



The Roadmap

Example: AluSq2

*Example: GULOP
(pseudogene)*

Example: Chromosome 2/PAX3

Conclusion:
A List of Databases

UCSC's Genome Browser
Tutorial

Entrez/BLAST Tutorial

The Contribution of Bioinformatics

History of Evolutionary Thought

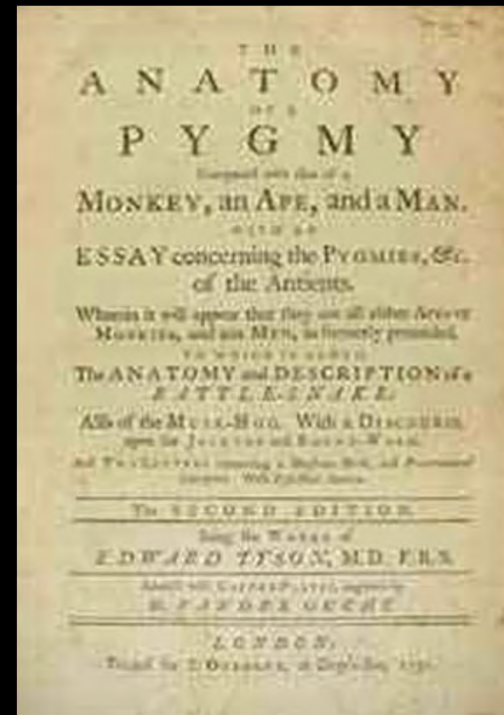
“

Biological evolution is the central organizing principle of modern biology...modern chimpanzees, other great apes, and humans are descended from a common ancestor that is now extinct.

”

-U.S. National Academy of Sciences,
Science, Evolution, and Creationism (2008)

The history of evolutionary thought with regards to common ancestry dates back to 1698...



...when the English anatomist Edward Tyson acquired the remains of a chimpanzee, and published his astonishment at the anatomical similarity between the chimpanzee and a human.

Pierre-Louis Moreau de Maupertuis, 1745



Maupertuis' *Vénus Physique* is an early attempt at a materialistic explanation of the origin of species, suggesting that natural variation and selection give rise to function.

Immanuel Kant, 1790



Wrote that the “analogy of animal forms” implies a common original type.

Charles Darwin published *On the Origin of Species* in 1859

Sixty years after his grandfather posed the question of common ancestry.

“

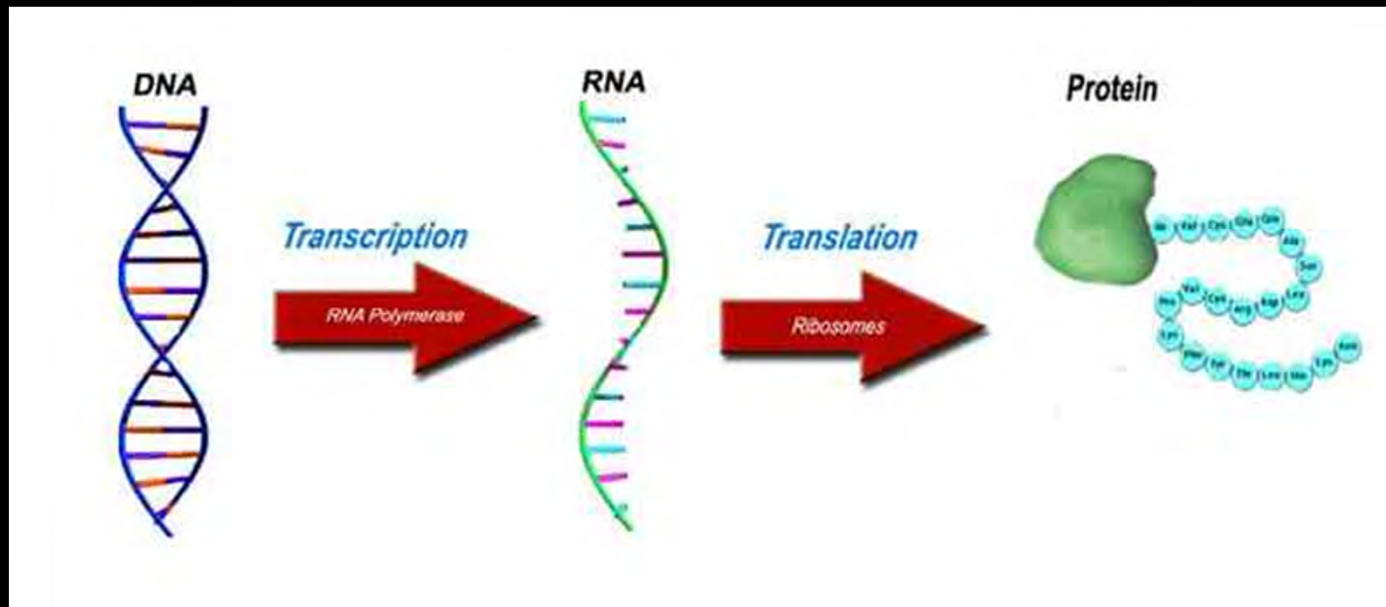
Therefore I should infer from analogy that probably all the organic beings which have ever lived on this earth have descended from some one primordial form, into which life was first breathed.

