Bioinformatic Resources

北京大学生物信息学中心 魏丽萍

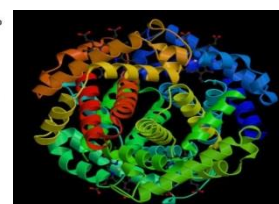Liping Wei, Ph.D.

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Unit 4:
UCSC Genome Bioinformatics

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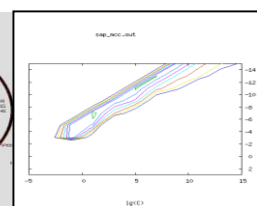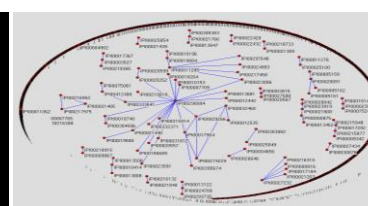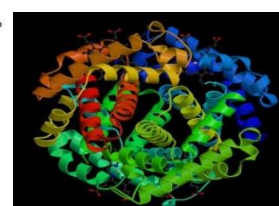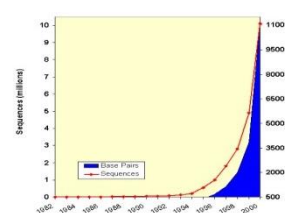# UCSC Genome Bioinformatics (http://genome.ucsc.edu/)

UCSC Genome Browser (http://genome.ucsc.edu/)

UCSC Genome Browser (http://genome.ucsc.edu/)

UCSC Genome Browser

http://genome.ucsc.edu/cgi-bin/hgTracks

ENCODE Project (http://www.genome.gov/10005107)

ENCODE data portal at UCSC (http://genome.ucsc.edu/encode/)

ENCODE

Encyclopedia of DNA Elements

About ENCODE Data

The Encyclopedia of DNA Elements (ENCODE) Consortium is an international collaboration of research groups funded by the National Human Genome Research Institute (NHGRI). The goal of ENCODE is to build a comprehensive parts list of functional elements in the human genome, including elements that act at the protein and RNA levels, and regulatory elements that control cells and circumstances in which a gene is active.
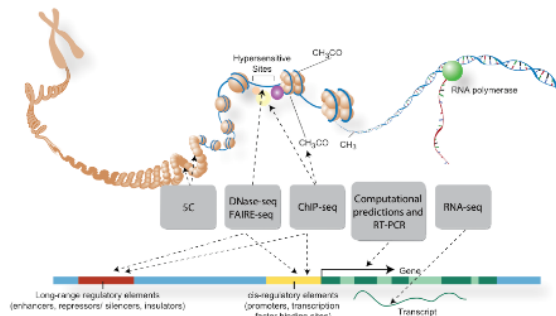
Click to enlarge

ENCODE data are now available for the entire human genome. *All ENCODE data are free and available for immediate use via* :

- Search for displayable tracks and downloadable files
- Download of data files
- Visualization in the UCSC Genome Browser (ENCODE data marked with the ⚒ NHGRI logo)
- Data mining with the UCSC Table Browser and other UCSC Genome Bioinformatics tools

To search for ENCODE data related to your area of interest and set up a browser view, use the UCSC Experiment Matrix or Track Search tool (*Advanced* features). The Experiment List (Human) and Experiment List (Mouse) links provide comprehensive listings of ENCODE data that is released or in preparation.

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Neandertal Genome (http://genome.ucsc.edu/Neandertal/)

UCSC Genome Bioinformatics

Home - Genomes - Blat - Tables - Gene Sorter - PCR - VisiGene - Session - FAQ - Help

Genome Browser
ENCODE
Blat
Table Browser
Gene Sorter
In Silico PCR
Genome Graphs
Galaxy
VisiGene
Utilities
Downloads

Neandertal Genome Analysis Consortium Tracks at UCSC

Neandertals are the closest extinct relatives of humans. They lived from several hundred thousand years ago until their disappearance approximately 30,000 years ago. The Neandertal genome sequence (published by Green *et al.* in *Science* May 2010) consists of short sequence fragments, usually about 50 base pairs long, mapped to the human reference genome. The DNA was extracted largely from three Neandertal bones, each about 40,000 years old, from the Vindija Cave in Croatia: Vi33.16, Vi33.25, and Vi33.26. The bulk sequencing was carried out on the Illumina GAII platform. Neandertal DNA was identified from among the background of microbial sequences in the bone by similarity to the human or chimpanzee genomes.

This portal provides access to the sequence data and alignments to the reference human genome (NCBI Build 36/hg18, GRCh37/hg19) as well as the reference chimpanzee genome (CGSC 2.1/panTro2) and several associated analyses (see Downloads and References).

The following annotations are available on the human hg18 and hg19 genome assemblies, except as noted:

- **Neandertal Alleles in Human/Chimp Coding Non-synonymous Differences in Human Lineage**: Displays Neandertal alleles for human-chimp protein-coding differences on the human lineage using orangutan as the outgroup to determine which allele is more likely to be ancestral.
- **Selective Sweep Scan (S) on Neandertal vs. Human Polymorphisms**: Shows the S score, an estimate

http://genome.ucsc.edu/cgi-bin/hgTracks

Neandertal Assembly and Analysis — refresh

18 **H-C Coding Diffs**
hide

18 **Sel Swp Scan (S)**
hide

18 **5% Lowest S**
hide

18 **S SNPs**
hide

18 **Cand. Gene Flow**
hide

Neandertal Seq
- hide
- dense
- squish
- pack
- full

18 **Neandertal Mito**
[No data-chr22]

Denisova Assembly and Analysis — refresh

Denisova Variants
hide

Mod Hum Variants
hide

Denisova Seq
hide

Modern Derived
hide

Variation and Repeats — refresh

Common SNPs(138)
dense

Flagged SNPs(138)
hide

Mult. SNPs(138)
hide

All SNPs(138)
hide

Common SNPs (137)
hide

Flagged SNPs (137)
hide

Mult. SNPs (137)

All SNPs(137)

Common SNPs (135)

Flagged SNPs (135)

Mult. SNPs(135)

All SNPs(135)

UCSC BLAT (http://genome.ucsc.edu/cgi-bin/hgBlat)

UCSC *In-Silico* PCR (http://genome.ucsc.edu/cgi-bin/hgPcr)

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生物信息学：导论与方法
Bioinformatics: Introduction and Methods

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https://www.coursera.org/course/pkubioinfo