

### **Functional RNAs:**

- Noncoding RNAs (ncRNA) are any RNA not translated into a protein, and include
  - o Transfer RNAs (tRNA), ribosomal RNAs (rRNA), long noncoding RNAs(lncRNA) , small nucleolar RNAs(snoRNA), small nuclear RNAs(snRNA), microRNAs(miRNA), short interfering RNAs(siRNA), and guide RNAs(gRNA)
- Functional RNA (fRNA) a more broad term than ncRNA, and includes functional secondary structures in mRNA, and those in exons listed as “coding fRNAs”
- PPfold: accepts multiple RNA aligns, uses phylo-SCFG methods(focus on entropy)
- Predicting miRNA targets:
  - o miRanda: specialized to find miRNA/mRNA targets by looking at 3'UTR and comparative genomics
  - o MANY other tools available

### **UCE and Conserved NC elements:**

- Ultraconserved Elements:
  - o Definition changes based on which organisms are being compared
  - o 2004 study found 481 regions of 200+ bp with 100% identity when comparing human, mouse, and rat. Not attributed to chance, most not in coding DNA and some in “gene deserts”
- SNPs and UCEs: very rare to see SNPs, as if UCE could mutate, there would be little to no variation between species that diverged 300 million years ago, making it have to be an SNP
- UCEs rarely seen outside of Chordates.
- UCE function unknown, but can be seen acting as an enhancer in uc322 within the SOX6 gene, enhancing expression in melanocytes.

### **CNE (conserved nc elements) Databases:**

- ANCORA: maintained by Boris Lenhard group, houses 11 species, with each having a browser with conservation tracks (HCNEs) and can be loaded into UCSC or Ensembl
- cneViewer: Access/display conserved regions between human and zebrafish, access info through gene name OR CNE ID
- UCNEBase: more comprehensive, hosted by swiss inst. Of bioinfo,
  - o 2013 paper describes ultraconserved nc elements
  - o Database holds 4351 UCNEs across 18 species
- CEGA: resource recently introduced, 5 species of vertebrate to find cons nc sequences(CNCs) from genomic alignments