

Alineamiento de genomas completos

Objetivo

Para dos genomas, *A* y *B*, mapear cada posición de *A* en su posición correspondiente de *B*

CCGGTAGGCTATTAAACGGGGTGAGGAGCGTTGGCATAGCA



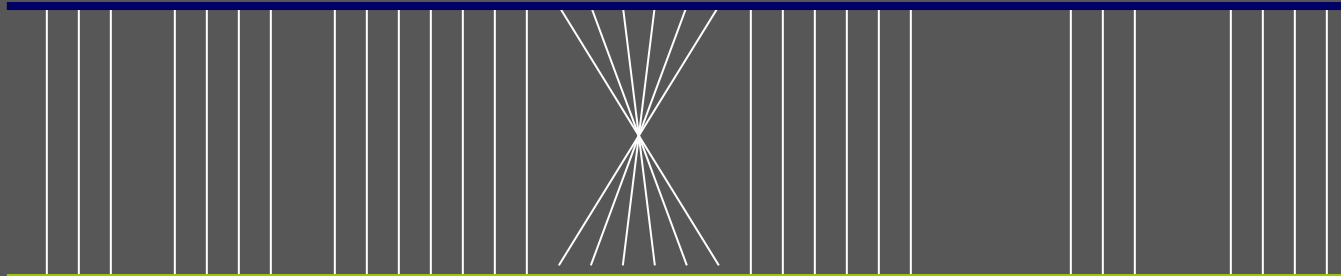
The diagram consists of two horizontal lines, one blue on top and one green on the bottom. Between these lines, there are 25 vertical white lines that connect the two horizontal lines at regular intervals, representing a 1:1 mapping between the two sequences.

