

CoGe: Comparative Genomics

<http://genomevolution.org>

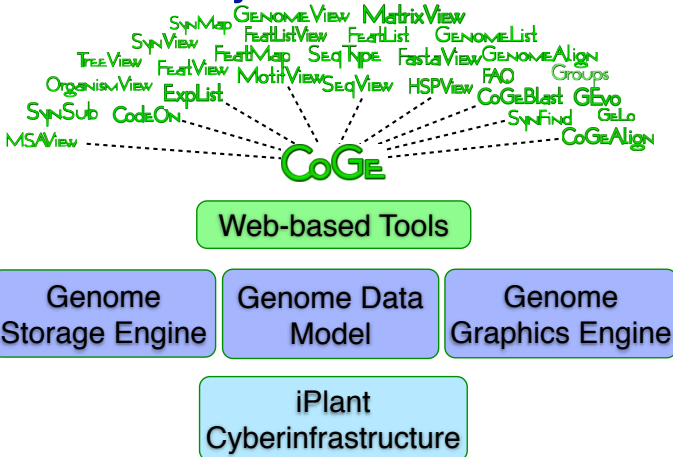
Eric Lyons

School of Plant Sciences; iPlant Collaborative
University of Arizona

What Makes CoGe Different?

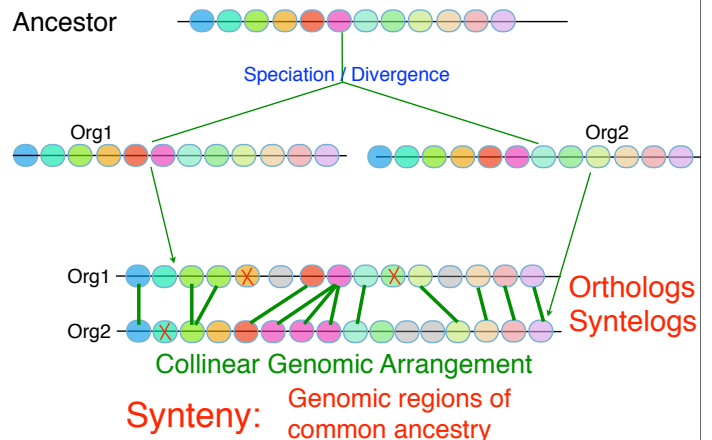
The screenshot shows the CoGe website with a navigation menu (Home, Applications, Forums, Preferences, Help) and a 'Welcome to CoGe!' message. It lists statistics: 14,993 Organisms, 19,145 Genomes, 699,602,542,768 Nucleotides, 226,461,884 Genomic Features, and 500,445,228 Annotations. A 'What is CoGe?' section lists key features like multi-domain analysis, easy data finding, analysis tools, synteny finding, and high-resolution analysis. A 'New to CoGe?' section offers guides and FAQs. The 'CoGe's Entrance Tools' list includes OrganismView, CoGeBlast, FeatView, SynMap, SynFind, and GEye. A visualization shows a 'Human-mouse syntenic comparison showing a conserved tandem gene cluster' with red lines connecting orthologous regions across two genomes.

CoGe's system architecture

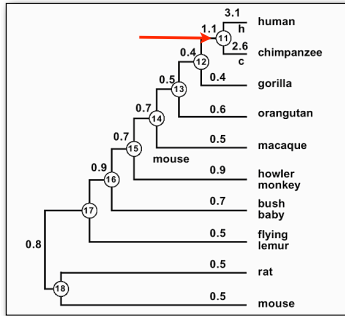
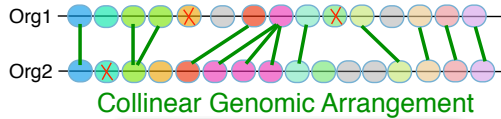


