TGAC Browser: visualisation solutions for big data in the genomic era

- Anil S. Thanki
Scientific Programmer – Sequencing Informatics
Anil.Thanki@tgac.ac.uk

@anilthanki and @tgacbrowser

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BOSC

#Poster 6

Genome Browsers

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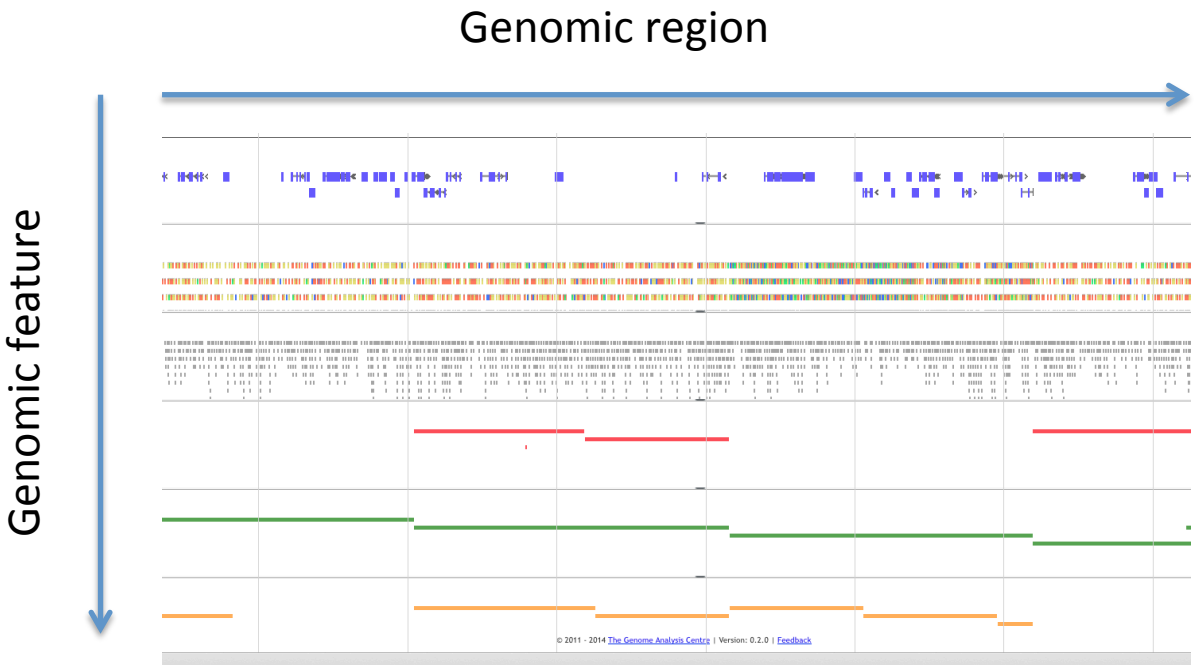
In bioinformatics, a **genome browser** is a graphical interface for display of information from a biological database for genomic data.



TGAC Browser

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TGAC Browser developed at TGAC from scratch, works on top of Ensembl Core database

TGAC Browser server-client

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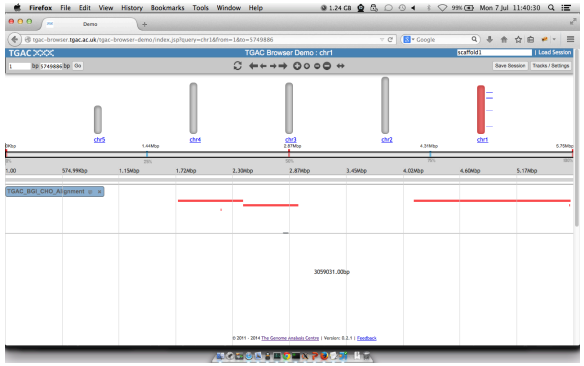
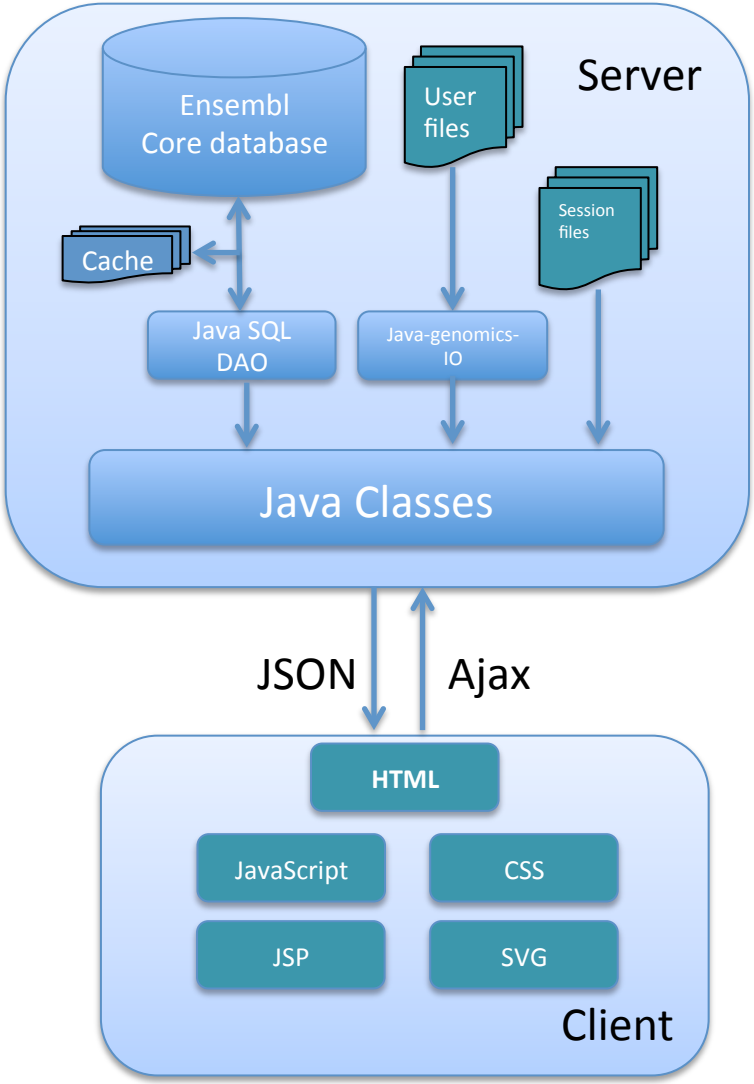
- Heavy database queries and parsing on server
- Transfer information in Text format
- Utilise Client system to generate and render images



- Performance and easy access of data from server implementation
- Flexibility of web Browsers for sharing data