CCGGTAGGCTATTAAACGGGGTGAGGAGCGTTGGCATAGCA

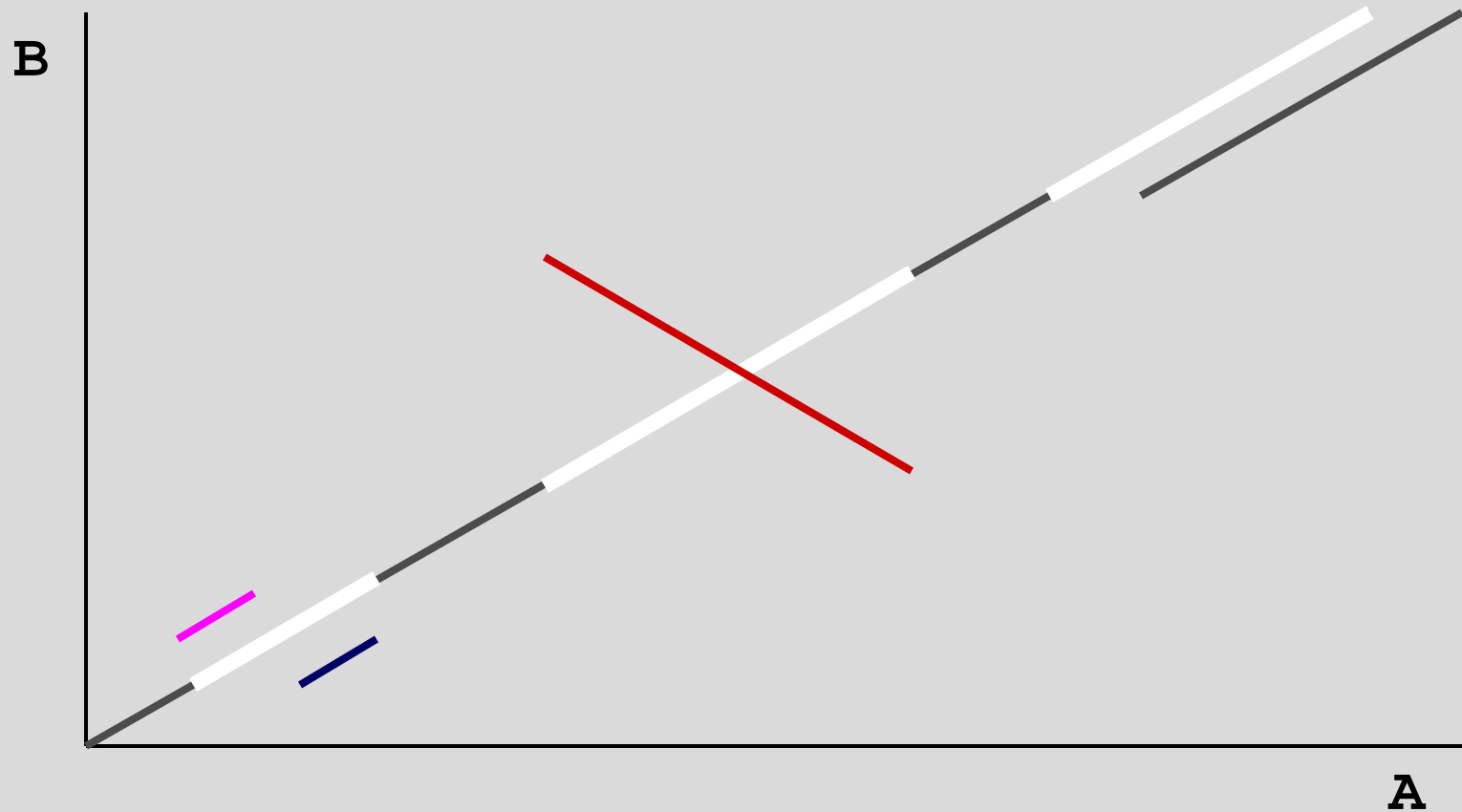
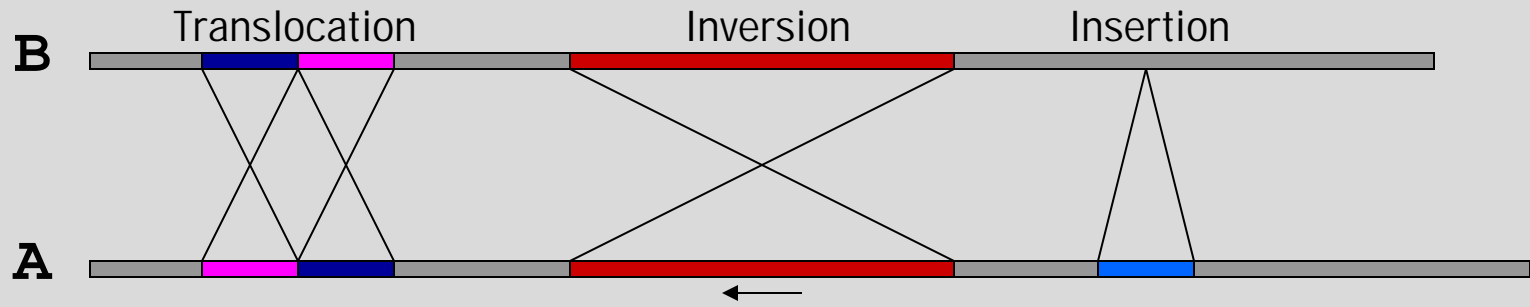
Pero no tan rápido...

Puede haber inserciones, deleciones,
translocaciones, inversiones,
duplicaciones, SNPs...