”

-Darwin, *On the Origin of Species*, 1859

Since then, biologists have discovered that...


...all life forms share the same fundamental biochemical organization:



It is such similarities that have prompted bioinformaticians to meticulously compare sequences, pseudogenes, and repeated sequences in the genomes of humans and chimpanzees.

Even more recently, the field of bioinformatics has begun to contribute to the search for answers...

bio·in·for·mat·ics  *noun pl but singular in constr* \bī-ō-in-fər-'ma-tiks\
: the collection, classification, storage, and analysis of biochemical and biological information using computers especially as applied to molecular genetics and genomics

— **bio·in·for·mat·ic**  \-tik\ *adjective*

<http://www.merriam-webster.com/dictionary/bioinformatics>

- In 2002, Ebersberger et al. aligned 1.9 million nucleotides of chimpanzee DNA with the human genome, and found a difference of a mere 1.24%.
- In 2003, Lie et al. compared 4.97 million nucleotides of human DNA from chromosome 7 to the corresponding chimpanzee DNA, and found that the sequences differed by 1.13%.
- The publication of a rough draft of the chimpanzee genome, also in 2003, provided even greater evidence for the similarity between chimpanzees and humans.

The entire sequence differs from the human genome by 86-89% (Tomkins, 2011); this statistic is a matter of live debate, and fluctuates regularly in the literature.

Using bioinformatics, we can examine the arguments for/against common ancestry for ourselves.

**This is an informational talk, I will not draw conclusions about the strength of the data.*

The Roadmap



Example: Chromosome 2/PAX3

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Example: Human Chromosome 2

- The structure of human chromosome 2 resembles the structure one might see if chimpanzee chromosomes 2a and 2b were fused together.
- Scientists accept that there is good evidence that chromosome 2 is composed of two fused chromosomes.

Regardless of the plausibility of a fusion event...

How similar are the genes on human chromosome 2 to those on chimpanzee chromosomes 2a and 2b?

PAX3 is a gene that belongs to the paired-box family of transcription factors, located on human chromosome 2, and chimpanzee chromosome 2b.

- Associated with ear, eye, and facial development.

Entrez BLAST

A tutorial

“Entrez is NCBI’s [National Center for Biotechnology Information] primary text search engine”

an
ot
ge

9

AST

[Organism Overview](#) ; [Genome Project Report](#) ; [Genome Annotation Report](#) ; [Organelle Annotation Report](#)



Pan troglodytes (chimpanzee)

The chimpanzee genome sequence is an important tool in understanding primate evolution

Lineage: Eukaryota[1622]; Metazoa[648]; Chordata[271]; Craniata[266]; Vertebrata[265]; Euteleostomi[260]; Mammalia[124]; Eutheria[120]; Euarchontoglires[66]; Primates[34]; Haplorrhini[30]; Catarrhini[27]; Hominidae[6]; Pan[2]; Pan troglodytes[1]

Pan troglodytes, or chimpanzee, is a primate very closely related to humans. The chimpanzee and other apes are most closely related to humans, followed by Old World monkeys; including the rhesus macaque and baboon. The chimpanzee is an important model to study biology, disease, and evolution. Research with *Pan troglodytes* has provided [More...](#)

Chromosomes



Click on chromosome name to open MapViewer

Genome Sequencing Projects

Organism	BioProject	Assembly	Status	Chrs	Organelles	Size (Mb)	GC%	Gene	Protein
Pan troglodytes	PRJNA10627, PRJNA12552, PRJNA13184	ICC22C chr21 ; Pan_troglodytes-2.1.4	◆	25	1	3,160.37	41.6	30,235	32,568
Pan troglodytes verus	PRJNA16845, PRJNA16847	ASM217v1 ; CCYSCv1	◆	1	-	12.26	40.5	84	42
Pan troglodytes	PRJNA11814	-	◆	-	-	-	-	-	-
Pan troglodytes	PRJNA13698	-	◆	-	-	-	-	-	-

Other BioProjects

Transcriptome or Gene expression 5

Tools

1. BLAST Genome

NCBI Resources

[Chimp Build Statistics](#)

[Map Viewer](#)

Related information

[BioProject](#)

[Gene](#)

[Protein Clusters](#)

[Components](#)

[Protein](#)

[PubMed](#)

[Taxonomy](#)

Search details

"Pan troglodytes"[Organism]

[See more...](#)

Recent activity

[Turn Off](#) [Clear](#)

[Pan troglodytes \(1\)](#)

Genome

[ref|NC_000002.11| \(243199373 letters\)](#)

BLAST

[Pan troglodytes](#)

Genome

[chimpanzee \(7\)](#)

10



Structure: three-dimensional [Go to Genome Results Page](#)



