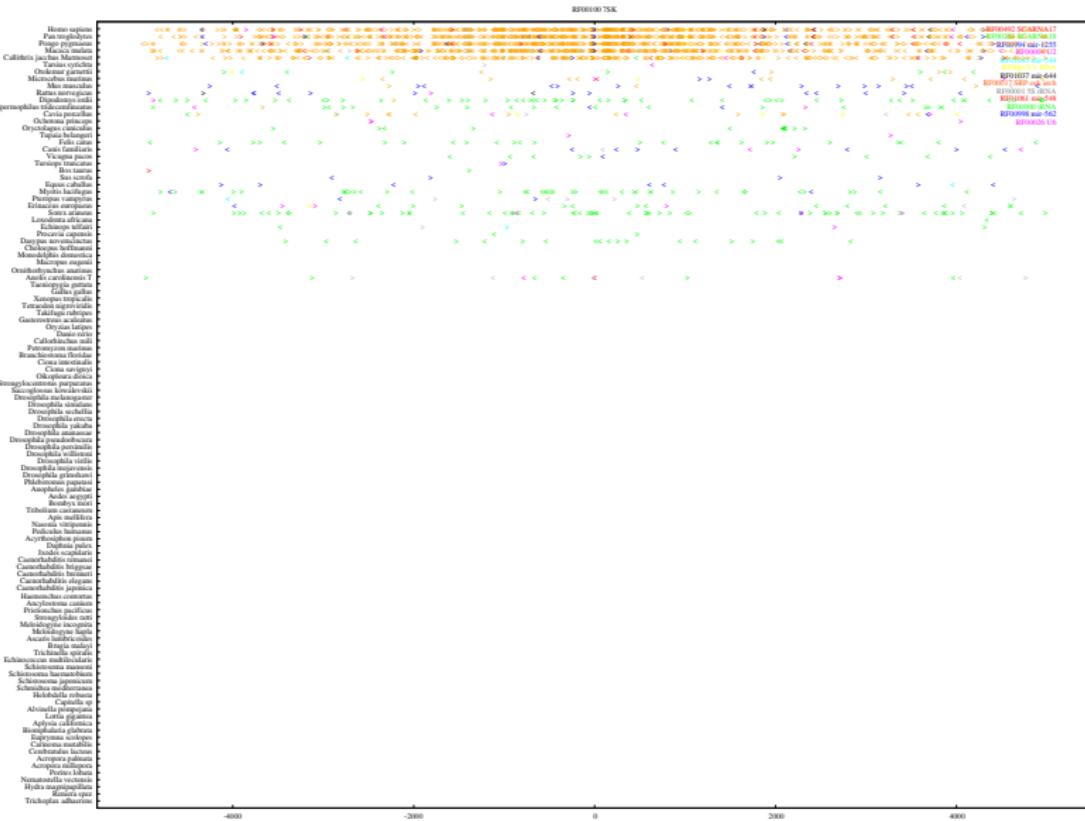
Some Preliminary Results: miRNA-649



Some Preliminary Results: 5S RNA



Some Preliminary Results: 7SK RNA



Identification of a mobile element (gene *p*)

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Identification of a mobile element (gene *p*)



Identification of a mobile element (gene *p*)



Identification of a mobile element (gene p)



Identification of a mobile element (gene *p*)



Identification of a mobile element (gene *p*)



Likelihood of a biological feature

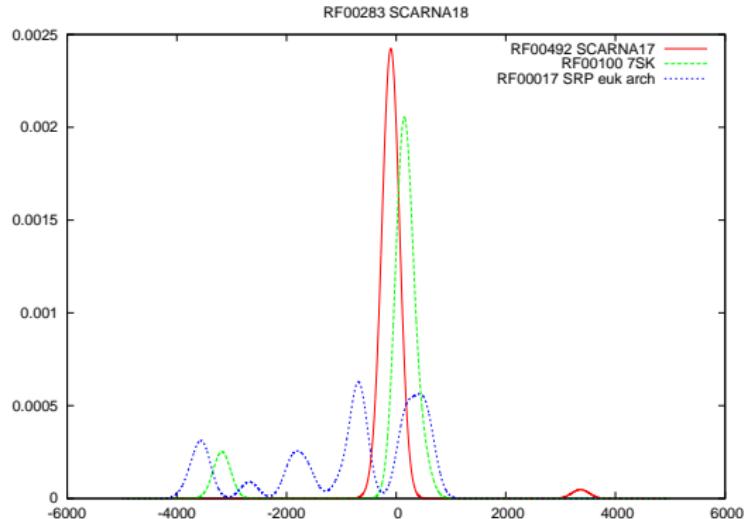
Assumptions:

- individual candidates for linkage between two genes are independently distributed
- each candidate can be modeled by a Gaussian $N(\mu, \sigma^2)$ with μ the distance between the two gene candidates and σ^2 chosen to be constant (independent of μ)

$$\mathcal{P}(I \geq k | n) = \sum_I \binom{n}{I} (4\sigma p)^k (1 - 4\sigma p)^{n-k}$$

confidence intervall $\phi = 0.9$

Statistically validation of SCARNA-17-18 linkage



RF00492 SCARNA17: $C_i = (-389, 175)$, $iL = 564$

RF00100 7SK: $C_i = (-2883, 756)$, $iL = 3639$

RF00017 SRP: $C_i = (-3613, 679)$, $iL = 4292$

Conclusion

Conclusion

easy

Conclusion

easy
gain many data

Conclusion

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gain many data
complete analysis never done before

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gain many data
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Conclusion

- Linkages of all known ncRNAs throughout all metazoans
- Correlation of Orientation and Distance
- Time point ncRNA linkage invention
- Occurrence in specific taxa?
- Identification of mobile elements
- Usage for divergent genes, pseudogenes
- Specific organism linkages and duplications

Acknowledgements

Thx 2:

e, f, j, l, p, s

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x