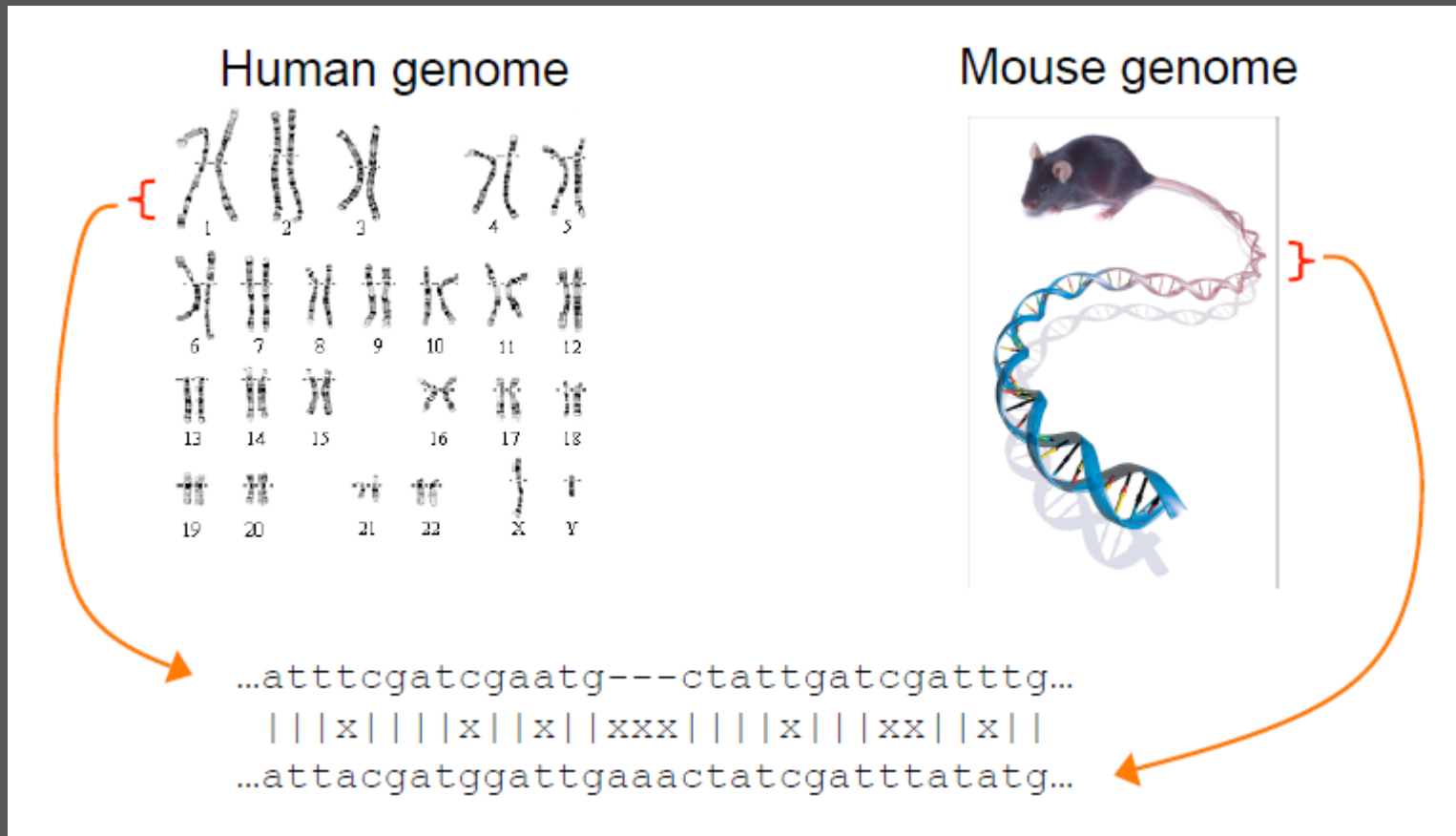
CCGGTAGGATATTAAACGGGGTGAGGAGCGTTGGCATAGCA



CCGCTAGGCTATTAAAACCCCGGAGGAG . . . GGCTGAGCA



El objetivo, por tanto, del alineamiento de genomas completos es encontrar y alinear las piezas similares entre dos genomas



LAST software

Query sequences

cgcgctctattaa
ctg**agcaagtaatg**gtag
atattctgtat
ctatgctatgc
ctagctagctgtgt
cgcgatgtaat
ctgatcgtgta
cctgcgaaaata
cgctgctgaacc
cgctgctgaacc
aatgctgatgctg
ctgatcgtgtagctgtaa

Reference sequences

ct**agctatgtgatg**a
ctcgttagctgtgtcgtgtg
ctcgtagctgatcgtgt
ctgatcgtacgtatataa
aatatagtttctattc
ctg**cctgcatgatcta**gcat
tgtagtcgtagctatgtogaac