TGAC Browser server-client



Supported Data

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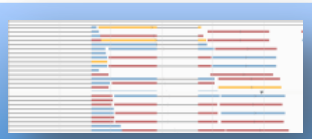
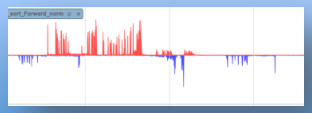
Genomics Data

Ensembl core



SAM/BAM



Wig/BigWig

GFF

VCF

Ensembl Data

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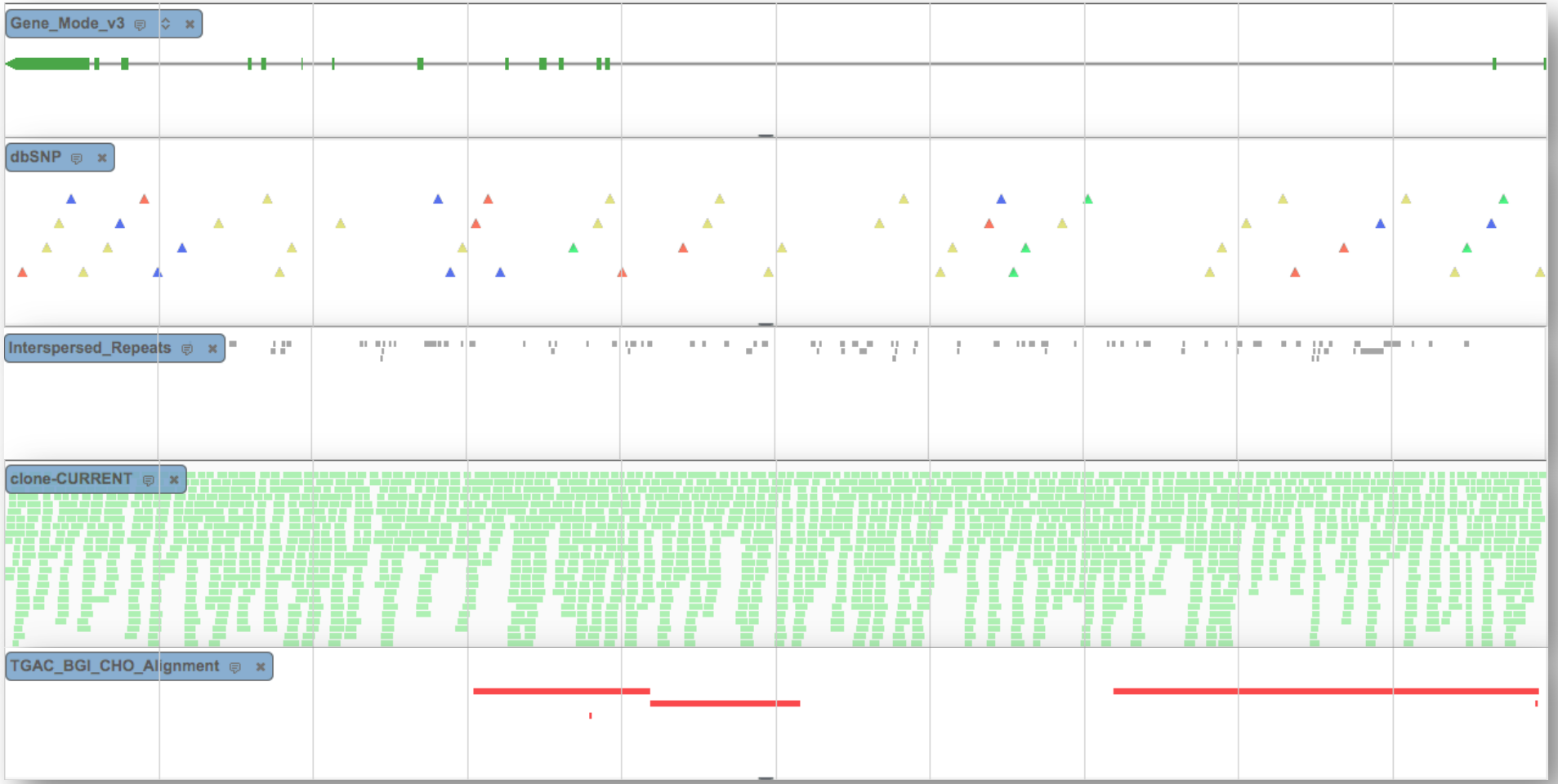
- Genomic features from Ensembl Database
  - Genes, SNPs, repeats, assembly, alignments, markers, etc



BAM/SAM

Visualising reads directly from SAM/BAM file

- Coloured Paired end reads
  - Blue First in Pair
  - Brown Second in Pair
  - Orange unpaired
  - Skipping deletions

Wig/bigwig

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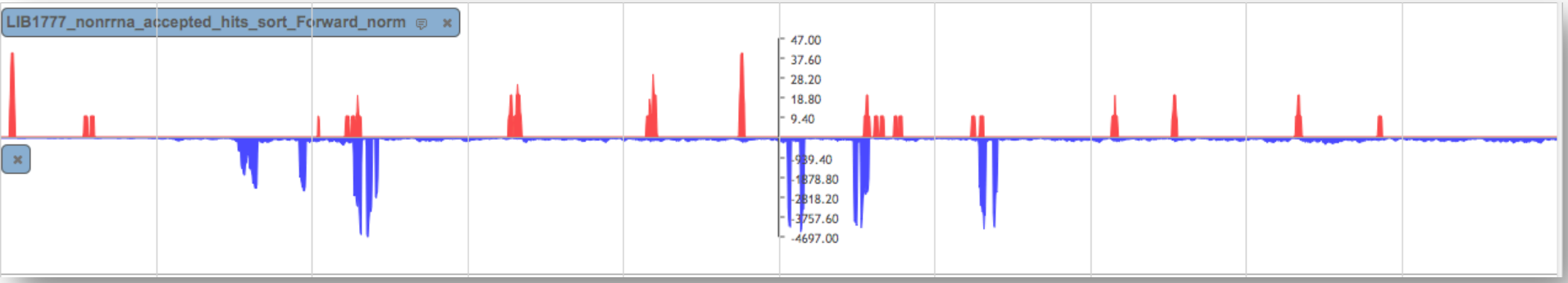
Visualising expression data directly from wig/bigwig file

- Coloured and oriented peaks
  - Upwards red are positive
  - Downwards blue are negative



VCF and GFF

- Visualising variant data directly from vcf file
- Coloured based on base pairs
- Visualise insertion, deletion, mutation