20828



PopSet: population study data sets

Entrez BLAST

A tutorial

The Basic Local Alignment Search Tool (BLAST) finds regions of local similarity between sequences. The program compares nucleotide or protein sequences to sequence databases and reports the position and similarity of the best matches. **Pan troglodytes (chimpanzee) Nucleotide BLAST**

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) [Query subrange](#)

From

To

Or, upload file no file selected [Choose File](#)

Job Title

Enter a descriptive title for your BLAST search [Choose File](#)

Choose Search Set

Database 27005 sequences [Choose File](#)

Exclude Models (XM/XP) Uncultured/environmental sample sequences

Entrez Query

Enter an Entrez query to limit search [Choose File](#)

Program Selection

Optimize for Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

Somewhat similar sequences (blastn)

Choose a BLAST algorithm [Choose File](#)

BLAST Search database **Genome (reference only) - Pan troglodytes** using **Megablast (Optimize for highly similar sequences)**

Show results in a new window

Entrez BLAST

A tutorial

NCBI

HOME SEARCH SITE MAP

Display Settings: Summary, 20 per page, Sorted by Default order [Send to:](#)

See **PAX3 paired box 3** in the Gene database
pax3 in [Homo sapiens](#) | [Mus musculus](#) | [Rattus norvegicus](#) | [All 24 Gene records](#)

Results: 1 to 20 of 233 << First < Prev Page 1 of 12 Next > Last >>

[PAX3, partial \[Homo sapiens\]](#)
1. 55 aa protein
Accession: AAA91849.1 GI: 1220350
[GenPept](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Pax3, partial \[Capra hircus\]](#)
2. 142 aa protein
Accession: AFD10414.1 GI: 379692648
[GenPept](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Pax3 \[Polyodon spathula\]](#)
3. 285 aa protein
Accession: ADZ48385.1 GI: 325980252
[GenPept](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[Pax3 \[Scyliorhinus canicula\]](#)
4. 319 aa protein
Accession: ABM89502.1 GI: 124054602
[GenPept](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[PAX3 \[Homo sapiens\]](#)
5. 80 aa protein
Accession: ACU60135.1 GI: 255046236
[GenPept](#) [FASTA](#) [Graphics](#) [Related Sequences](#)

[paired box protein Pax-3-B \[Xenopus laevis\]](#)
6. 461 aa protein
Accession: NP_001088994.1 GI: 147903833
[GenPept](#) [FASTA](#) [Graphics](#) [Related Sequences](#) [Identical Proteins](#)

Result counts displayed: 1091, 1852, 7, 332, 16, 3554, 233, 1, none, 3552, 61, 153

BLAST

Entrez BLAST

A tutorial

► NCBI/ BLAST/ blastn suite Pan troglodytes (chimpanzee) Nucleotide BLAST

[blastn](#) [blastp](#) [blastx](#) [tblastn](#) [tblastx](#)

BLASTN programs search nucleotide databases using a nucleotide query. [more...](#)

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [Clear](#) Query subrange [↕](#)

ACU00135.1 From

To

Or, upload file no file selected [↕](#)

Job Title

Enter a descriptive title for your BLAST search [↕](#)

Choose Search Set

Database 27005 sequences [↕](#)

Exclude Models (XM/XP) Uncultured/environmental sample sequences

Optional

Entrez Query

Optional

Enter an Entrez query to limit search [↕](#)

Program Selection

Optimize for

Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)



Somewhat similar sequences (blastn)

Choose a BLAST algorithm [↕](#)

Search database **Genome (reference only)** - Pan troglodytes using Megablast (Optimize for highly similar sequences)

