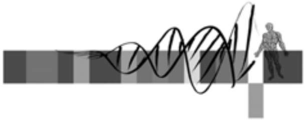

Sequence Analysis

III:

Genomics and Genome Browsers

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WIBR Bioinformatics and Research Computing

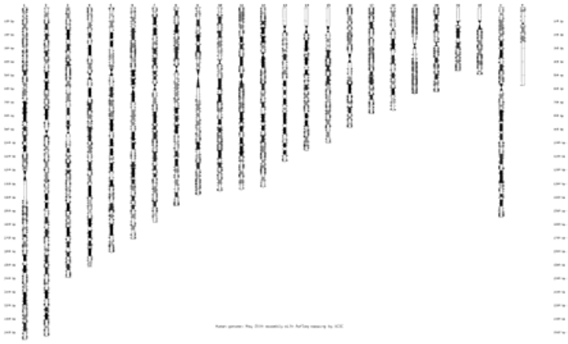
Genomics and Genome Browsers

- Introduction to genomics
- Genomics with genome browsers
- Conservation and evolution
- Introduction to comparative genomics
- Genome-wide data analysis

Genomics: some big questions

- What is a gene?
  - one definition: a region of DNA that encodes functional RNA or protein.
- What is the sequence of the genome? SNPs?
- Where are all of the genes?
- What are the proteins they encode? What do they do?
- Where's the regulatory sequence? What does it do?
- How can one integrate all of this information?

The human genome



The human genome

- Last assembly: May 2004 ("NCBI 35")

  3.0 billion bases, mostly complete
  Ensembl annotation: 24,194 genes; 35,838 transcripts
  Heterochromatin (light staining) is not sequenced

Mean GC content:	41%
Repetitive DNA:	50%
Coding sequence:	1.5%
Under selection:	5%

- Reference genome sequence comprises one strand of each chromosome.

Identifying genes

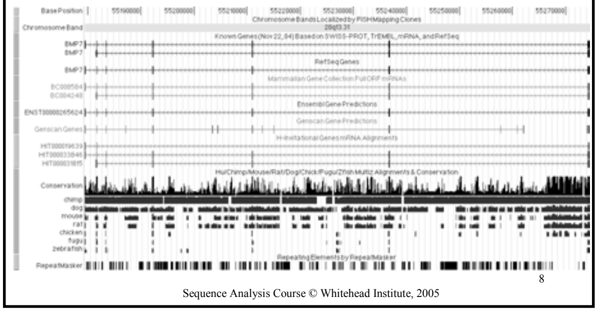
- Optimal protocol: Collect all RNA from all cell types in all conditions, sequence it and map it to the genome.
- Practical protocols:
  - predict genes de novo
  - cluster ESTs
  - sequence full-length clones
  - search with known genes in another species
  - a combination of those techniques above
- Still problems with pseudogenes

How many genes and transcripts?

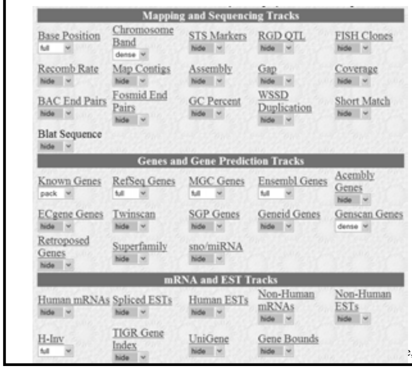
- Gene-centric databases (one entry per gene)
  - Ensembl (Hs= 24,194; Mm=28,069)
  - LocusLink (32,688; 67,653) incl. other “stuff”
- Human-curated full-length cDNA resources (one entry per transcript)
  - RefSeq (23,534; 30,462)
  - Mammalian Gene Collection (17,747; 14,639)
- EST-centric clusters (one entry per cluster)
  - UniGene (52,888; 45,719)
  - TIGR Gene Indices (227,631; 161,499)

Genome Browsers

Examples: UCSC, Ensembl, NCBI, WIBR



Genome Browser tracks



Mapping and Sequencing Tracks				
Base Position full	Chromosome Band dense	STS Markers hide	RGD QTL hide	FISH Clones hide
Recomb Rate hide	Map Contigs hide	Assembly hide	Gap hide	Coverage hide
BAC End Pairs hide	Fosmid End Pairs hide	GC Percent hide	WSSD Duplication hide	Short Match hide
Blat Sequence hide				

Genes and Gene Prediction Tracks				
Known Genes pack	RefSeq Genes full	MGC Genes full	Ensembl Genes full	Acembly Genes hide
ECgene Genes hide	Twinscan hide	SGP Genes hide	Geneid Genes hide	Genscan Genes dense
Retroposed Genes hide	Superfamily hide	sno/miRNA hide		

mRNA and EST Tracks				
Human mRNAs hide	Spliced ESTs hide	Human ESTs hide	Non-Human mRNAs hide	Non-Human ESTs hide
H-Inv full	TIGR Gene Index hide	UniGene hide	Gene Bounds hide	

Other groups:

•Expression and Regulation

•Comparative Genomics

•ENCODE Tracks

•Variation and Repeats

Genome Browser data

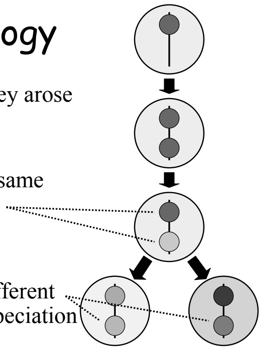
- Potential to show any data that can be mapped to a genome.
- Visual examination can be more powerful than any automated analysis tool.
- Positive strand of reference chromosome is shown.
- Conventions: gene “start” < “end”
- Coordinates change with each assembly.
- Sequence is often soft- or hard-masked for repetitive DNA.