Visualising Genes data directly from gff file

- Exons, Introns, CDS

Non Ensembl Data

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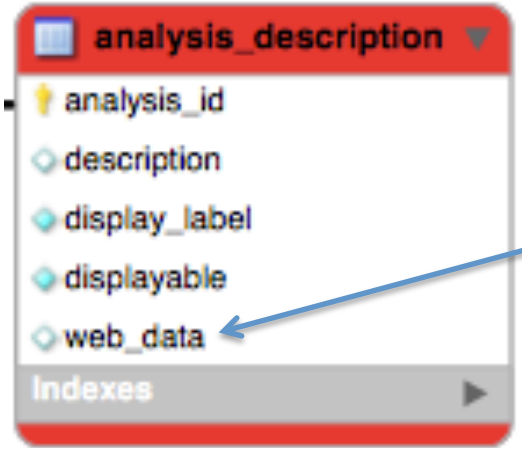
- Adding non Ensembl data in TGAC Browser
- *analysis_description* table of Ensembl Core schema
- *web_data* column for file information




```
{
"colour": "blue",
"source": "file",
"filepath": "/storage/browser/test.bw",
”track-group": LIB1777,
}
```

Visual Types

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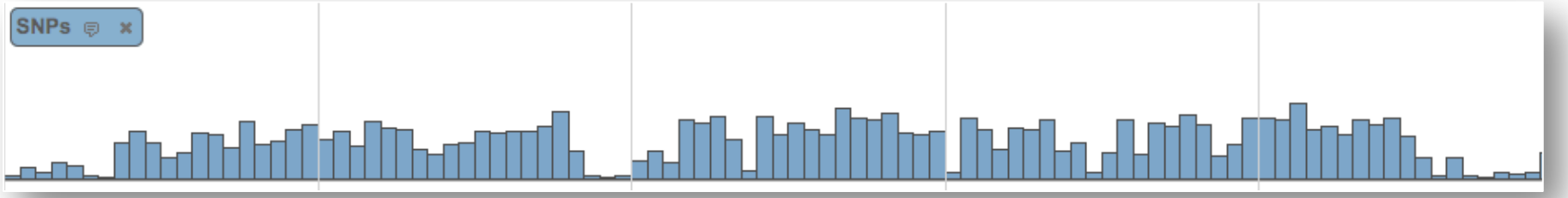
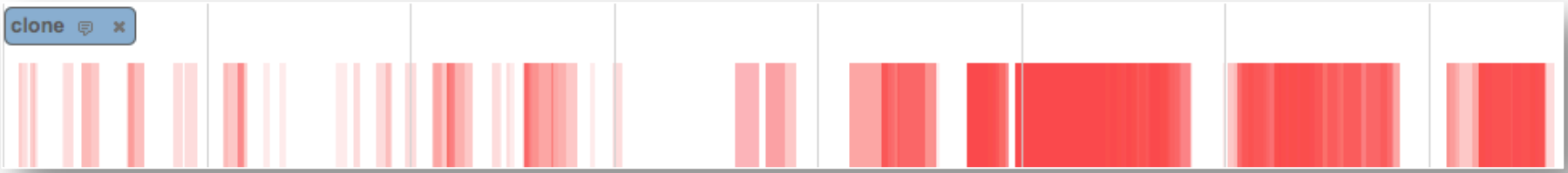
- Select Visual types based on amount of feature
  - Bar charts
  - Heat Map



- Graphical presentation of large data e.g. SNPs, alignments density



- Heat map presentation of large data

Search

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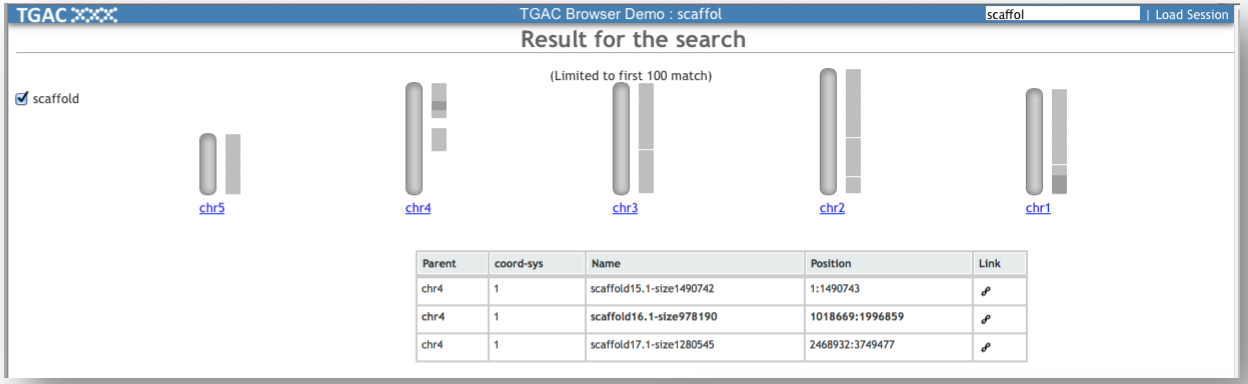
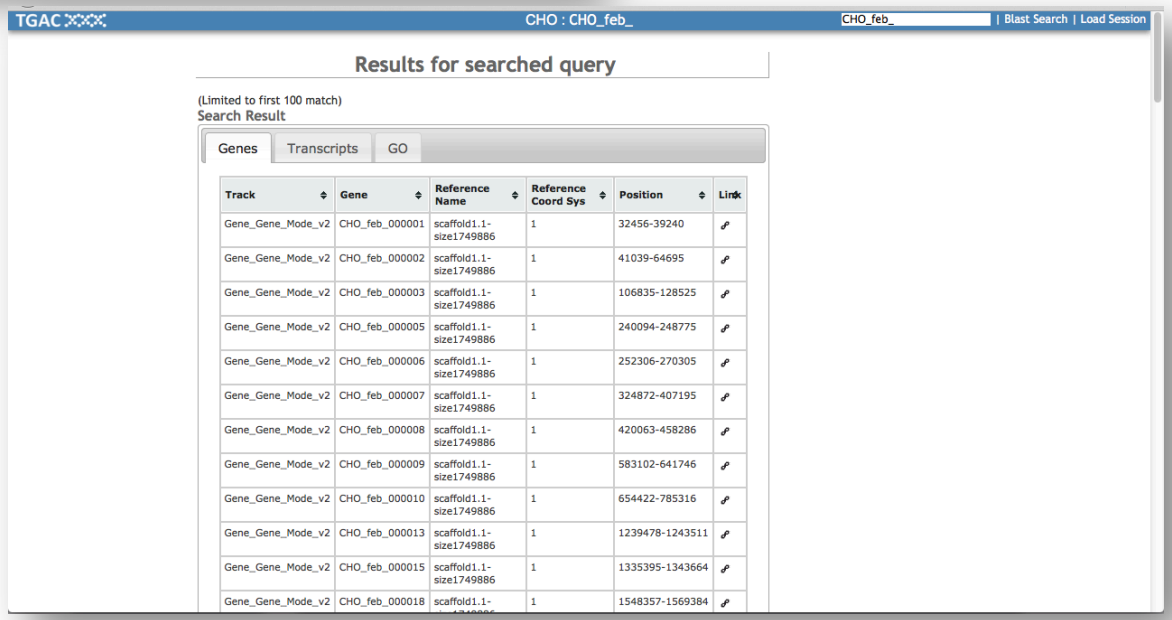
- Search with keyword among data



