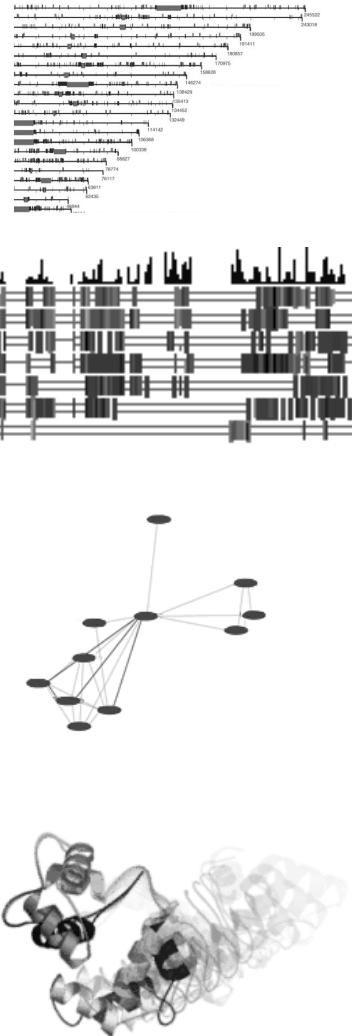


# Gerstein Lab Overview



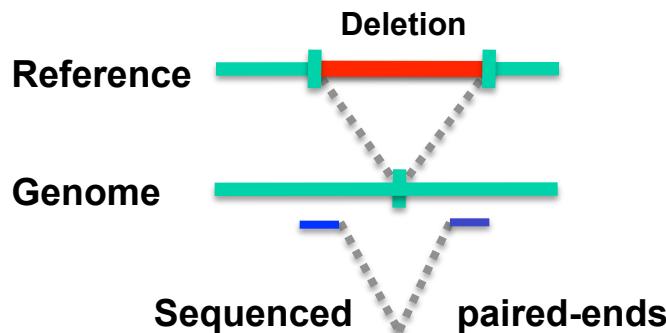
- Biological Knowledge Representation & Literature Mining
- Genome Structural Variation & Personal Genomics
- Human Genome Annotation
- Networks of Genes  
& Protein Pathways
- Macromolecular Structures & Motions

