Transforming genomic coordinates between plant reference assemblies

www.gramene.org **plants.ensembl.org**

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Assembly Conversion Tool

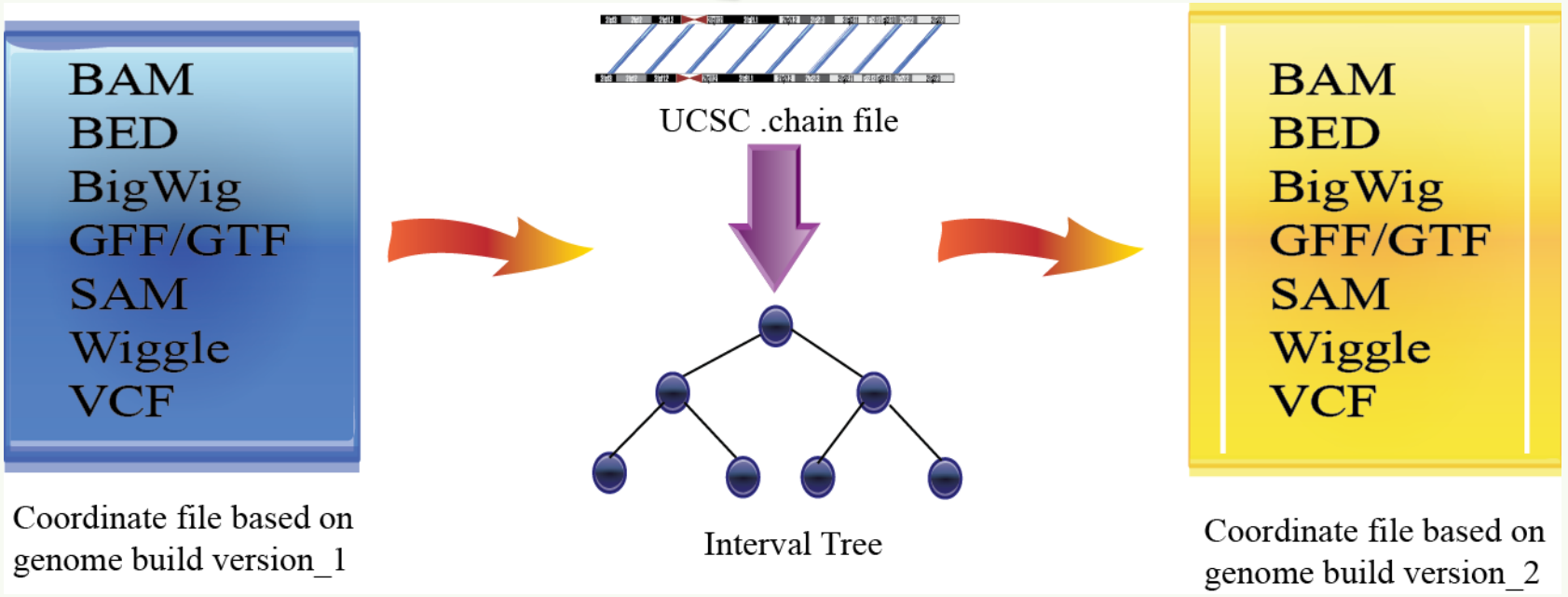
Converts genome coordinates between assemblies to facilitate meta-analysis, direct comparison, data integration and visualization

Why?

- Reference genome assemblies are subjected to change from time to time
- Convert results from old assemblies to newer versions and *viceversa*

CrossMap Tool

Assembly converter tool in Gramene uses CrossMap!!