Result on Chromosomes

Result as list



BLAST Integration

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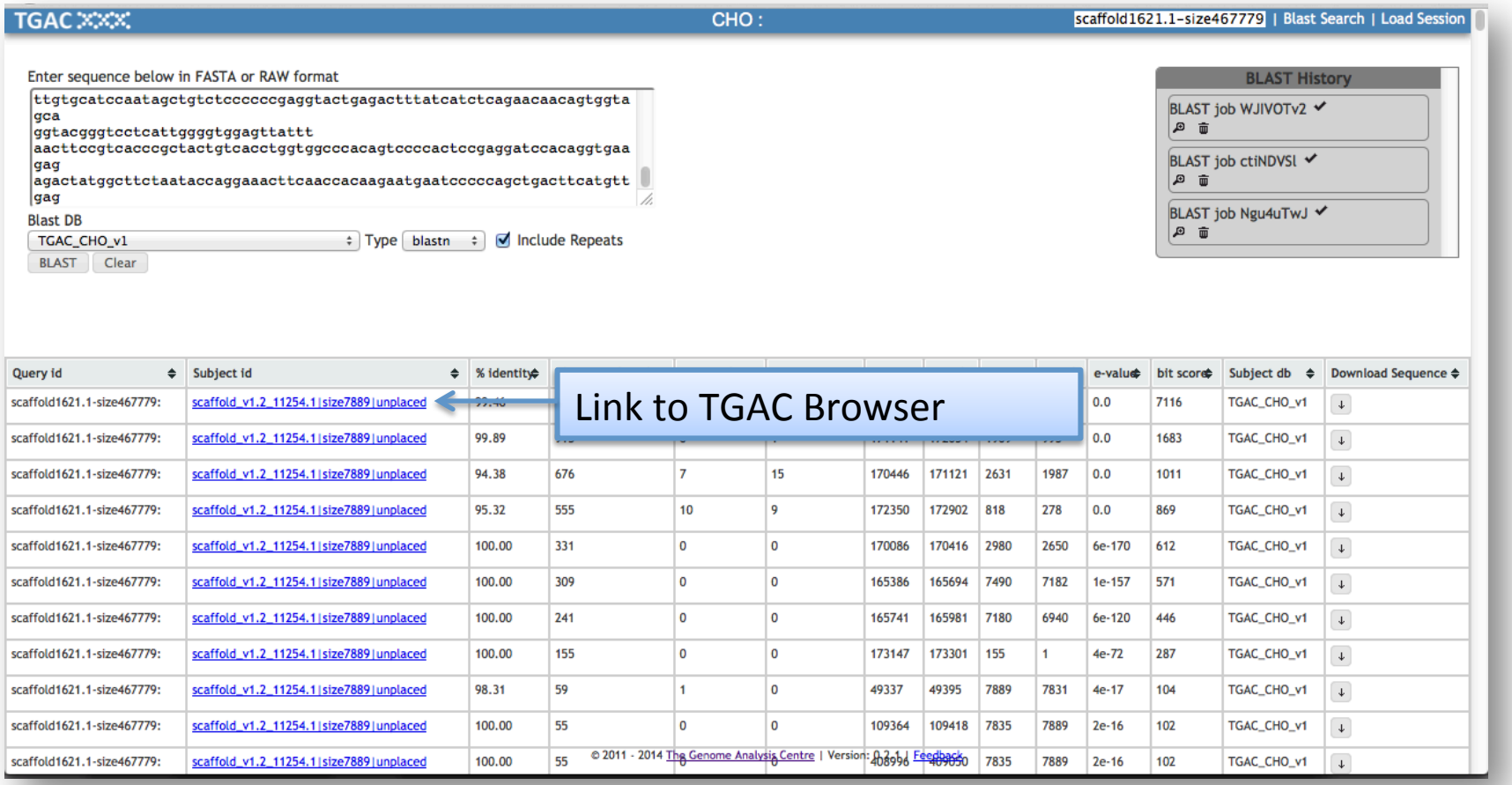
- BLAST results for sequence search
- BLAST Manager
  - BLAST history logs
  - Run multiple BLAST simultaneously and toggle between result



Query id	Subject id	% identity								e-value	bit score	Subject db	Download Sequence
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced									0.0	7116	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	99.89								0.0	1683	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	94.38	676	7	15	170446	171121	2631	1987	0.0	1011	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	95.32	555	10	9	172350	172902	818	278	0.0	869	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	100.00	331	0	0	170086	170416	2980	2650	6e-170	612	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	100.00	309	0	0	165386	165694	7490	7182	1e-157	571	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	100.00	241	0	0	165741	165981	7180	6940	6e-120	446	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	100.00	155	0	0	173147	173301	155	1	4e-72	287	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	98.31	59	1	0	49337	49395	7889	7831	4e-17	104	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	100.00	55	0	0	109364	109418	7835	7889	2e-16	102	TGAC_CHO_v1	
scaffold1621.1-size467779:	scaffold_v1.2_11254.1|size7889|unplaced	100.00	55	0	0	408996	409050	7835	7889	2e-16	102	TGAC_CHO_v1	

BLAST Integration

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- BLAST run on a track or selected region
- BLAST results showing as a track run
- Coloured based on score and with indel information