Conservation and evolution

- Functional regions of a genome can be difficult to find in a large, repetitive sequence.
- During evolution, pressure for selection leads to greater conservation of some regions of a genome.
- Searching for regions of purifying selection is hoped to lead to elements of functional significance.

Homology

- Genes are *homologous* if they arose from the same ancestor.
- Paralogs: homologs (in the same species) that arose from a duplication event
- Orthologs: homologs (in different species) that arose from a speciation event



Quantifying evolution of coding regions

1. Percentage of AA identity or similarity
   For human-mouse orthologs, median identity = 79%
2. The K_a/K_s ratio

$$\frac{\text{AA substitution rate}}{\text{Neutral substitution rate}} = \frac{\text{Non-synonymous substitution rate}}{\text{Synonymous substitution rate}}$$

For human-mouse orthologs, median $K_a/K_s = 0.12$

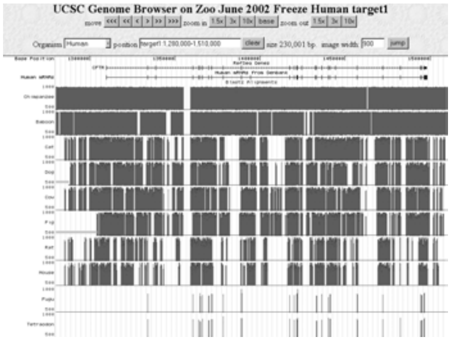
=> 88% of AA-changing mutations are deleterious

- Domain-containing regions have evolved less.
- Pseudogenes have a K_a/K_s ratio close to 1.

Comparative genomics

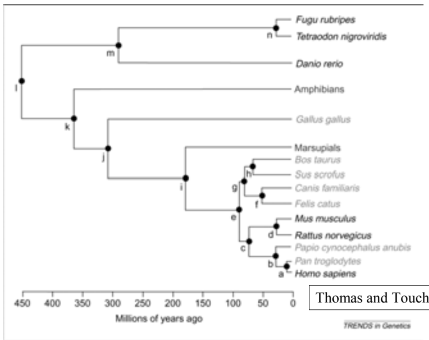
- Conservation between genomes is a very effective way to identify genes and regulatory regions.
- Comparison of multiple genomes can identify functional elements without any previous understanding of their function.
- With increasing conservation of a region of interest, comparisons between more distant species becomes more informative.
- Comparison of two species is rarely as effective as that of multiple species.

Multiple-species comparisons



UCSC Genome Browser on Zoo June 2002 Freeze Human target1

Vertebrate sequencing projects



Thomas and Touchman, 2002

Conserved synteny

Nature 420(6915):520-62, 2002

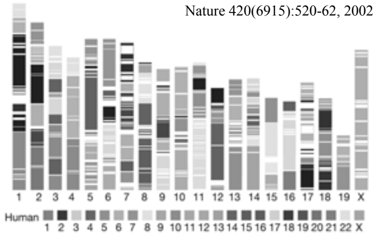


Figure 3 Segments and blocks >300 kb in size with conserved synteny in human are superimposed on the mouse genome. Each colour corresponds to a particular human chromosome. The 342 segments are separated from each other by thin, white lines within the 217 blocks of consistent colour.

Finding orthologous genes

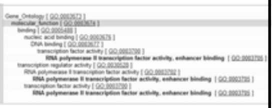
- Traditional method 1: reciprocal best BLASTP hits in all vs. all searches
- Traditional method 2: synteny maps
- Current methods: sequence analysis and conserved synteny
- Resources:
  Ensembl, NCBI, genome browsers
- Complicated by paralogous genes

What do all the genes do?

Q: How can every molecular function and biological process be systematically organized?

A: The Gene Ontology Consortium

- The three GO ontologies:
  - Molecular function
  - Biological Process
  - Cellular Component



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Gene_Ontology [ GO:0003673 ]
  molecular_function [ GO:0003674 ]
    binding [ GO:0005488 ]
      nucleic acid binding [ GO:0003676 ]
        DNA binding [ GO:0003677 ]
          transcription factor activity [ GO:0003700 ]
            RNA polymerase II transcription factor activity, enhancer binding [ GO:0003705 ]
    transcription regulator activity [ GO:0030528 ]
      RNA polymerase II transcription factor activity [ GO:0003702 ]
        RNA polymerase II transcription factor activity, enhancer binding [ GO:0003705 ]
      transcription factor activity [ GO:0003700 ]
        RNA polymerase II transcription factor activity, enhancer binding [ GO:0003705 ]
```

- Components of the ontologies are like hierarchies except that a “child” can have more than one “parent”.
- Evidence for annotation varies.

Genome-wide data analysis

- Ensembl and UCSC genome downloads
- NCBI flat file downloads
- EnsMart for genome-wide queries on the web
- Ensembl and WIBR LocusLink for SQL queries
- Analyzing sequence vs. annotations
- Transitivity of sequences and annotations?
- Check with BaRC about data on their servers

Summary

- Introduction to genomics
- Genomics with genome browsers
- Conservation and evolution
- Introduction to comparative genomics
- Genome-wide data analysis

Selected references

- Initial sequencing and analysis of the human genome. Nature. 409:860-921, 2001.

- Initial sequencing and comparative analysis of the mouse genome. Nature. 420:520-62, 2002.

- A User's Guide to the Human Genome II. Nature Genetics. 35 Suppl 1:4, 2003. (“web special”)

Exercises

- Browsing for genomic information
- Extracting annotated genomic sequence
- Gene-finding with comparative mammalian genomics
- Gene and genome analysis through annotation
- Command-line applications