

Time-course Gene expression Analysis

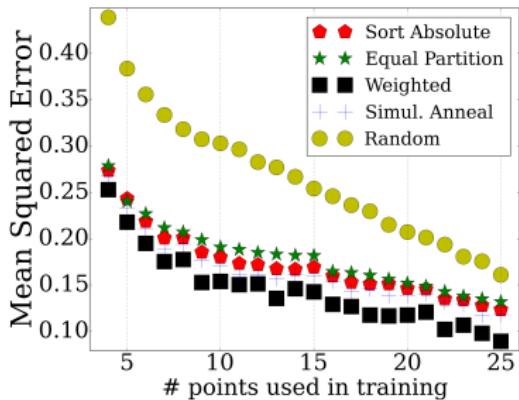


Selected Time Points

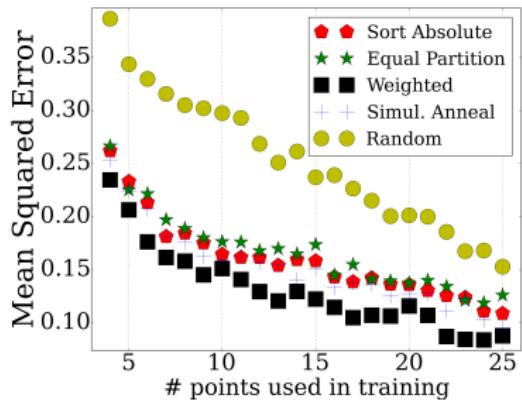
- ▶ Selected 15 time points from mRNA is:
0.5, 1.0, 1.5, 2.5, 3.0, 4.5, 6.0, 7.5, 8.5, 9.5, 10.0, 12.5, 18.0, 24.0, 28.0
- ▶ Top 10 solutions are similar to these selected points
- ▶ Initialize by points that sorted by increasing absolute differences.
- ▶ Keep adding and removing points until there is no improvement.

Error By Increasing Sampled Points

- ▶ Major performance improvement over randomly selected points



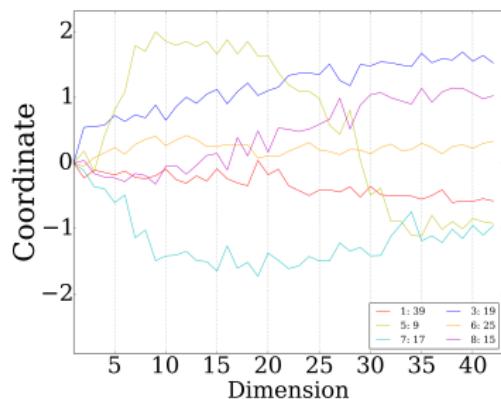
(a) Performance analysis



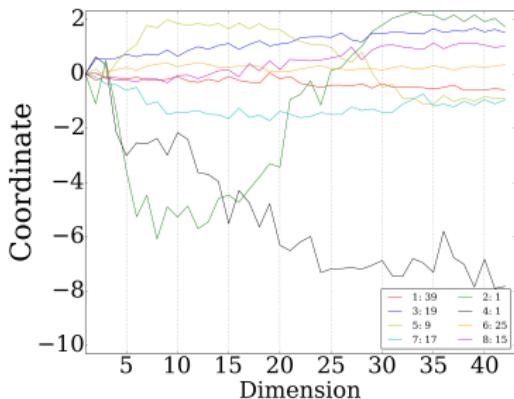
(b) Remove last two points

mRNA Cluster Analysis

- ▶ 6 stable clusters
 - ▶ One cluster corresponds to the genes with non-monotonic expression over time

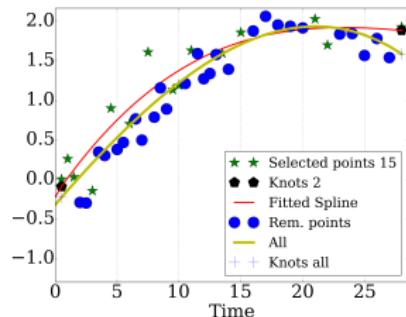


(c) 6 stable clusters

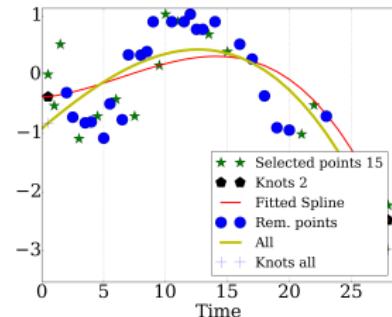


(d) Centroids

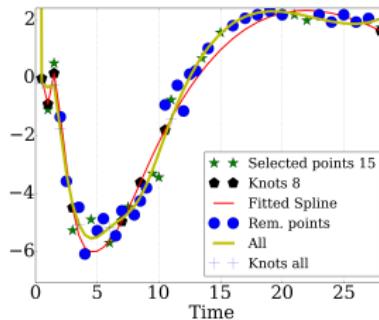
Detailed mRNA Gene Analysis



(e) PDGFRA



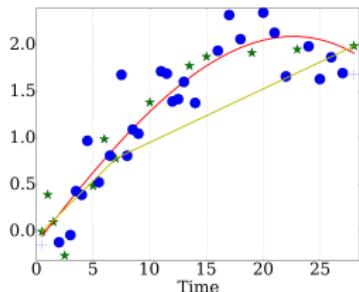
(f) ELN



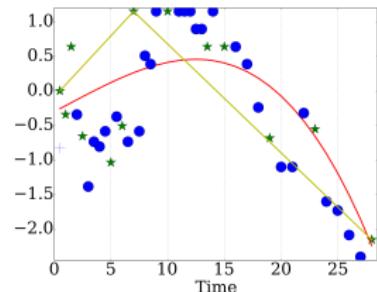
(g) INMT

Spline vs Linear Error

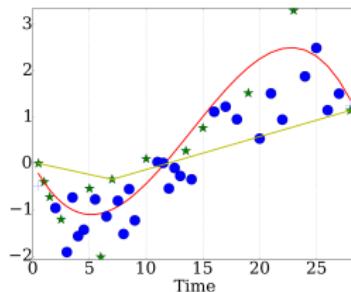
- Area difference is larger than 1.0 for 102 genes.