Show results in a new window

A BLAST comparison of the protein sequences yields...

```
>  ref|XP_001165390.1|  PREDICTED: paired box protein Pax-3 isoform 6 [Pan troglodytes]  
Length=505
```

```
GENE ID: 459971 PAX3 | paired box 3 [Pan troglodytes]
```

```
Score = 977 bits (2526), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 474/474 (100%), Positives = 474/474 (100%), Gaps = 0/474 (0%)
```

```
Query 1 MTTLAGAVPRMMPGPGQNYPRSGFPLEVSTPLGQGRVNQLGGVFINGRPLPNHIRHKIV 60  
Sbjct 1 MTTLAGAVPRMMPGPGQNYPRSGFPLEVSTPLGQGRVNQLGGVFINGRPLPNHIRHKIV 60  
Query 61 EMAHHGIRPCVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQVTTPDVEKKIEE 120  
Sbjct 61 EMAHHGIRPCVISRQLRVSHGCVSKILCRYQETGSIRPGAIGGSKPKQVTTPDVEKKIEE 120  
Query 121 YKRENPGMFSWEIRDKLLKDAVCDRNTVPSVSSISRILRSKFGKGESEADLERKEAEE 180  
Sbjct 121 YKRENPGMFSWEIRDKLLKDAVCDRNTVPSVSSISRILRSKFGKGESEADLERKEAEE 180  
Query 181 EKKAKHSIDGILSERASAPQSDGSDIDSEPDLPKRKQRRSRTTFTAEQLEELERAFA 240  
Sbjct 181 EKKAKHSIDGILSERASAPQSDGSDIDSEPDLPKRKQRRSRTTFTAEQLEELERAFA 240  
Query 241 THYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQLMAFNHLIPGGFPPTAMP 300  
Sbjct 241 THYPDIYTREELAQRAKLTEARVQVWFSNRRARWRKQAGANQLMAFNHLIPGGFPPTAMP 300  
Query 301 TLPTYQLSETSYQPTSIPQAVSDPSSTVHRPQPLPPSTVHQSTIPSNPDSSSAYCLPSTR 360  
Sbjct 301 TLPTYQLSETSYQPTSIPQAVSDPSSTVHRPQPLPPSTVHQSTIPSNPDSSSAYCLPSTR 360  
Query 361 HGFSSYTDSFVPPSGPSNPMNPTIGNGLSPQVMGLLNHGGVPHQPQTDYALSPLTGGLE 420  
Sbjct 361 HGFSSYTDSFVPPSGPSNPMNPTIGNGLSPQVMGLLNHGGVPHQPQTDYALSPLTGGLE 420  
Query 421 PTTTVSASCSQRLDHMKSLSLPTSQSYCPPTYSTTGYSMDPVTGYQYGQYQGS 474  
Sbjct 421 PTTTVSASCSQRLDHMKSLSLPTSQSYCPPTYSTTGYSMDPVTGYQYGQYQGS 474