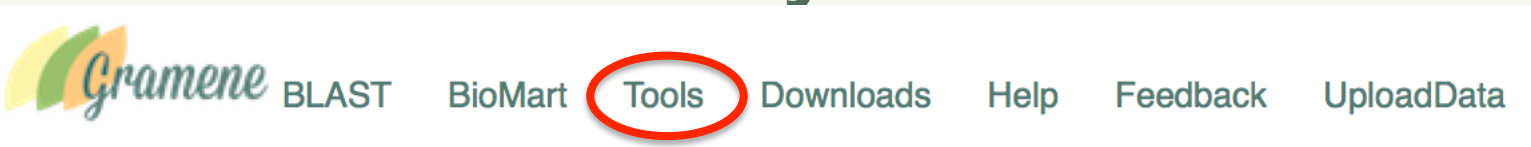
- Chain file describes the pair-wise alignments between two genomes
- CrossMap run time increases linearly to the size of input file

Zhao, H., Sun, Z., Wang, J., Huang, H., Kocher, J.-P., & Wang, L. (2013). CrossMap: a versatile tool for coordinate conversion between genome assemblies. Bioinformatics (Oxford, England), btt730

Other conversion tools

- UCSC liftover tool only supports BED input
- NCBI remap support BED, GFF, GTF, VCF, etc.
- Galaxy (based on UCSC liftover tool) supports BED, GFF, GTF input
- Pyliftover only does conversion of point coordinates; unlike liftOver, it does not convert ranges, nor does it provide any special facilities to work with BED files

Tools: Assembly converter



Tools

We provide a number of ready-made tools for processing both our data and yours. We routinely delete results from our servers after 10 days, but if you have an gramene genome account you will be able to save the results for about 2-3 months until next release.

http://ensembl.gramene.org/tools.html

Processing your data

Name	Description	Online tool	Upload limit	Download script	Documentation
Variant Effect Predictor VeP	Analyse your own variants and predict the functional consequences of known and unknown variants via our Variant Effect Predictor (VEP) tool.	🔧	50MB*	⬇	
HMMER	Quickly search our genomes for your protein sequence.	🔧			
BLAST/BLAT	Search our genomes for your DNA or protein sequence.	🔧	50MB		
Assembly Converter	Map (liftover) your data's coordinates to the current assembly.	🔧	50MB		

* For larger datasets we provide an API script that can be downloaded (you will also need to install our Perl API, below, to run the script).

Accessing Gramene data

Name	Description	Get it from:	Documentation
BioMart	Use this data-mining tool to export custom datasets from Gramene.	Gramene BioMart	ℹ
Ensembl Perl API	Programmatic access to all Ensembl data using simple Perl scripts	GitHub or FTP download (current release only)	ℹ
Ensembl Genomes Virtual Machine	Pre-configured VirtualBox virtual machine (VM) running the latest Ensembl Genomes browser.		ℹ
Ensembl Genomes REST server	Access Ensembl data using your favourite programming language		ℹ

Tools: Assembly converter

This online tool currently uses CrossMap, which supports a limited number of formats (see our online documentation for details of the individual data formats listed below). CrossMap also discards metadata in files, so track definitions, etc, will be lost on conversion.

Important note: CrossMap converts WIG files to BedGraph internally for efficiency, and also outputs them in BedGraph format.

Species: Oryza glaberrima

Assembly mapping: 1.0 -> AGI1.1

Name for this job (optional): Oglab_chr12

Input file format: GFF

Either paste data:

Or upload file: Browse... No file selected.

Click here to download the previously uploaded file.

Or provide file URL:

Run › Clear Close form

Methods to upload data

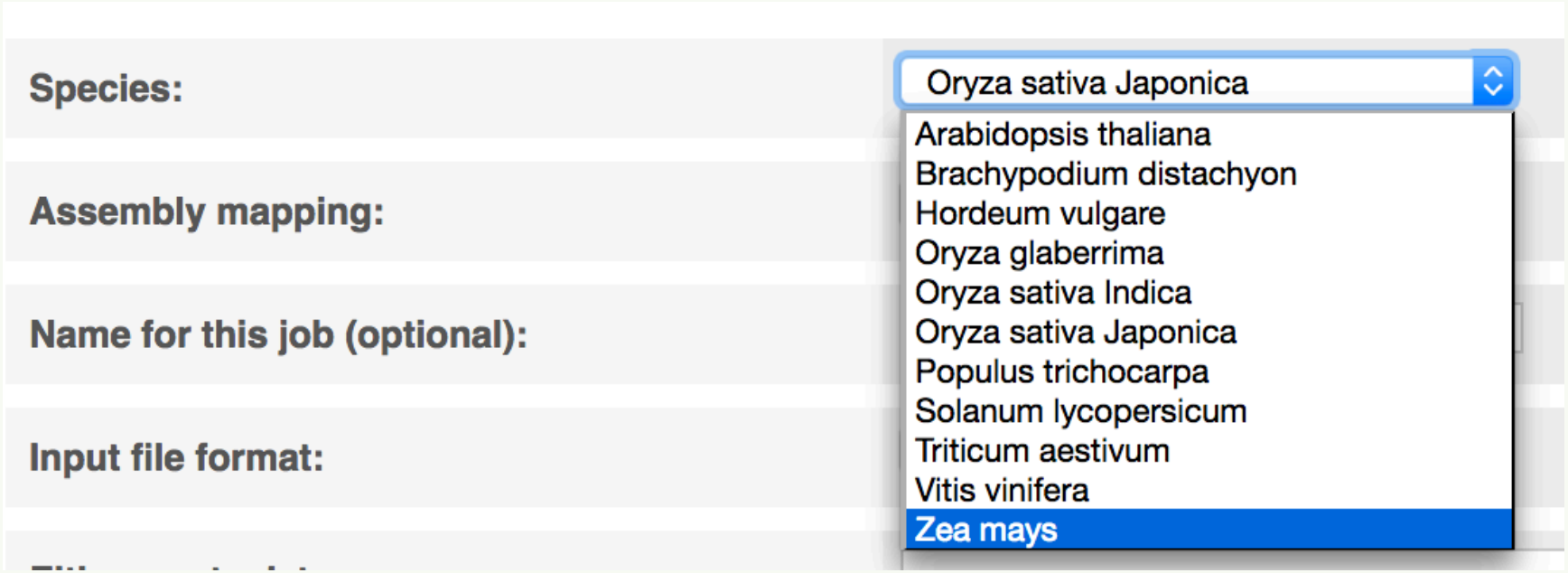
Recent jobs

1 Refresh

Show/hide columns (1 hidden) Filter

Analysis	Jobs	Submitted at
Assembly Converter	Assembly conversion of Oglab_chr12 in Oryza_glaberrima Queued	30/11/2016, 00:49 (GMT)
Assembly Converter	Assembly conversion of Oglab_chr12 in Oryza_glaberrima Done [Download results]	29/11/2016, 16:59 (GMT)
Assembly Converter	Assembly conversion of Oglab in Oryza_glaberrima Failed	29/11/2016, 16:51 (GMT)

Species supported for assembly mapping



Chain files provided at ensemble FTP

ftp://ftp.ensemblgenomes.org/pub/release-33/plants/assembly_chain/

Convert GFF/GTF format files

- GFF (General Feature Format) is plain text file used to describe gene structure
- GTF (Gene Transfer Format) is a refined version of GFF

Sample GFF:

```
10      gramene gene    130112  134842  .       +       .       ID=gene:Zm00001d023208
10      gramene gene    218781  220384  .       -       .       ID=gene:Zm00001d023210
10      gramene gene    265243  271813  .       -       .       ID=gene:Zm00001d023211
10      gramene lincRNA_gene    271217  272132  .       -       .       ID=gene:Zm00001d023035
```

- Each feature (exon, intron, UTR, etc.) is processed separately and independently
- Plain text, compressed plain text, and URLs pointing to remote files are all supported
- Only chromosome and genome coordinates are updated

Convert BED format files

- BED (Browser Extensible Data) file is a tab-delimited text file describing genome regions or gene annotations

Sample BED:

chr	start	end
1	1630	1760
1	1982	9815
1	10217	11435
1	10371	11284
1	11720	14685

- It consists of one line per feature, each containing 3-12 columns (chr, start, end are required)
- Regions of old assembly which to multiple locations on new assembly will be split
- Compressed remote files are not supported!