**Big Data Analysis & Mining**

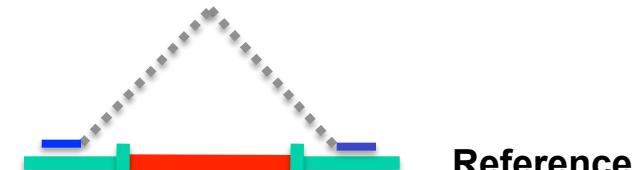
**Simul-  
ation &  
Modeling**

# Finding Variants (SVs) in Personal Genomes

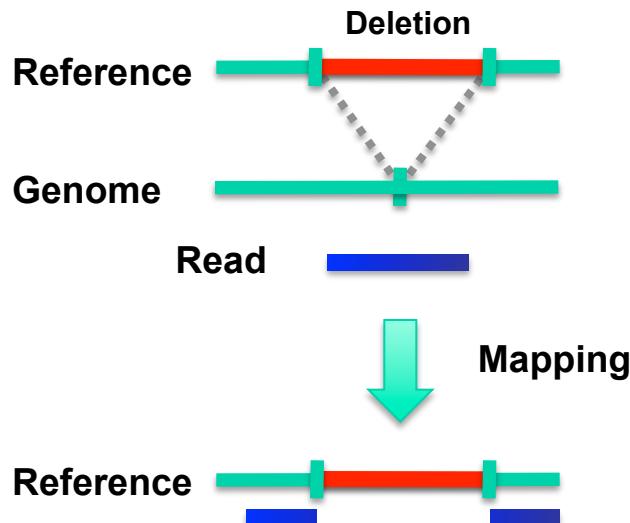