```

The query and the subject sequences are identical.

The Roadmap



*Example: GULOP
(pseudogene)*

UCSC's Genome Browser
Tutorial

Entrez/BLAST Tutorial

Example: Chromosome 2/PAX3

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UCSC's Genome Browser

A tutorial

This site contains the reference sequence and working draft assemblies for a large collection of genomes.

Human (*Homo sapiens*) Genome Browser Gateway

The UCSC Genome Browser was created by the [Genome Bioinformatics Group of UC Santa Cruz](#).
Software Copyright (c) The Regents of the University of California. All rights reserved.

clade	genome	assembly	position or search term	gene
Mammal	Human	Feb. 2009 (GRCh37/hg19)	chr2:223064606-223163715	PAX3

[set the browser user interface settings to their defaults.](#)

[track hubs](#) [configure tracks and display](#) [clear position](#)

Human Genome Browser – hg19 assembly ([sequences](#))

The February 2009 human reference sequence (GRCh37) was published in the [Genome Reference Consortium](#). For more information about this assembly, see [GRCh37](#) in the NCBI Assembly database.

Sample position queries

A genome position can be specified by the accession number of a contig or keywords from the GenBank description of an mRNA. The following are examples of valid position queries for the human genome. See the [User's Guide](#) for more information.

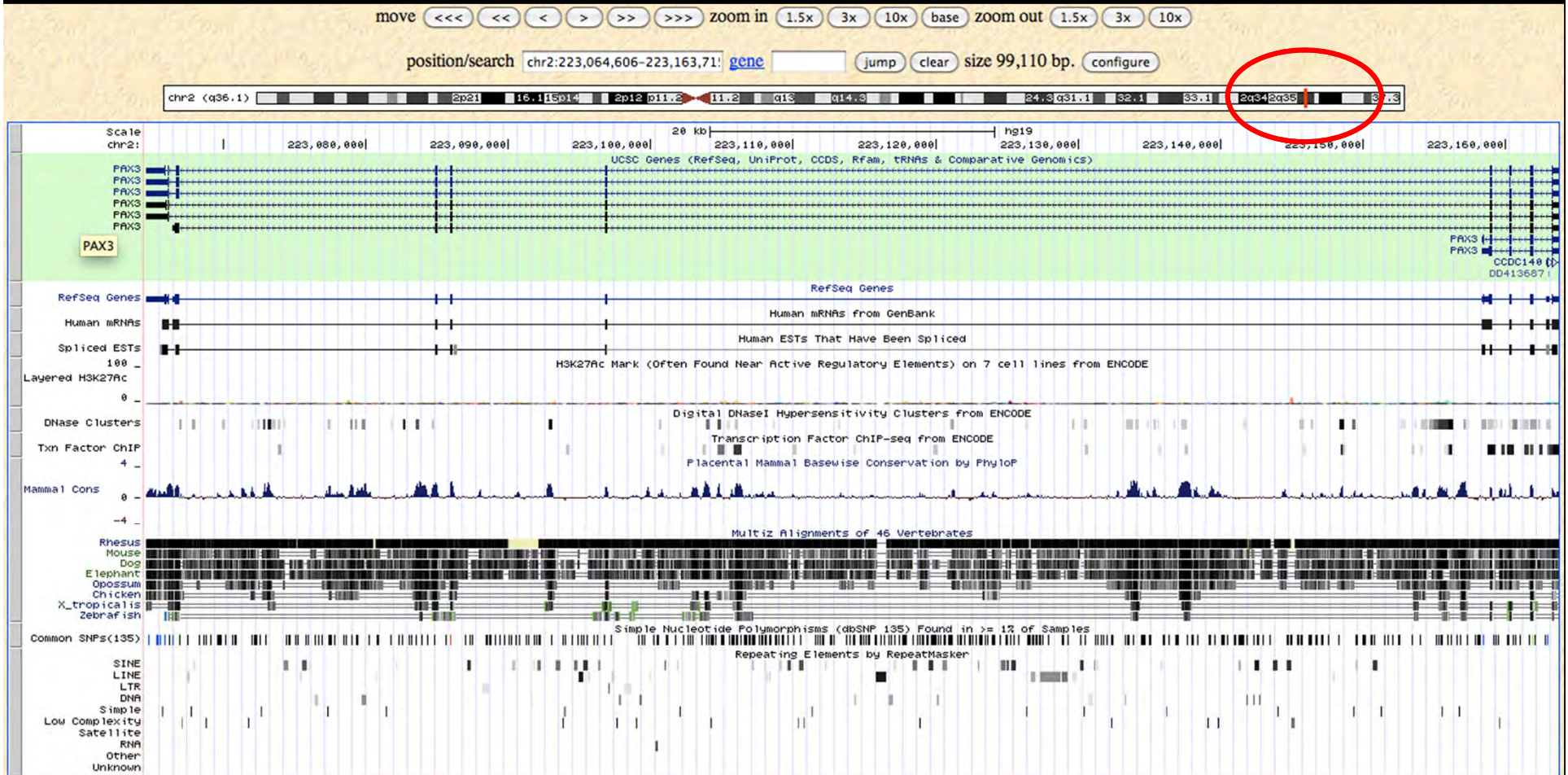
Request:	Genome Browser Response:
chr7	Displays all of chromosome 7
chrUn_g1000212	Displays all of the unplaced contig g1000212
20p13	Displays region for band p13 on chr 20