BLAST Integration

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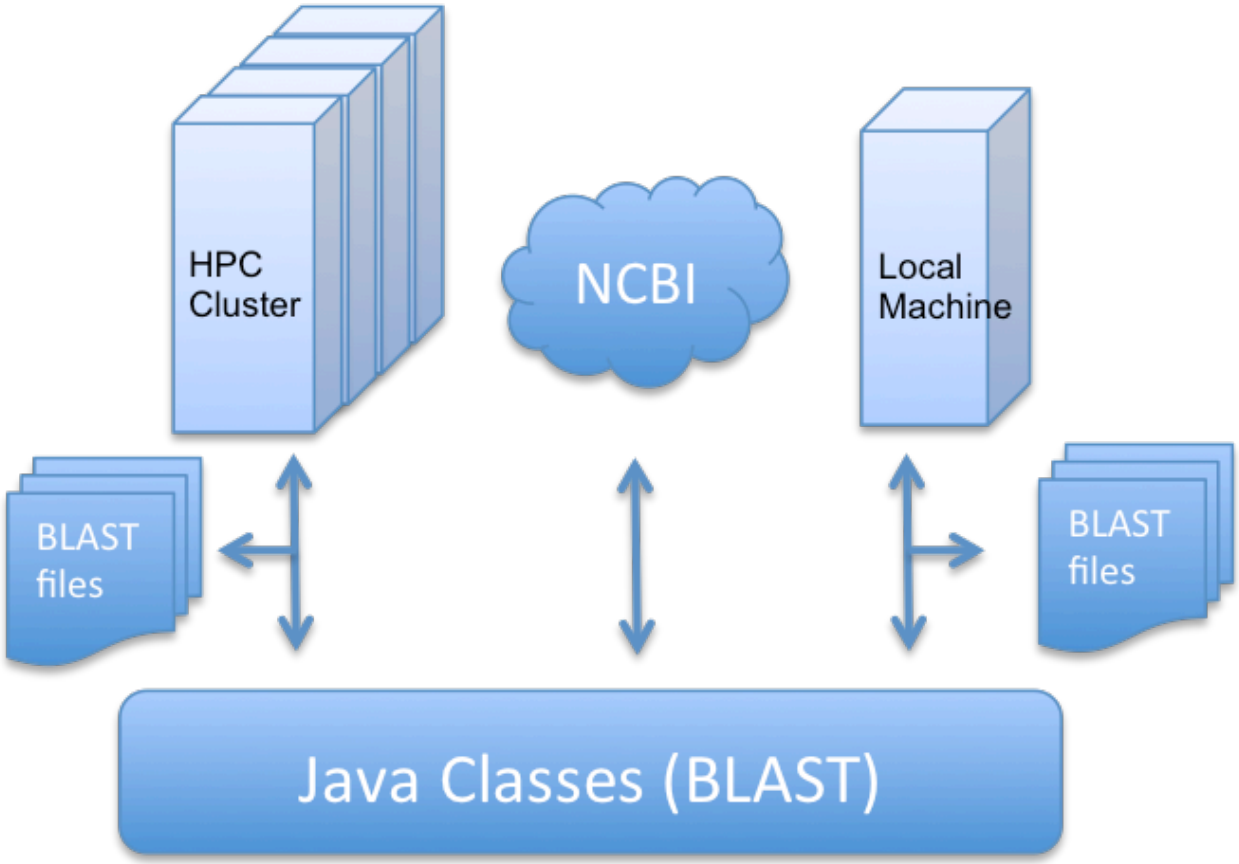
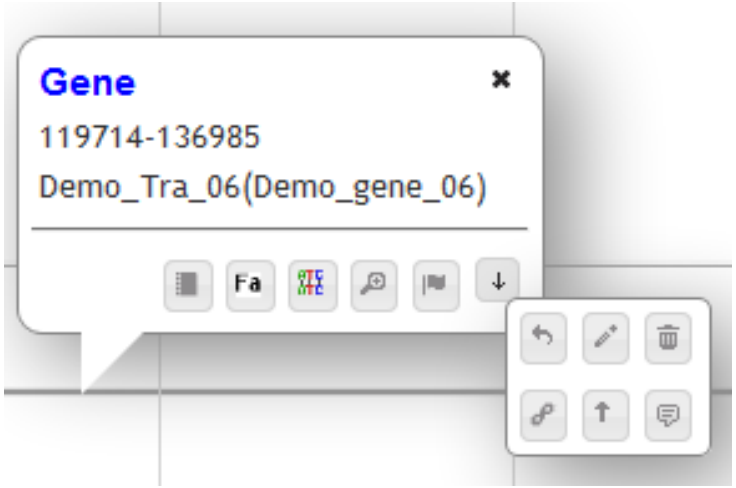
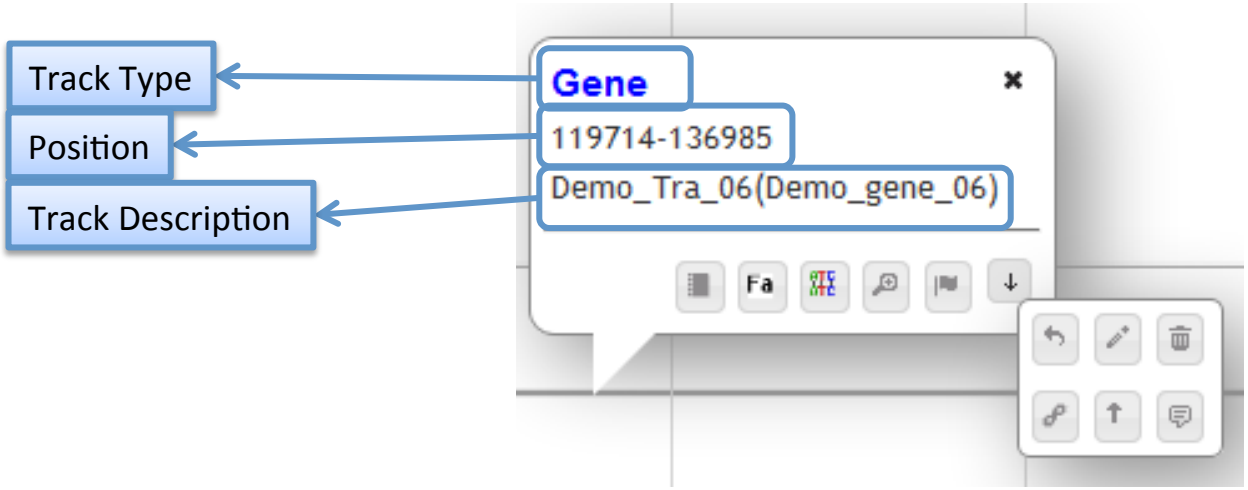