## 1. Paired ends



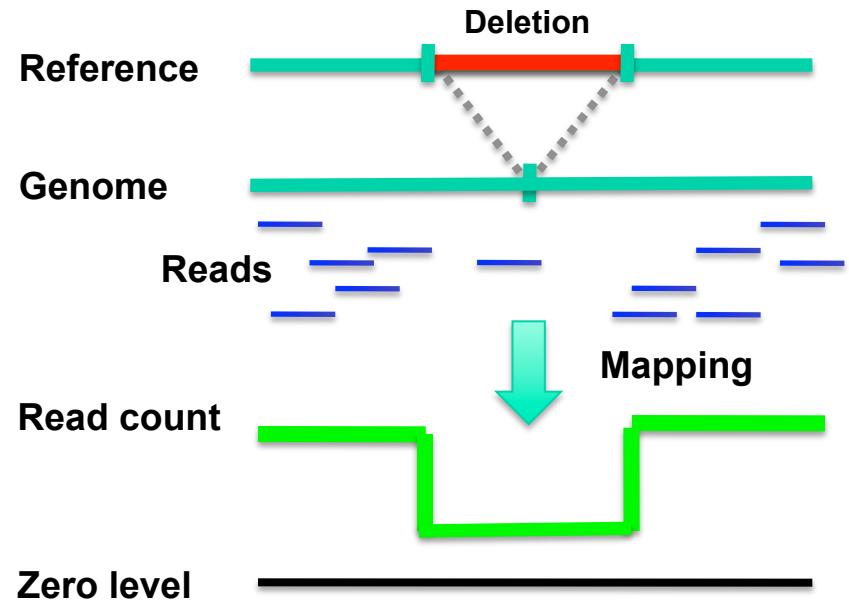
Mapping



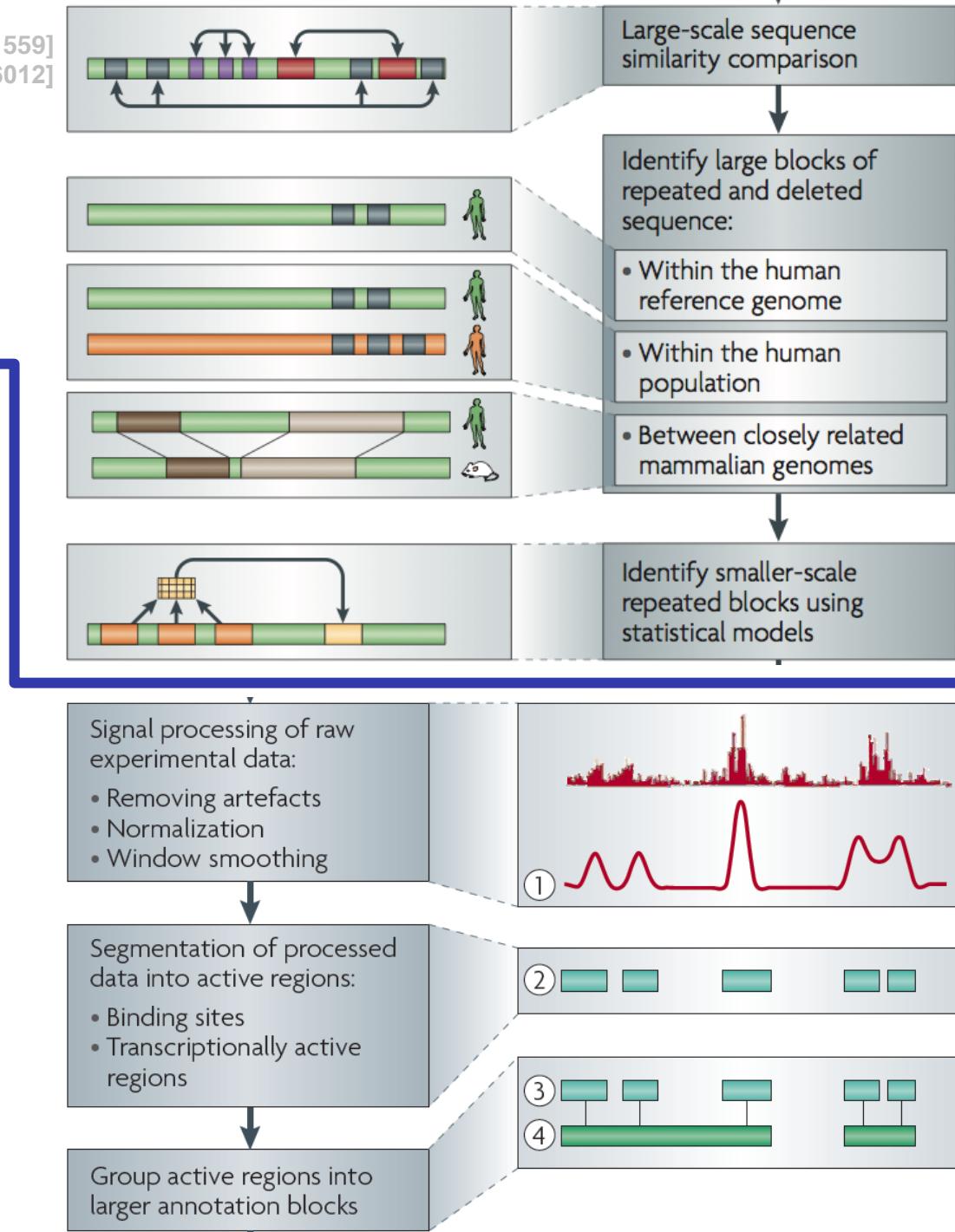
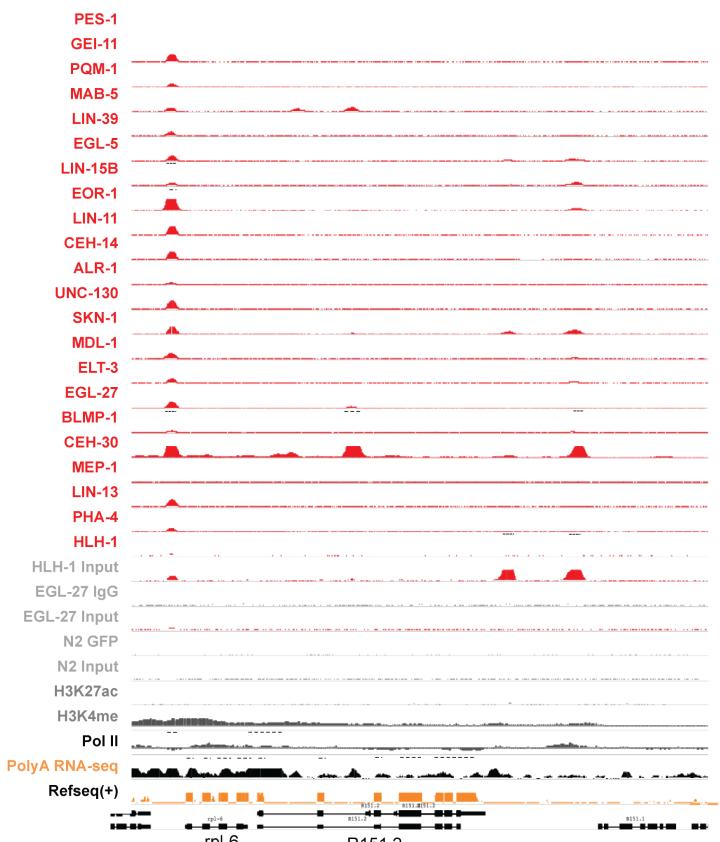
## 2. Split read