(h) PDGFRA(8.3488)



(i) ELN(9.5703)



(j) LRAT(25.24)

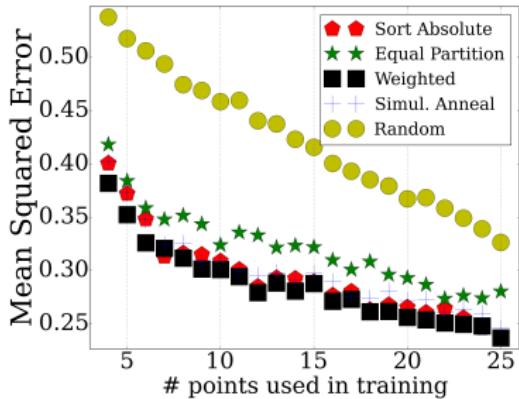
Similarity of miRNA to mRNA

- ▶ Using mRNA points gives 0.3312 error for miRNA
- ▶ Optimal points for miRNA are quite similar(error 0.3042)

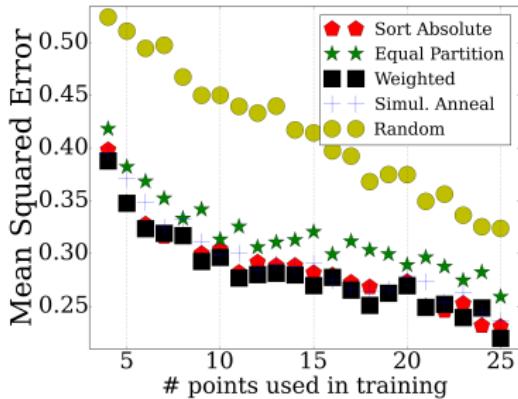
0.5, 1.0, 1.5, 2.5, 4.0, 5.0, 7.0, 8.5, 10.0, 12.0, 15.0, 19.0, 23.0, 28.0

Comparing miRNA and mRNA Errors

- Error is decreasing by increasing number of selected points in both datasets



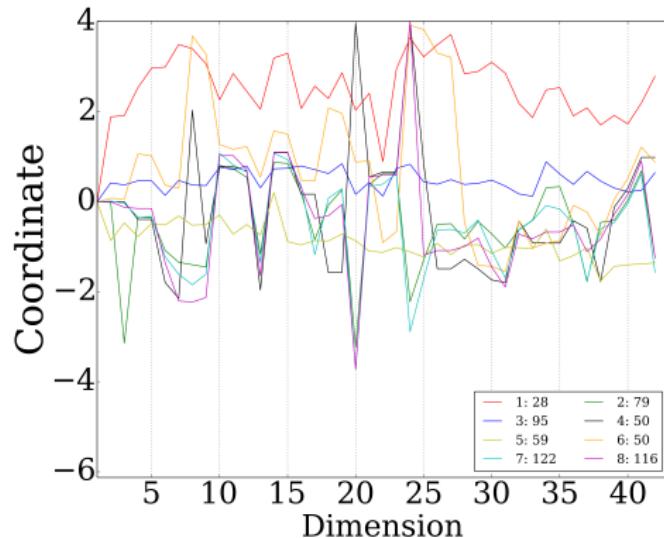
(k) Performance analysis



(l) Remove 27.0 and 28.0

miRNA Cluster Analysis

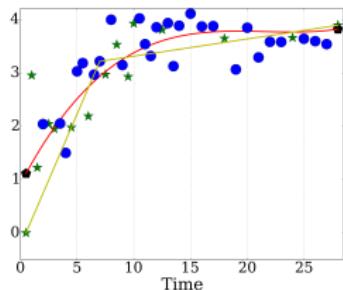
- ▶ 8 stable clusters
- ▶ Clusters change more frequently than mRNA data.
 - ▶ miRNA is noisier than mRNA data.



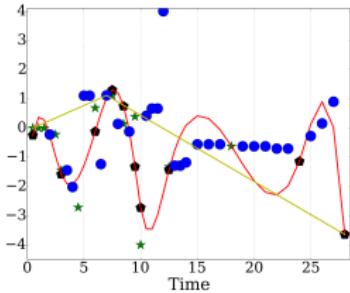
(m) 8 stable clusters

Detailed Analysis of miRNA Genes

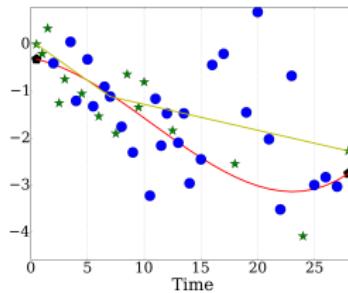
- Spline reconstruction performs better than linear one similar to mRNA dataset.



(n) mmu-miR-100



(o) mmu-miR-124



(p) mmu-miR-377

Conclusion

- ▶ Carefully selected subset of time points is important in reconstructing whole gene-expression over time
- ▶ Spline based reconstruction outperforms simpler linear reconstruction
- ▶ Analysis of mRNA is a nice representative of larger miRNA study
 - ▶ Similar subset of time points can reconstruct both data