GeLo: Genome Location Visualization

Speciation and Synteny



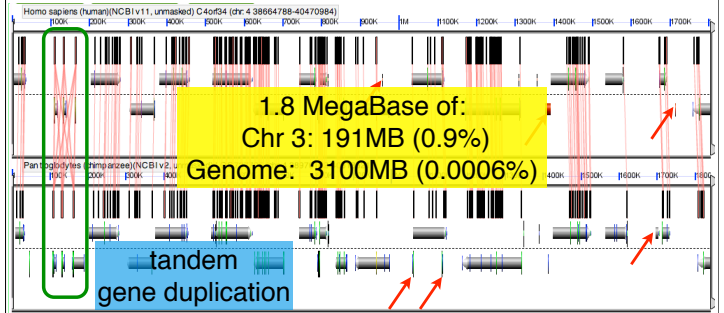
Speciation and Synteny



Human-Chimp Synteny

Collinear Genomic Arrangement

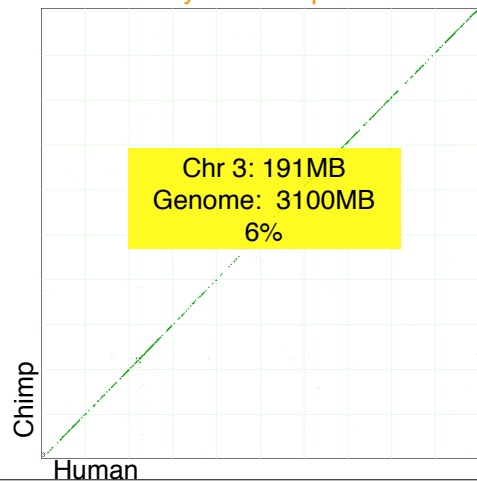
Human



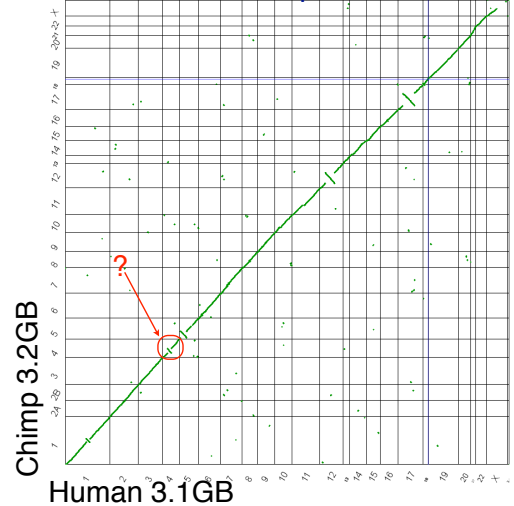
Chimp

Human versus Chimp Chromosome 3

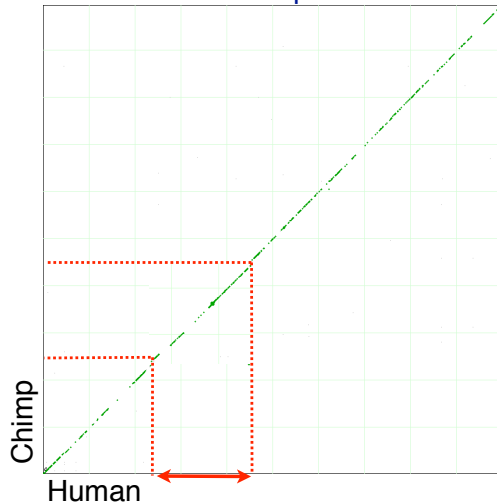
Syntenic dotplot



Human versus Chimp Whole Genome



Human versus Chimp Chromosome 4



CoGe The Place to Compare Genomes

Welcome to CoGe! Organisms: 8,782 Genomes: 9,343 Nucleotides: 182,723,425,568

What is CoGe?

- CoGe is a comparative genomics platform for all genomes across all domains of life in any state of assembly
- CoGe allows you to easily find and analyze genomic data from any organism
- CoGe provides analysis tools for finding and comparing homologous sequences from any set of organisms
- CoGe allows you to find syntenic regions from between or within an organism
- CoGe allows high-resolution sequence analysis for multiple genomic regions

New to CoGe?

- How to get started
- Tutorials
- CoGePedia docs
- FAQs
- Latest News

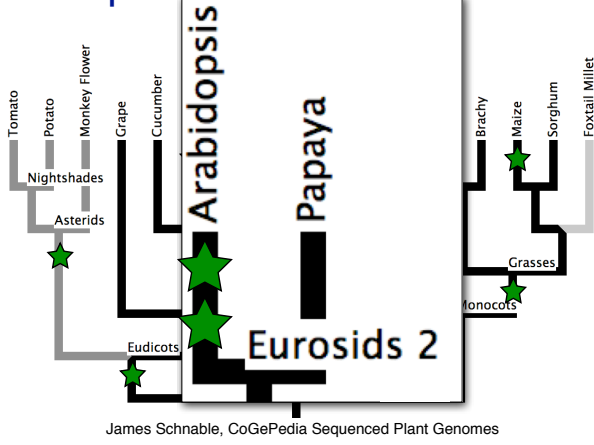
CoGe's Entrance Tools:

- OrganismView: Search for organisms and perform analyses on their genomes
- CoGeBlast: Blast sequences against any number of genomes of your choosing
- FeatView: Searching for genomic features by name
- SynMap: Whole genome syntenic dotplot analyses
- G Evo: High-resolution sequence analysis of genomic regions
- Latest Genomes

NSF

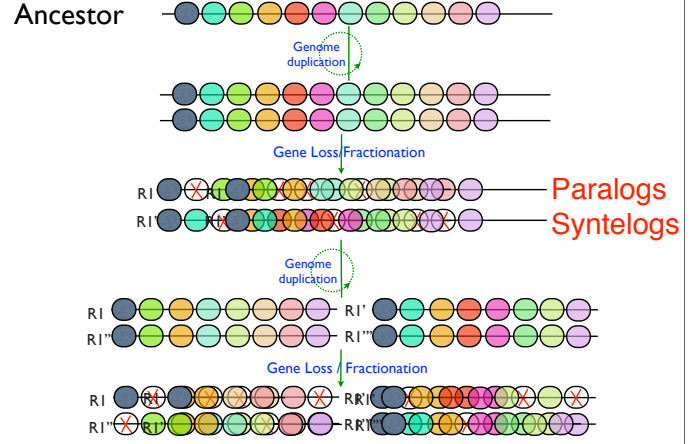
Currently logged in as: Eric Lyons Sign-out
Date: 2010-06-20 10:39 AM
Warning: This site uses AJAX. Don't press your browser's back button!