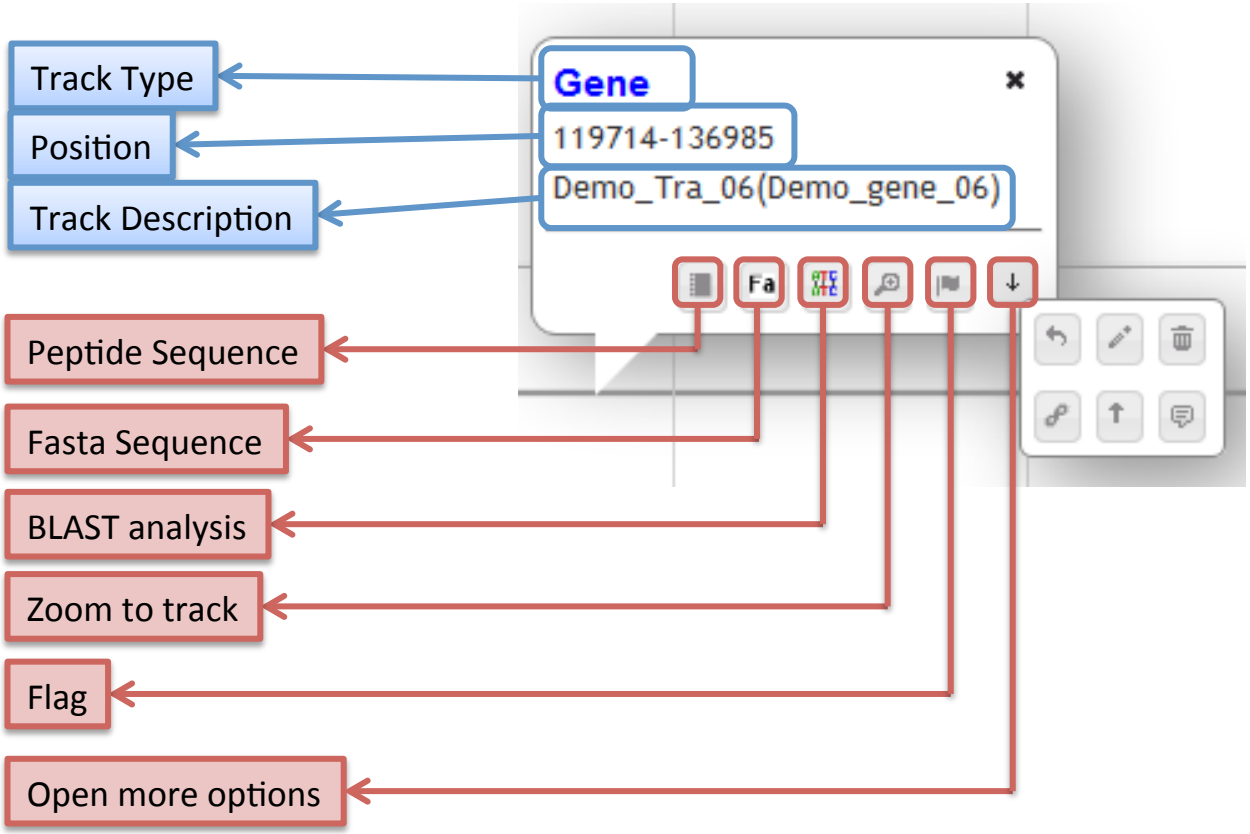
Popup



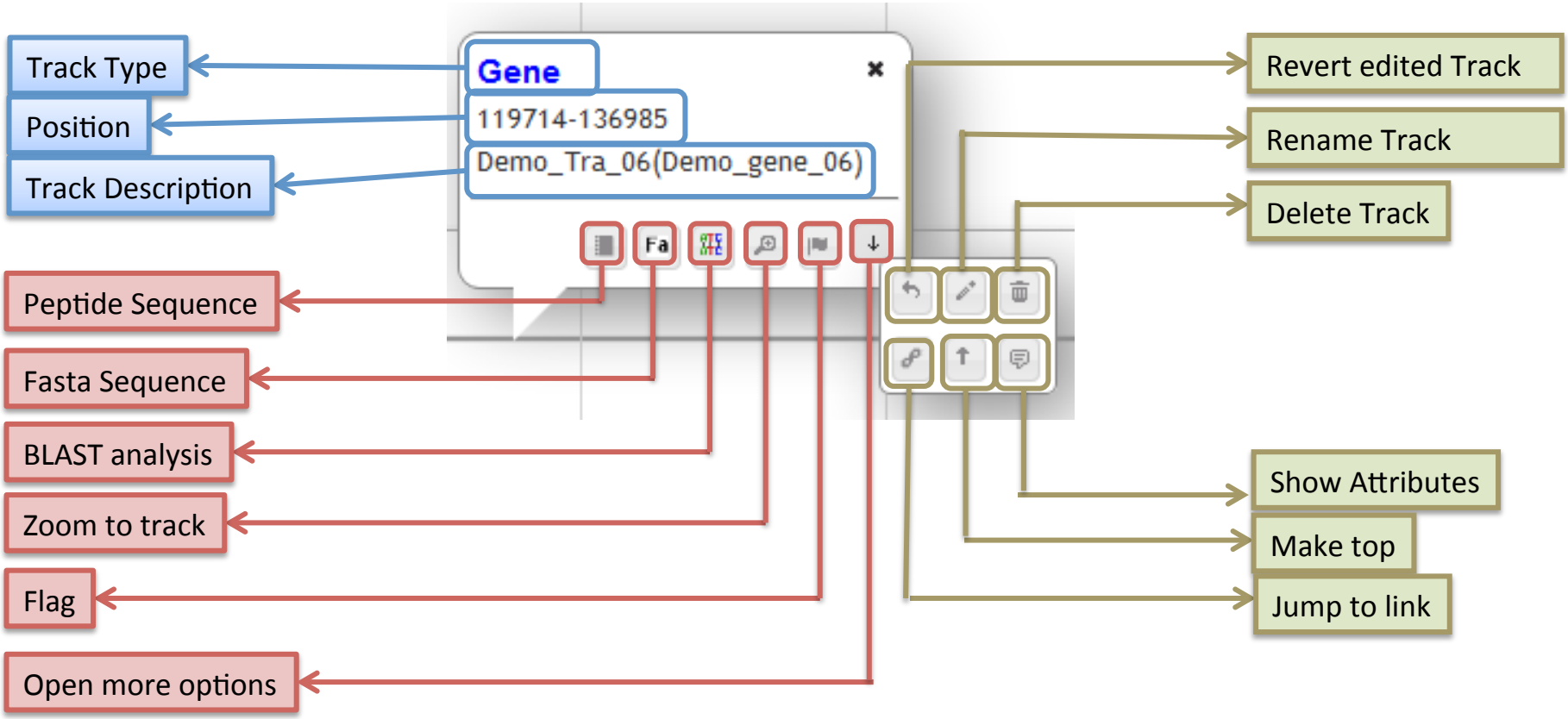
Popup


Track Type
Position
Track Description
Gene
119714-136985
Demo_Tra_06(Demo_gene_06)
Fa

Popup


Track Type
Position
Track Description
Gene
119714-136985
Demo_Tra_06(Demo_gene_06)
Fa
Peptide Sequence
Fasta Sequence
BLAST analysis
Zoom to track
Flag
Open more options

Popup


Track Type
Position
Track Description
Gene
119714-136985
Demo_Tra_06(Demo_gene_06)
Fa
Peptide Sequence
Fasta Sequence
BLAST analysis
Zoom to track
Flag
Open more options
Revert edited Track
Rename Track
Delete Track
Show Attributes
Make top
Jump to link