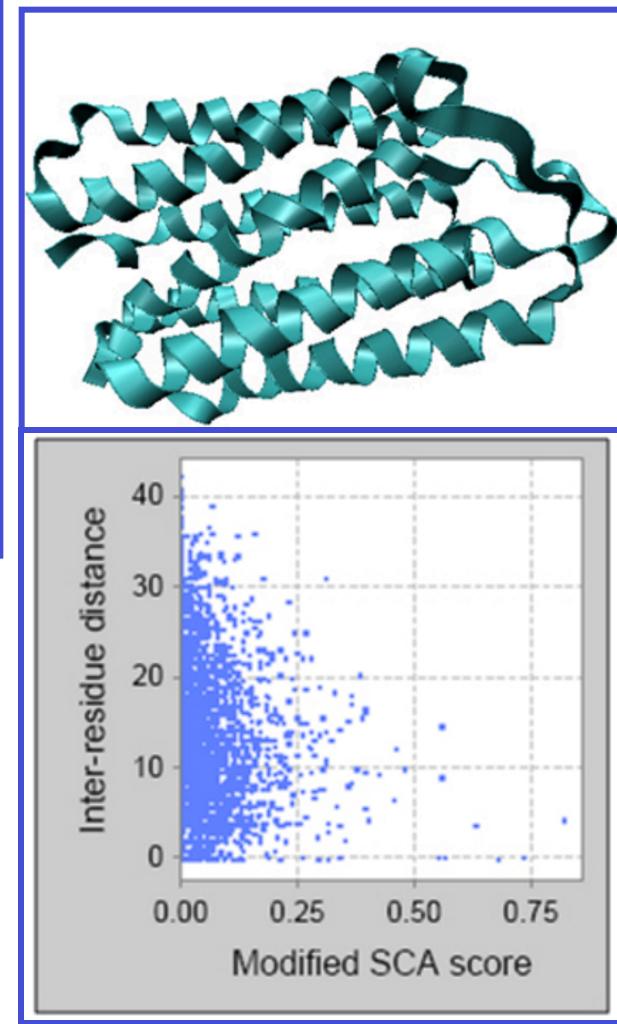
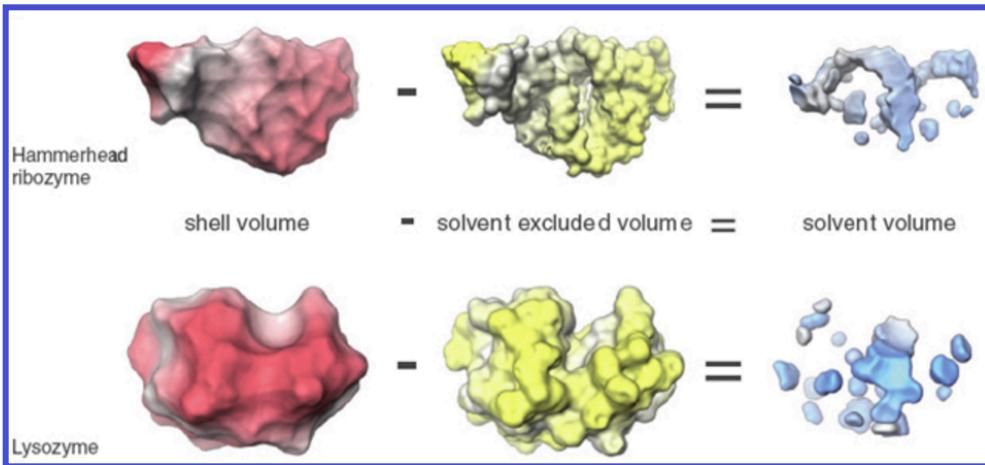