agctatgtgatg
||| | || |||
agcaa-gtaatg

cctgcatgatcta
||||| || ||
cctgc--gaaata

Example 3

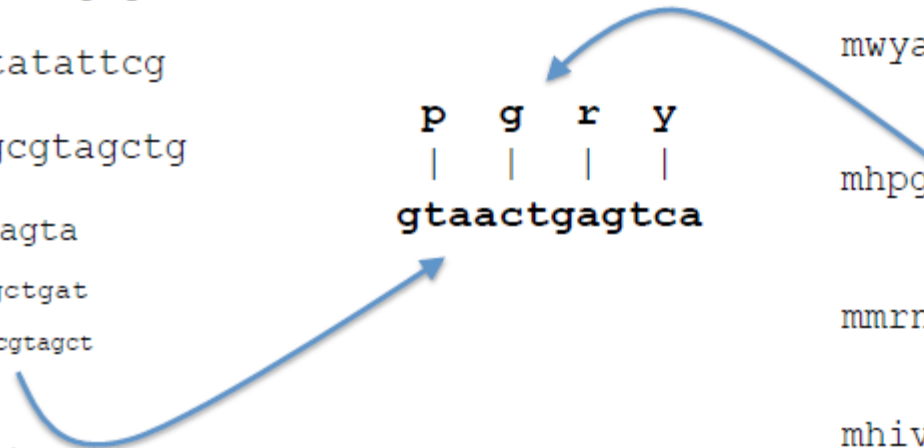
Metagenome DNA reads

aactgatgctgta
ctatgctagtgctg
cgcaaaagtgta
ccggctatattcg
gcggcgtagctg
cccgatgctagta
gtcgtagctgat
atgatcgtagct
gcggcgtagctg
gcggcgtagctg
aaaaaaaaaaaa