Limitations

- Size limit 50 MB
- Need to convert chromosome IDs to numerical chromosome numbers (*i.e.* strip off the prefix)
  - *e.g.* OglabChr01 -> 1
  - OglabChr02 -> 2
- Does not support VCF, BAM, BigWig & Wiggle format yet

Demo

Converting GFF coordinates

IRGSP1 => MSU6

Input

```
1    agi     ncRNA_gene    2631    2760    .    -    .    ID=gene:EPlOSAG00000002326
1    irgsp   gene    2983    10815    .    +    .    ID=gene:OS01G0100100
1    irgsp   gene    11218    12435    .    +    .    ID=gene:OS01G0100200
1    irgsp   gene    11372    12284    .    -    .    ID=gene:OS01G0100300
1    irgsp   gene    12721    15685    .    +    .    ID=gene:OS01G0100400
```

Output

```
1    agi     ncRNA_gene    1631    1760    .    -    .    ID=gene:EPlOSAG00000002326
1    irgsp   gene    1983    9815    .    +    .    ID=gene:OS01G0100100
1    irgsp   gene    10218    11435    .    +    .    ID=gene:OS01G0100200
1    irgsp   gene    10372    11284    .    -    .    ID=gene:OS01G0100300
1    irgsp   gene    11721    14685    .    +    .    ID=gene:OS01G0100400
```