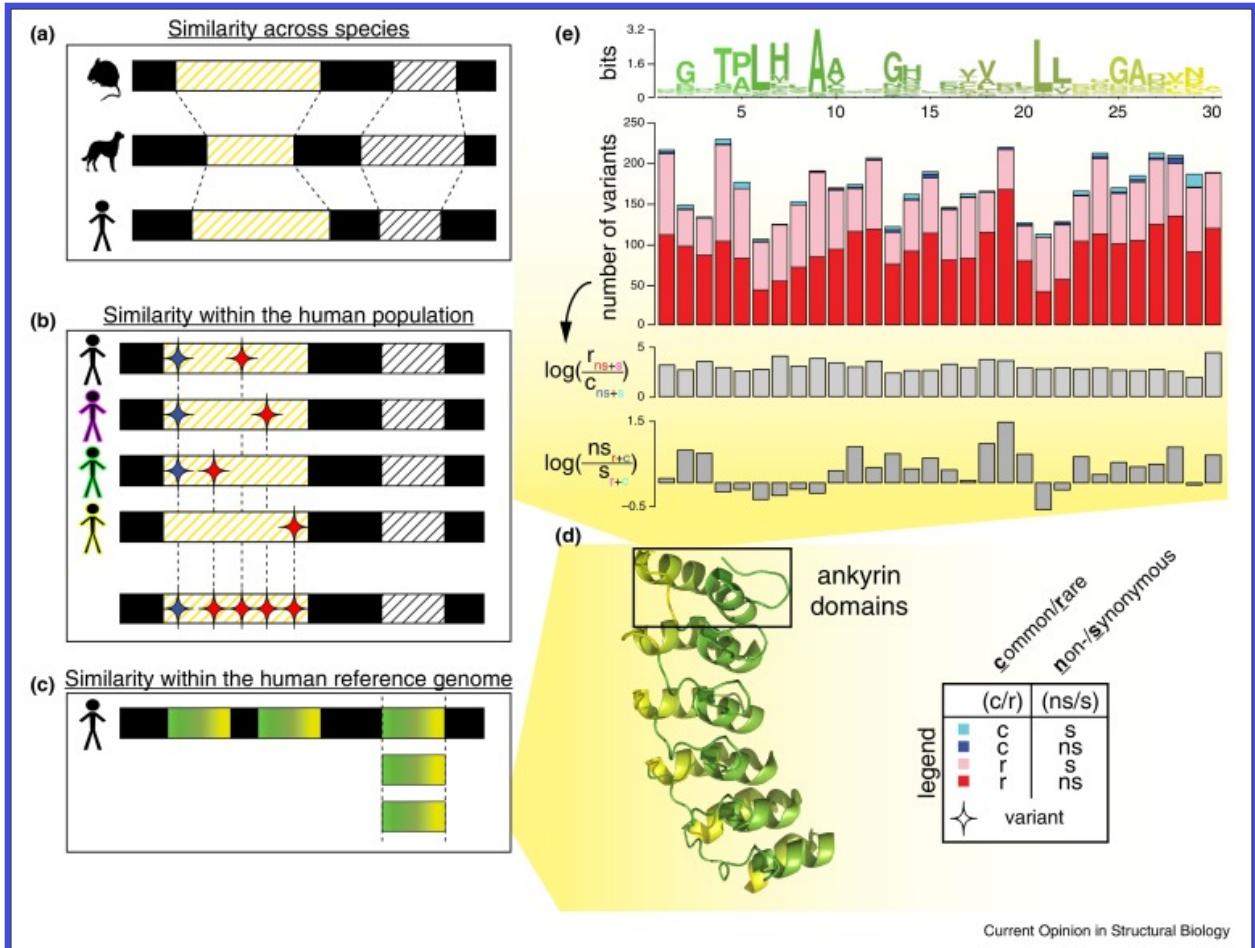
## 3. Read depth (or aCGH)