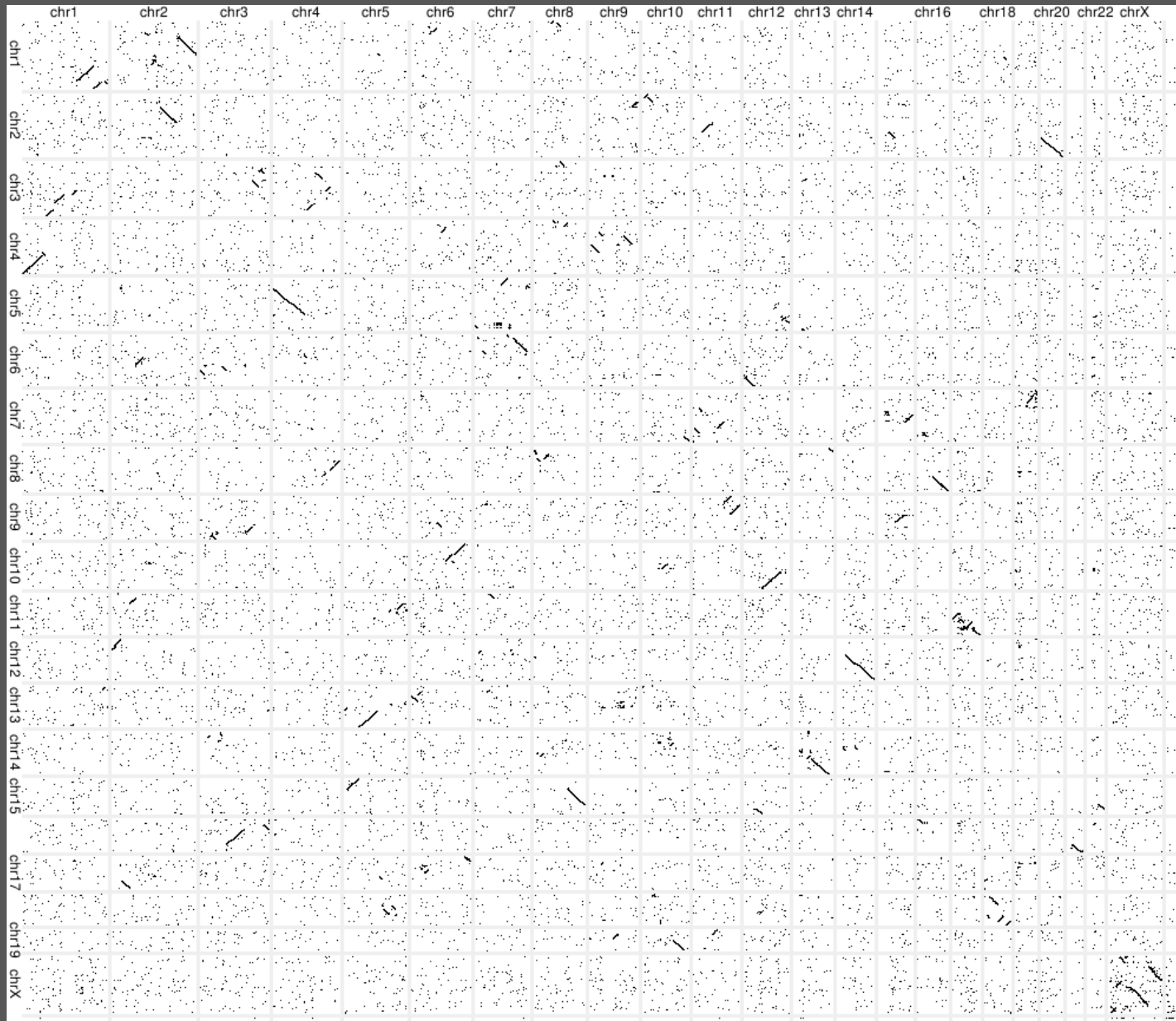
Protein database

mtghedfiklppaqwyttagtlf
myedefaagpkmvvcgrrcw
mwyaggqddhivinnaiievkky
mhpgrycyfhhgapa
mmrnhfagpilvpqerratelsss
mhivilfagaafviprcwt