Converting BED coordinates

IRGSP1 => MSU6

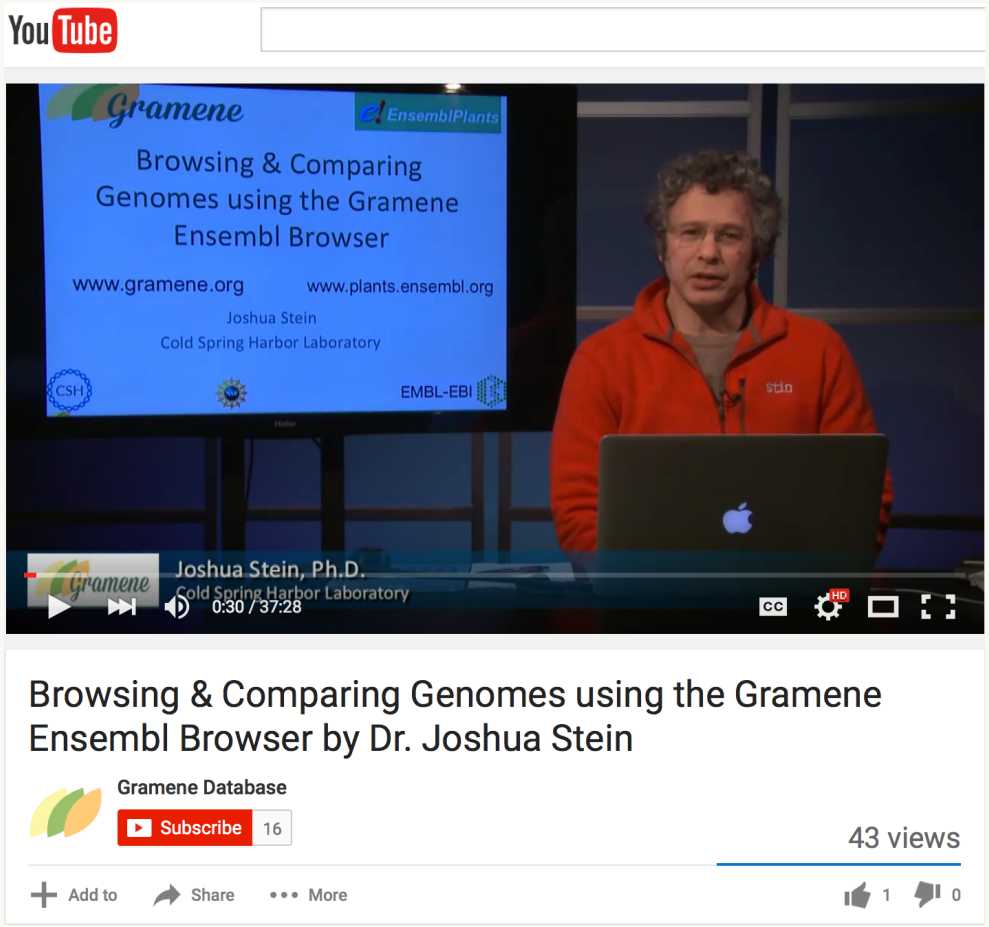
Input

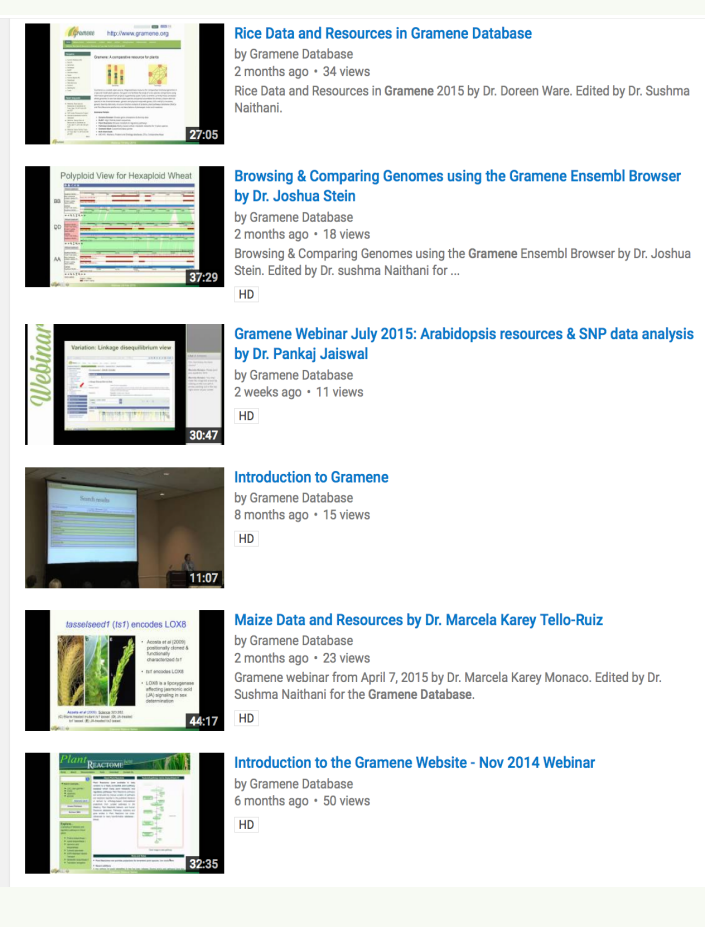
1	2630	2760	gene:EPlOSAG00000002326	.	-	agi	ncRNA_gene	.	ID=gene:EPlOSAG00000002326
1	2982	10815	gene:OS01G0100100	.	+	irgsp	gene	.	ID=gene:OS01G0100100
1	11217	12435	gene:OS01G0100200	.	+	irgsp	gene	.	ID=gene:OS01G0100200
1	11371	12284	gene:OS01G0100300	.	-	irgsp	gene	.	ID=gene:OS01G0100300
1	12720	15685	gene:OS01G0100400	.	+	irgsp	gene	.	ID=gene:OS01G0100400

Output

1	1630	1760	gene:EPlOSAG00000002326	.	-	agi	ncRNA_gene	.	ID=gene:EPlOSAG00000002326
1	1982	9815	gene:OS01G0100100	.	+	irgsp	gene	.	ID=gene:OS01G0100100
1	10217	11435	gene:OS01G0100200	.	+	irgsp	gene	.	ID=gene:OS01G0100200
1	10371	11284	gene:OS01G0100300	.	-	irgsp	gene	.	ID=gene:OS01G0100300
1	11720	14685	gene:OS01G0100400	.	+	irgsp	gene	.	ID=gene:OS01G0100400

Gramene Database @ YouTube





- 21 recorded webinars (topic specific or targeted to plant communities, *e.g.*, Arabidopsis, rice, maize, grape)
- Master mailing list of over 1,100 plant researchers

How to reach us

- E-mail: webinars@gramene.org
- Contact form: http://www.gramene.org/contact
- Gramene YouTube channel
- Announcements mailing list

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Gramene - Exploring Function through Comparative Genomics and Network Analysis

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