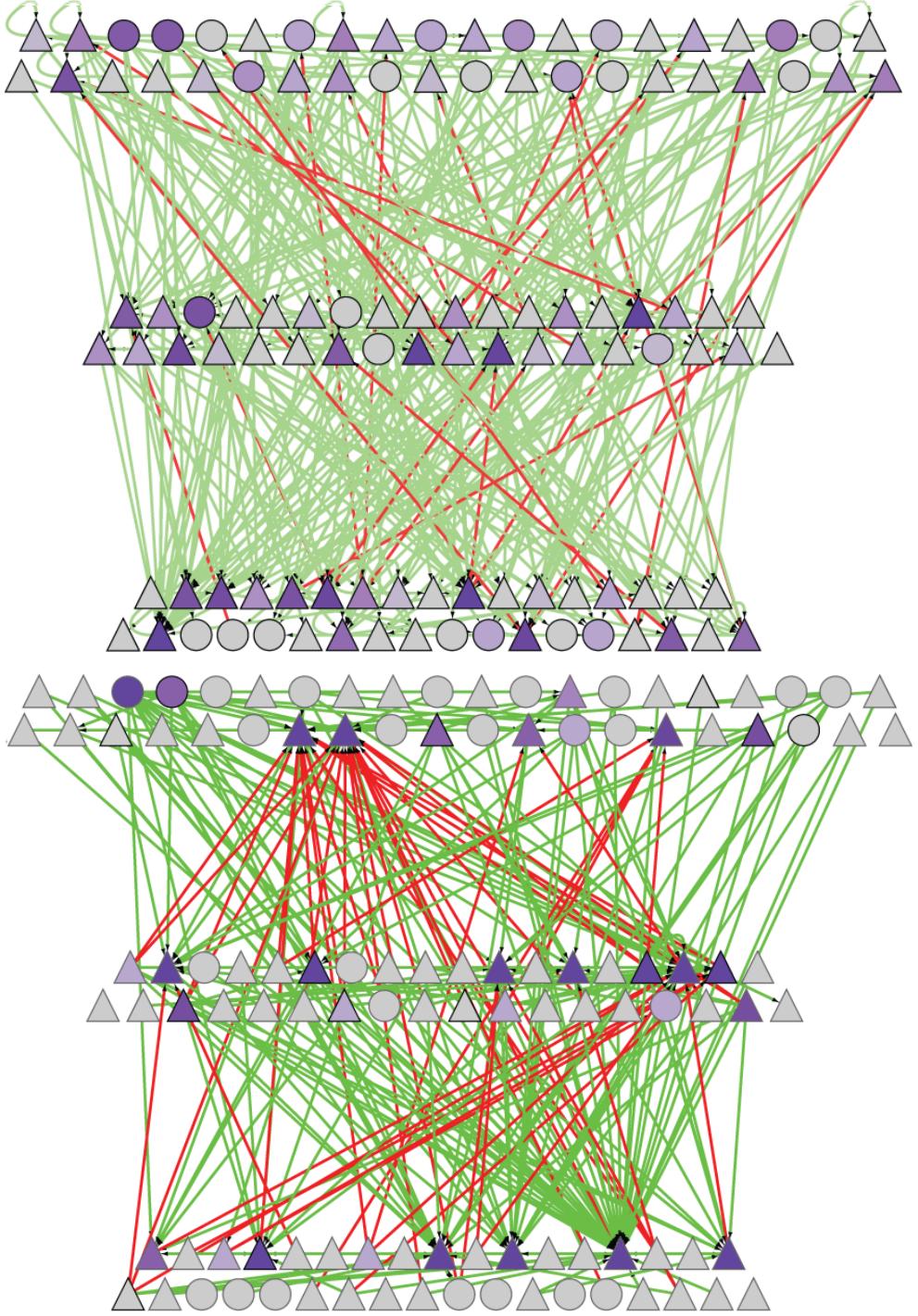


# Annotating the Human Genome: Comparative & Functional

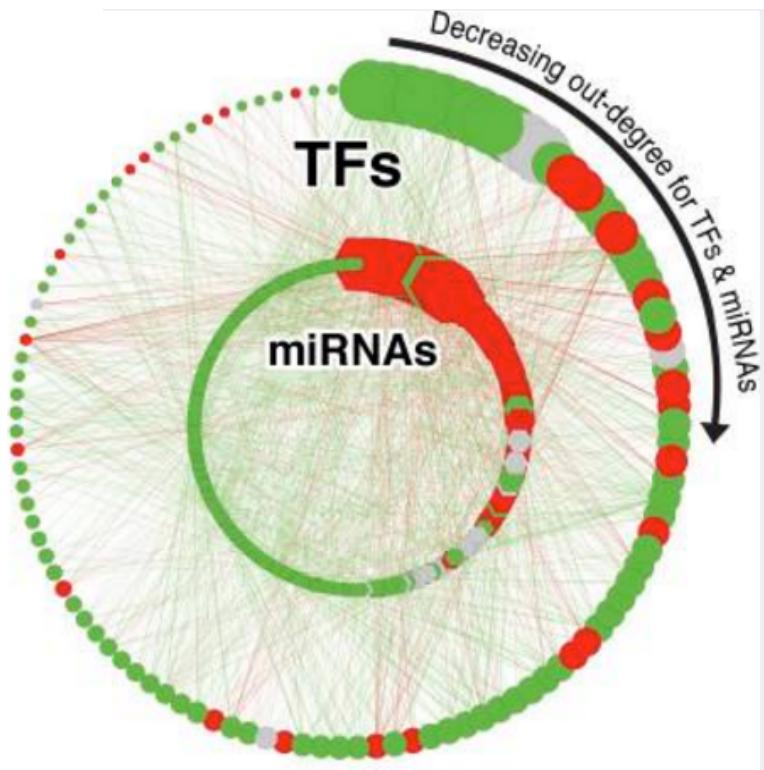


# Protein Structure & Function: Macromolecular Motions





# Recasting Genome Annotation as Networks: Comparing Proximal & Distal Networks



[ Gerstein et al. Nature (in press, '12) ]

# Application to cancer genome:

## identification of non-coding candidate