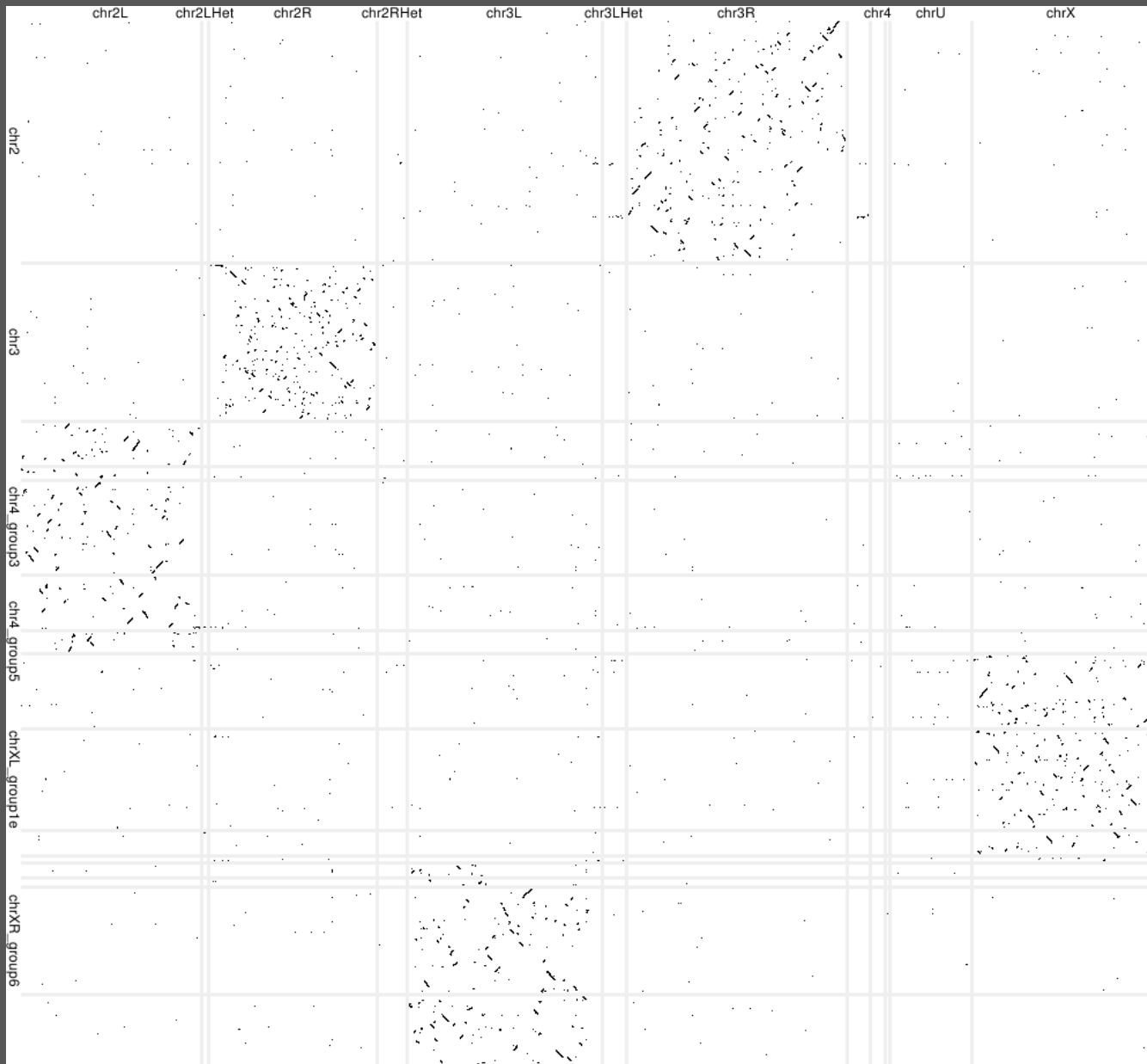
p g r y
| | | |
gtaactgagtca



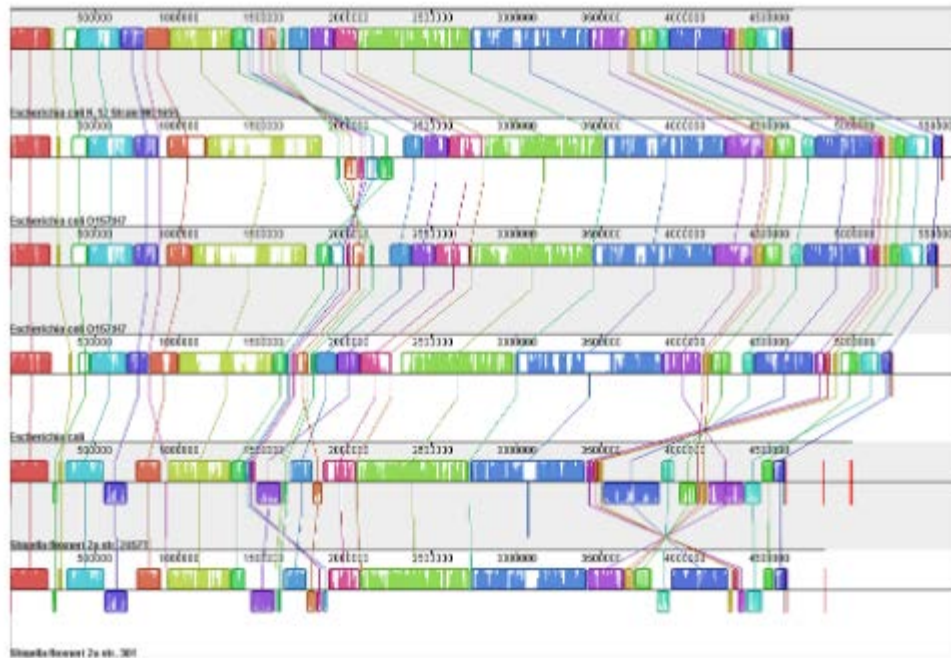
Matriz de puntos entre humanos (hg18) y ratón (mm9)



Matriz de puntos entre *D. melanogaster* y *D. pseudoobscura*

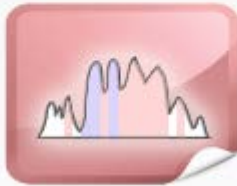


Mauve Alignment of 9 Enterobacteria (*Shigella* and *E. coli*)



Precomputed Alignments

VISTA Browser



<http://pipeline.lbl.gov/cgi-bin/gateway2>



Tools for Comparative Genomics



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
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[Help](#)

Clade: Genome: Release: Position:

- VISTA-Point
 VISTA Browser (Requires Java2)

 [Java 2 installation instructions](#)

 [Help](#)

Whole Genome Comparative Analysis of the *Human Feb. 2009 Genome*

From this page you can access the results of:

the **multiple alignments**

- [Human Feb. 2009](#), [Chimp Mar. 2006](#), [Callithrix jacchus v.2.0.2](#), [Rhesus Jan. 2006](#) and [Pongo pygmaeus abelii v.2.0.2](#) genomes.

UCSC Genome Browser on Human Feb. 2009 (GRCh37/hg19) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr22:31,217,701-34,573,570 3,355,870 bp.

chr22 (q12.2-q12.3) 22p13 22p12 22p11.2 22q11.21 q11.23 22q12.1 22q12.2 22q12.3 22q13.1 22q13.2 22q13.31 13.33