Sequenced Plant Genomes

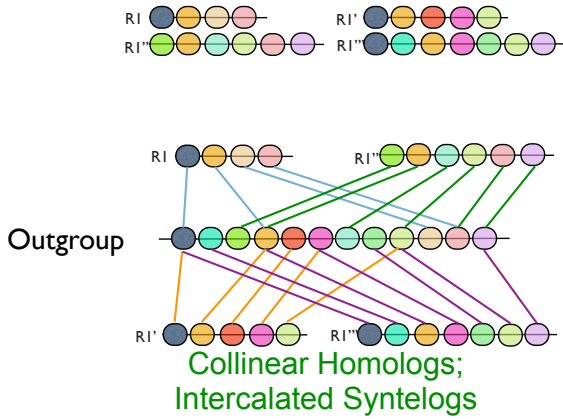


★ Whole genome duplications

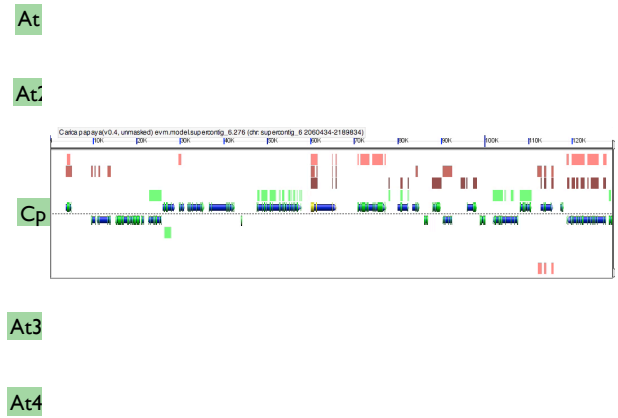
(WGD & Fractionation) x 2



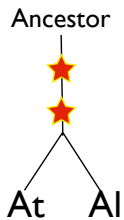
WGD & Fractionation x2



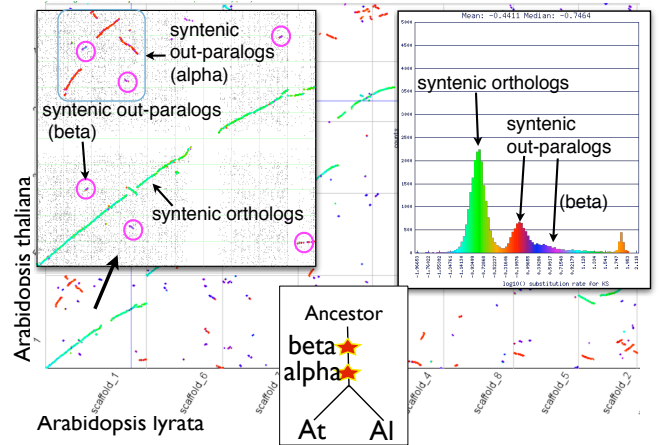
Fractionation: Intercalated syntelogs



Two Shared WGDs A. thaliana - A. lyrata

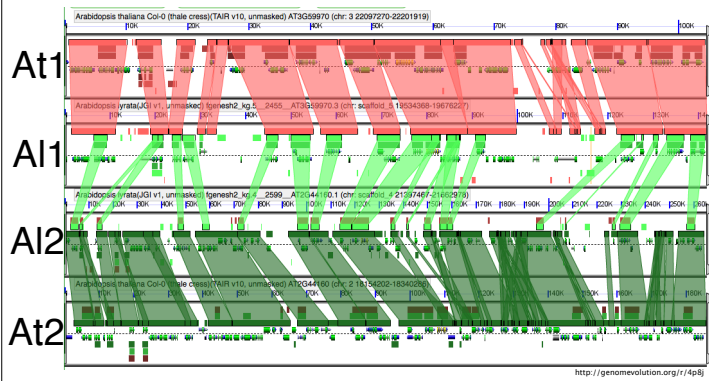


Two Shared WGDs A. thaliana - A. lyrata



Orthologs and Out-Paralogs

Structural Evidence



Hands-on

Go to: <http://genomeevolution.org>

Overview: <http://genomeevolution.org/r/6mkw>

Tutorials: <http://genomeevolution.org/r/4a3>

Download this presentation:

PDF (15M): <http://genomeevolution.org/r/6ml0>

Keynote (45M): <http://genomeevolution.org/r/6mky>