- Chimp
- Gorilla
- Orangutan
- Gibbon
- Rhesus
- Marmoset
- Mouse
- Rat
- Naked mole-rat
- Guinea pig
- Rabbit
- Pig
- Sheep
- Cow
- Horse
- Cat
- Dog
- Panda
- Microbat
- Tenrec
- Elephant
- Opossum
- Wallaby
- Platypus



UCSC's Genome Browser

A tutorial



Example: GULOP (pseudogene)

Darwinian scientists claim that much non-coding DNA is functionless “genetic flotsam and jetsam” (i.e., junk) that has accumulated many random mutations.

Pseudogenes, genes that have lost their protein-coding ability, are often called “junk DNA”.

"At face value, pseudogenes hardly seem like genomic features that would be designed by a wise engineer....given the relative ease of origin of pseudogenes, their persistence in genomes is understandable in the light of evolutionary reasoning."

-John C. Advise

(From John C. Avise, *Inside the Human Genome: A Case for Non-Intelligent Design* [Oxford University Press, 2010, pp. 115-6])

Using Genome Browser:

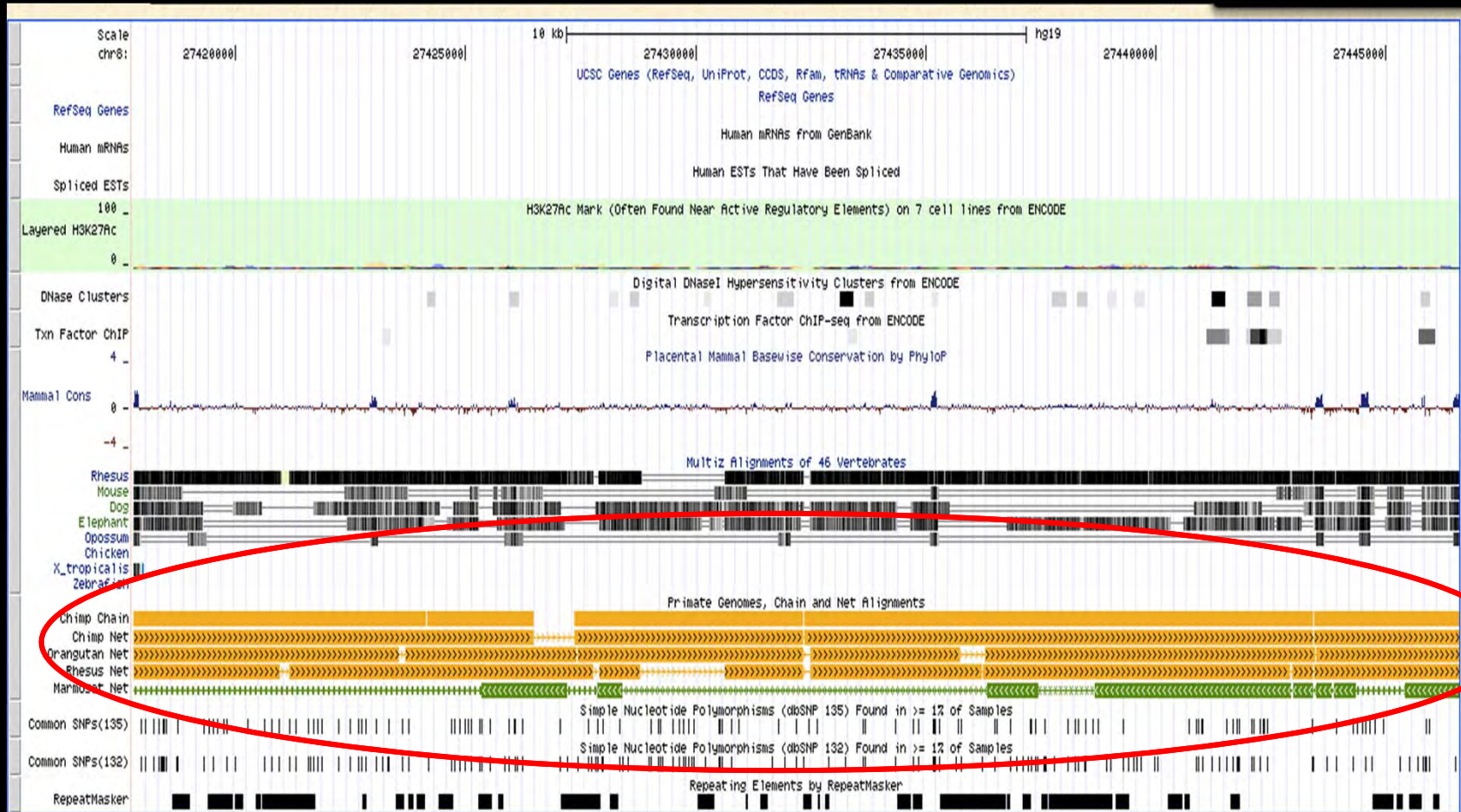
A gene that presumably encoded the L-gulono- γ -lactone oxidase enzyme in primates (GULO) exists as a pseudogene (GULOP) in both humans and chimpanzees...

UCSC's Genome Browser

A tutorial

The screenshot displays the UCSC Genome Browser interface with several tracks and their visibility settings:

- Regulation** (collapse icon):
 - ENCORE Regulation... (show)
 - ENC Histone... (hide)
 - SUNY SwitchGear (hide)
 - Vista Enhancers (hide)
 - 18 CD34 DnaseI (hide)
 - ENC RNA Binding... (hide)
 - 17 SwitchGear TSS (hide)
 - 18 NKI Nuc Lamina... (hide)
 - CpG Islands (hide)
 - ENC TF Binding... (hide)
 - TFBS Conserved (hide)
 - 18 UCSF Brain Methyl (hide)
 - ENC Chromatin... (hide)
 - FSU Repli-chip (hide)
 - TS miRNA sites (hide)
 - 18 ENC DNA Methyl... (hide)
 - OREgAnno (hide)
 - UMMS Brain Hist (hide)
 - ENC DNase/FAIRE... (hide)
 - Stanf Nucleosome (hide)
 - UW Repli-seq (hide)
- Comparative Genomics** (collapse icon):
 - Conservation (full)
 - hg19Patch2 Chain/Net (hide)
 - 18 Cons Indels MmCf (hide)
 - Vertebrate Chain/Net (hide)
 - GERP (hide)
 - 18 Evo Cpg (hide)
 - Primate Chain/Net** (hide) - circled in red
 - Placental Chain/Net (hide)
- Neandertal Assembly and Analysis** (expand icon)
- Variation and Repeats** (collapse icon):
 - Common SNPs(135) (dense)
 - Flagged SNPs(135) (hide)
 - Mult. SNPs(135) (hide)
 - All SNPs(135) (hide)
 - Common SNPs(132) (hide)
 - Flagged SNPs(132) (hide)
 - Mult. SNPs(132) (hide)
 - All SNPs(132) (hide)
 - SNPs (131) (hide)
 - Arrays (hide)
 - 18 SNP Arrays (hide)
 - HGDP Allele Freq (hide)
 - 18 HapMap SNPs (hide)
 - DGV Struct Var (hide)
 - Segmental Dups (hide)
 - RepeatMasker (full)
 - Interrupted Rpts (hide)
 - Simple Repeats (hide)
 - Microsatellite (hide)
 - Self Chain (hide)
 - 18 Genome Variants (hide)
 - NumtS Sequence (hide)
 - GIS DNA PET (hide)
 - HAIB Genotype (hide)



Human position: [chr8:13909-146302299](#) size: 146288391
Strand: +
Chimp position: [chr8:3911-143967758](#) size: 143963848
Chain ID: 6
Score: 11541415440 **Approximate Score within browser window:** 2569589