Future Work

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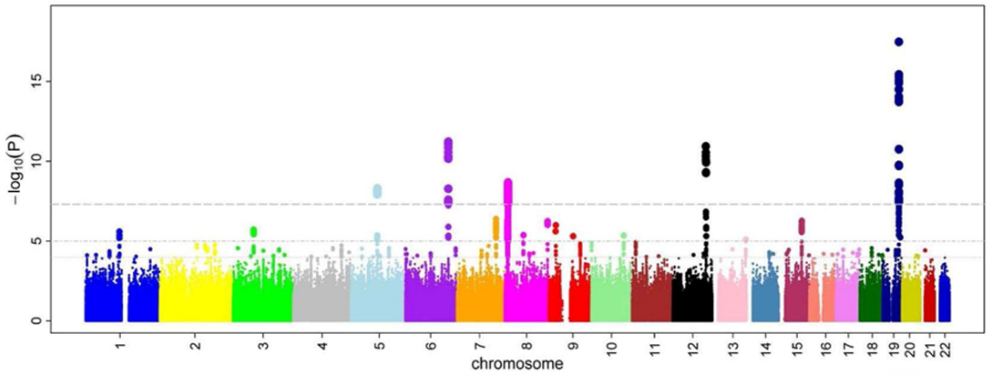
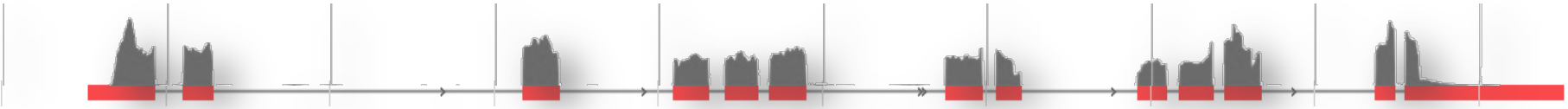
- **Manual Annotation**
- **Aequatus Browser integration**
- Upload user's data
- New Visuals
  - Manhattan Plots,
  - Expression data on Genes
- Integrate HMMER and BLAT analysis
- Data Download from TGAC Browser
- REST API to load data from Ensembl
- Write a Paper





Manual Annotation

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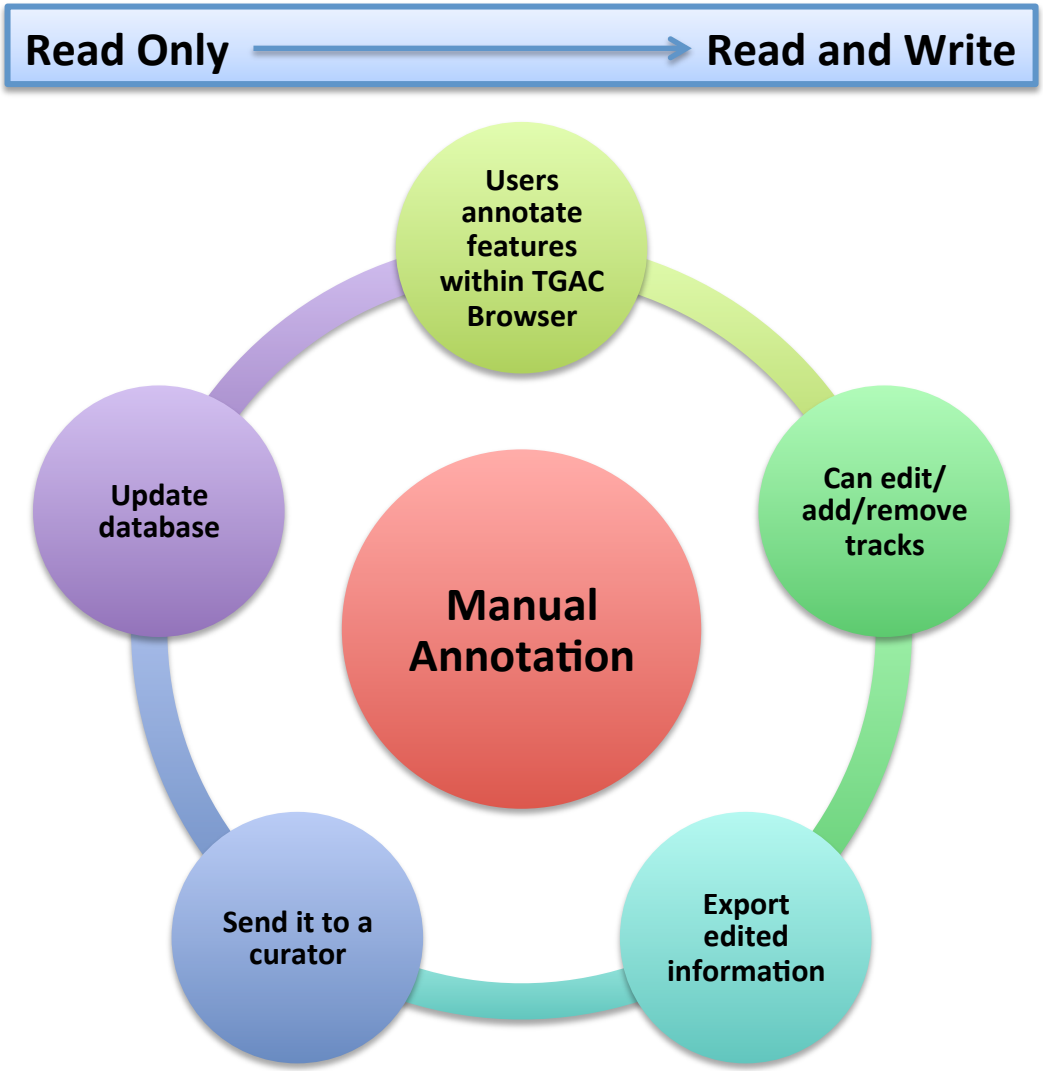