A BLAST comparison of the two sequences reveals a high sequence similarity, though the two are not identical:

```
Query 1189 AACAgtt-tttttgtttgtttgtttgtttgtttgtttgtttgtttgAAATGA 1247
          ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 118378 AACAA-TTCTTTTTGTTT-TGT-TTGTTTTGTTTT-TTTTTTTTTTTTTTTGAGACGGA 118323

Query 1248 GTCTCGCTCTGTCACCCAAGCTGGAGTGCAGTGGCGGGTCTCAGCTCACTGCCAGCTCC 1307
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 118322 GTCTCGCTCTGTCGCCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAGCTCC 118263

Query 1308 ACCTCCCAGGTTACACCAATTCTCCTTCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTG 1367
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 118262 GCCTCCCAGGTTACAGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCG 118203

Query 1368 CCCGCCACCACCCCAGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCGTGTT 1427
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 118202 CCCGCTACCACGCCCGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCGTGTT 118143

Query 1428 AGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGCCTGCCTCGGCCTCC-AAAGTGC 1486
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 118142 AGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCCGCCCGCCTCGGCCTCCCAAAGTGC 118083

Query 1487 TGGGATTACAGGTGTGAGCCACTGTGCCCGGCACTC 1522
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Sbjct 118082 TGGGATTACAGGCGTGAGCCACCGCGCCCGGC-CTC 118048
```

The Roadmap



Example: AluSq2

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(pseudogene)*

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Example: Alu Sequence (AluSq2)

Alu sequences are mobile genetic elements that appear to insert into the genome at random...

The vast majority of them are found in identical locations in the human and chimp genomes, which strongly suggests they were inserted in the common ancestor of humans and chimpanzees before they diverged.

Using Genome Browser:

AluSq2 is an SINE located in the SPTLC2 gene in humans...

Example: Alu Sequence (AluSq2)

The image shows a screenshot of a genomic data browser interface, likely UCSC Genome Browser, displaying various tracks for an Alu sequence (AluSq2). The interface is organized into several sections, each with a collapse/expand icon and a 'refresh' button.

- Regulation** (collapse icon):
 - ENCORE Regulation... (show)
 - ENC Histone... (hide)
 - SUNY SwitchGear (hide)
 - Vista Enhancers (hide)
 - CD34 DnaseI (hide)
 - ENC RNA Binding... (hide)
 - SwitchGear TSS (hide)
 - NKI Nuc Lamina... (hide)
 - CpG Islands (hide)
 - ENC TF Binding... (hide)
 - TFBS Conserved (hide)
 - UCSF Brain Methyl (hide)
 - ENC Chromatin... (hide)
 - FSU Repli-chip (hide)
 - TS miRNA sites (hide)
 - ENC DNA Methyl... (hide)
 - OREgAnno (hide)
 - UMMS Brain Hist (hide)
 - ENC DNase/FAIRE... (hide)
 - Stanf Nucleosome (hide)
 - UW Repli-seq (hide)
- Comparative Genomics** (collapse icon):
 - Conservation (full)
 - hg19Patch2 Chain/Net (hide)
 - Cons Indels MmCf (hide)
 - Vertebrate Chain/Net (hide)
 - GERP (hide)
 - Evo Cpg (hide)
 - Primate Chain/Net (hide)
 - Placental Chain/Net (hide)
- Neandertal Assembly and Analysis** (expand icon)
- Variation and Repeats** (collapse icon):
 - Common SNPs(135) (dense)
 - Flagged SNPs(135) (hide)
 - Mult. SNPs(135) (hide)
 - All SNPs(135) (hide)
 - Common SNPs(132) (hide)
 - Flagged SNPs(132) (hide)
 - Mult. SNPs(132) (hide)
 - All SNPs(132) (hide)
 - SNPs (131) (hide)
 - Arrays (hide)
 - GIS DNA PET (hide)
 - HAIB Genotype (hide)
 - SNP Arrays (hide)
 - HGDP Allele Freq (hide)
 - HapMap SNPs (hide)
 - DGV Struct Var (hide)
 - Segmental Dup (hide)
 - RepeatMasker (full) **(highlighted with a red circle)**
 - Interrupted Rpts (hide)
 - Simple Repeats (hide)
 - Microsatellite (hide)
 - Self Chain (hide)
 - Genome Variants (hide)
 - NonS Sequence (hide)

Example: Alu Sequence (AluSq2)

Home Genomes Blat Tables Gene Sorter PCR DNA Convert PS/PDF Session Ensembl NCBI Help