Manual Annotation

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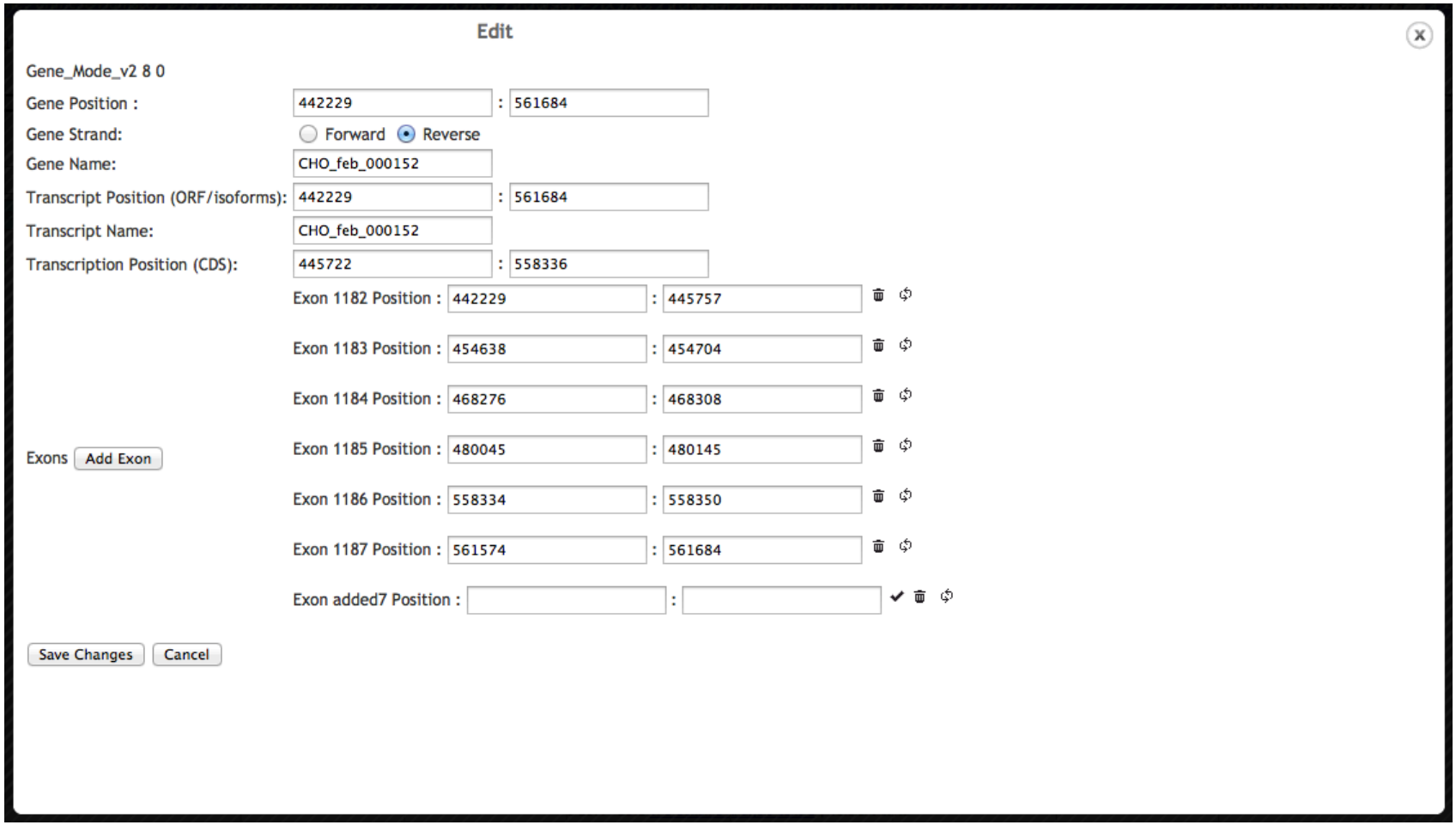
- Edit various genomic track credentials
- Add new tracks



Aequatus Browser

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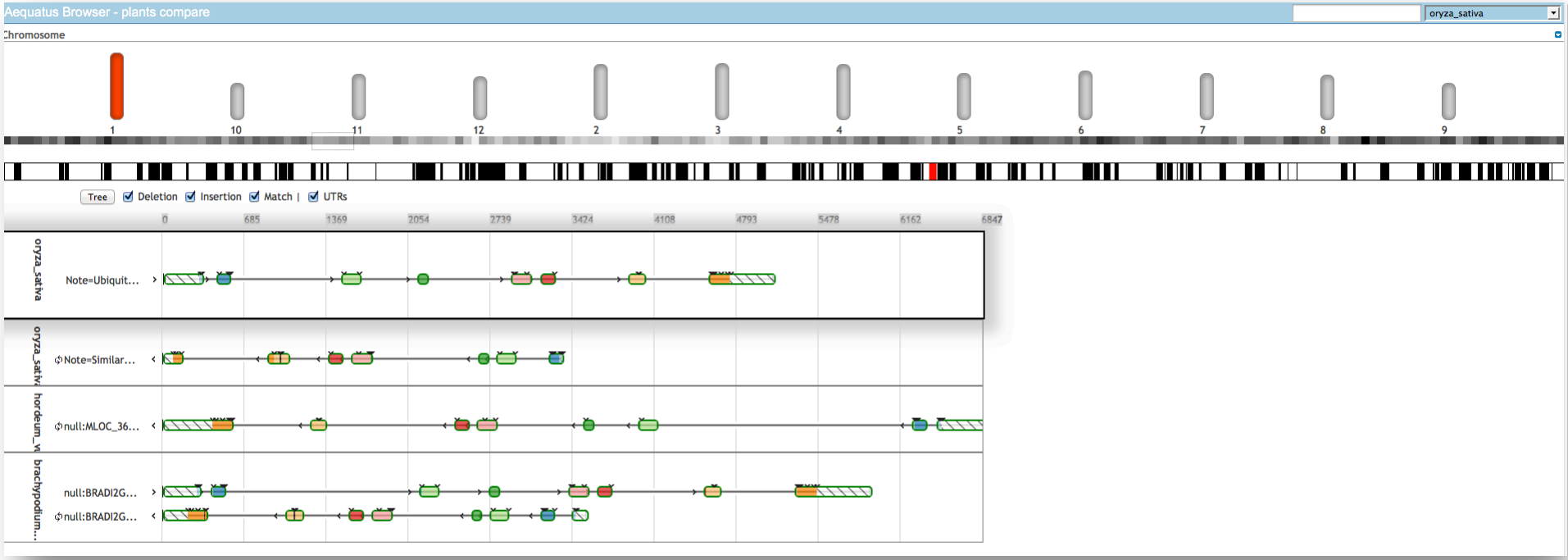
- Integration of Aequatus Browser within TGAC Browser
  - Under development at TGAC



- Visualising complex similarity relationships among species
- Beta: http://tgac-browser.tgac.ac.uk/plants_compara
- Slides: **http://tinyurl.com/aequatous-browser**

TGAC Browser

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Started	• Oct 2011
Presented at NGS DeepSeq	• August 2012
V0.1.1	• May 2013
Presented at ISMB	• July 2013
v0.1.2	• Aug 2013
Presented at UK Genome Science	• Sept 2013
V0.2.0	• Dec 2013
Presented at VizBi	• March 2014
v0.2.1	• May 2014
Presenting at BOSC 2014	• July 2014
V0.2.2	• Soon…

Instances:

- TGAC Browser Demo
- Chinese Hamster
- Wheat Yellow Rust
- Chalara Fraxinus
- Brassica
- Homo Sapiens
- Vietnamese Rice
- Lactobacillus salivarius
- IWGSC Wheat
- Hordeum
- Oryza Sativa
- Brachypodium

Documentation: **https://documentation.tgac.ac.uk/display/TB/TGAC+Browser**

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Trinity College Dublin — Paul Linehan

International Wheat Genome Sequencing Consortium

http://tgac-browser.tgac.ac.uk
tgac.browser@tgac.ac.uk
@anilthanki and @tgacbrowser

BBSRC bioscience for the future

transPLANT