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg10) Assembly

Repeat 3x 10x

move <<< << < position/search chr

chr14 (q24.3) 14p13 14p12 14p11.2 14q11.2

Scale chr14: 77,999,000| 1 kb|

SPTLC2

RefSeq Genes

Human mRNAs

Spliced ESTs 100 _

Layered H3K27Ac 0 _

DNase Clusters

Txn Factor ChIP 4 _

Mammal Cons 0 -4 _

Rhesus Mouse Dog Elephant Opossum Chicken X_tropicalis Zebrafish

Common SNPs(135) | | |

SINE LINE LTR DNA Simple Low Complexity Satellite RNA Other Unknown

RepeatMasker Information

Name: AluSq2
Family: Alu
Class: SINE
SW Score: 2259
Divergence: 11.5%
Deletions: 0.0%
Insertions: 0.7%
Begin in repeat: 2
End in repeat: 303
Left in repeat: 9
Position: [chr14:77999360-77999663](#)
Band: 14q24.3
Genomic Size: 304
Strand: +
[View DNA for this feature \(hg19/Human\)](#)
[View table schema](#)
[Go to RepeatMasker track controls](#)
Data last updated: 2009-04-24

hg19 78,000,500|

ENCODE

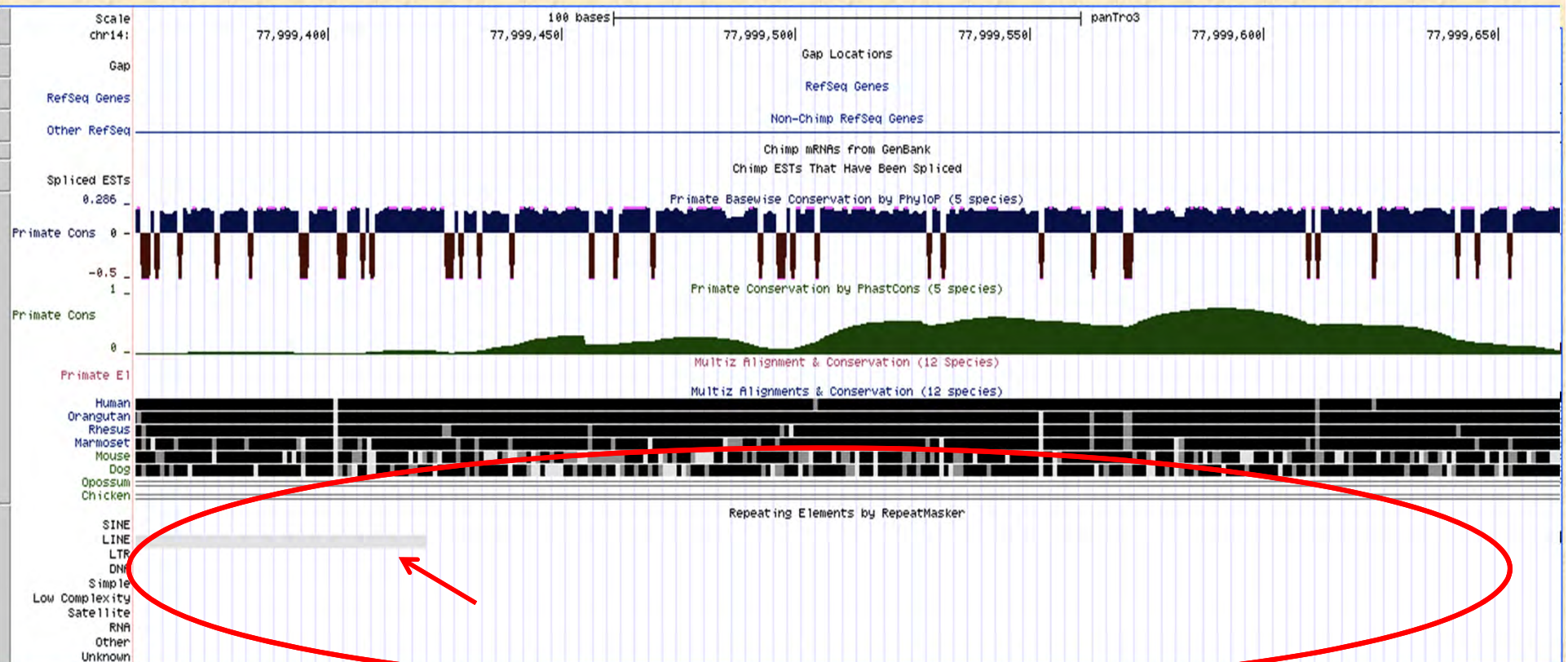
Example: Alu Sequence (AluSq2)

Home Genomes Blat Tables PCR DNA Convert PS/PDF Session Ensembl Help

UCSC Genome Browser on Chimp Oct. 2010 (CGSC 2.1.3/panTro3) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x

position/search chr14:77,999,360-77,999,663 [gene](#) size 304 bp.



In the new age of technology, bioinformatics has become the battleground of choice for evolutionary biologists...

The field is a collaborative effort among scientists all over the globe, and provides a wealth of information about comparative genomics:

- Blogs
- Articles
- Papers



Yet the plethora of genetic information about common ancestry already available is only just the beginning...

The Roadmap

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Conclusion:
A List of Databases

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Tutorial

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A List of Useful Databases

- NCBI
 - PubMed
 - Entrez
 - BLAST
- Ensembl (European)
- UCSC's Genome Browser

“

Genetic mechanism in all its happenstance has produced the genetic *basis* of humanness. *Genetics describes the process, ordained and upheld by God, to make the creature that expresses God's 'image and likeness'...*

”

-Graeme Finlay
(*emphasis added*)

