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IWGSC sequence repository: how to facilitate pseudomolecule assembly?

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IWGSC Sequence Repository: How to facilitate pseudomolecule assembly ?

Michael Alaux



Wheat@URGI website



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Wheat@URGI

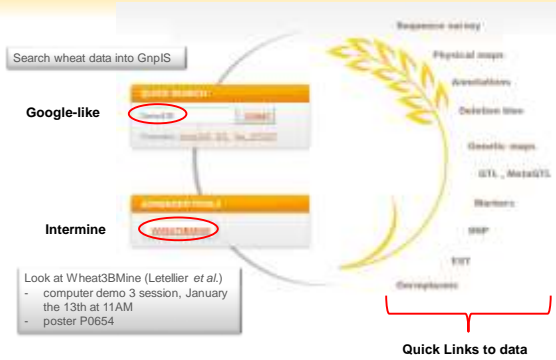


<http://wheat-urgi.versailles.inra.fr>



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Sequence Repository

The screenshot shows the 'Sequence Repository' website. On the left is a vertical navigation menu with items: 'Create an account', 'Home', 'Access Status', 'FAQ', 'BLAST', 'Accessories', 'Reference sequences', 'Genes & annotations', 'Physical maps', 'Transcriptome', 'BIM-Seq', 'Publication', and 'Support to assembly and data submission'. The main content area includes sections for 'New sequences', 'Publications', 'Reference sequences', and 'BIM-Seq'.



<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Sequence Repository: 3B example

This collage shows several screenshots from the Sequence Repository website. Red arrows highlight various features: a search bar, a list of sequences, a detailed view of a sequence with its alignment, and a visualization of sequence data. The screenshots demonstrate the user interface for searching and viewing genomic data.



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BLAST

BLAST



- **Public BLAST**
<https://urgi.versailles.inra.fr/blast/>
- More than 250 000 BLAST searches the past 2 years !



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<https://urgi.versailles.inra.fr/blast/>

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BLAST

This screenshot shows the BLAST search interface. The 'Database' dropdown menu is open, showing a list of databases. The 'wheat-urgi' database is highlighted with a red circle, indicating it is the selected database for the search.



<https://urgi.versailles.inra.fr/blast/>

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BLAST

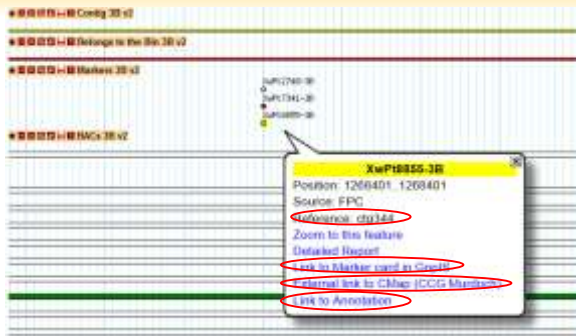
This screenshot shows the 'Advanced search' options in the BLAST interface. It includes settings for 'Expect threshold', 'Matrix', 'Mask', 'Alignment', and 'Output format'. The 'Expect threshold' is set to 0.01, and the 'Matrix' is set to BLOSUM62.



<https://urgi.versailles.inra.fr/blast/>

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Physical maps



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_phys_pub/

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3B reference sequence annotation



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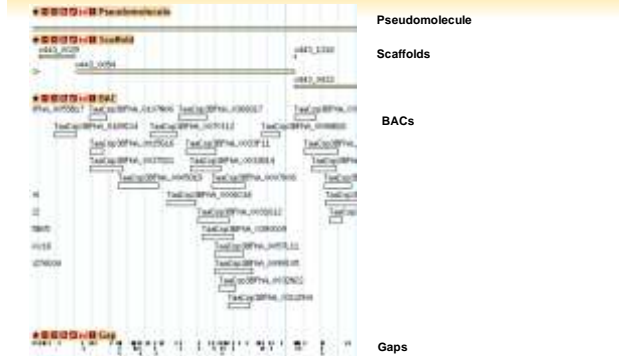
3B annotation



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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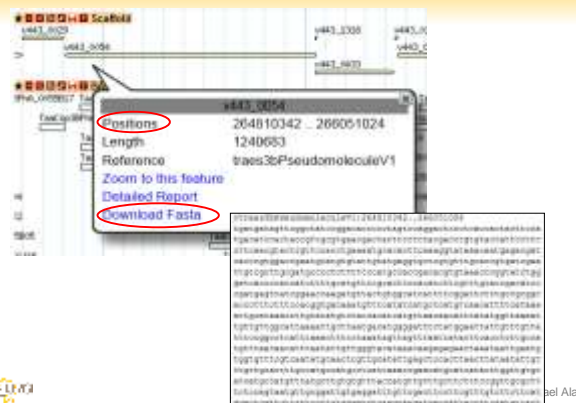
3B annotation



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

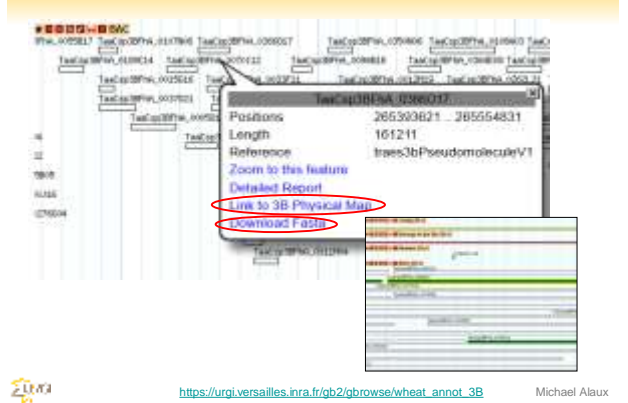
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3B annotation: Scaffold



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3B annotation: BAC



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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3B annotation



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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3B annotation: Marker



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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3B annotation: Gene



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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3B annotation: TE



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_annot_3B

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Survey sequence browser



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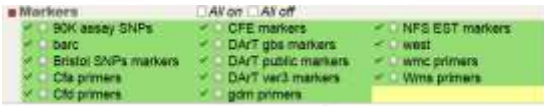
Survey sequence



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_survey_sequence_annotation

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Survey sequence



Support to assembly and data submission



https://urgi.versailles.inra.fr/gb2/gbrowse/wheat_survey_sequence_annotation

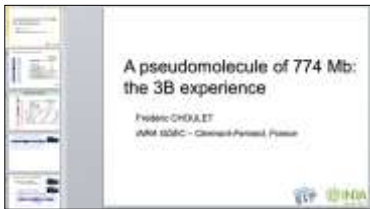
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BAC sequence assembly

4 BAC (sequence assembly)
 Frédéric Chouaïet, 2014
<http://urgi.versailles.inra.fr/Seq-Repository>



- 3B MTP BAC sequencing
- 3B physical map
- Assembly and scaffolding
- Ordering scaffolds
- Perform the Annotation
- Bioinformatic tools

BAC sequence assembly

What are the needs?
 i.e. distribute the bioinformatics softwares



<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Data submission



Wheat dataflow overview



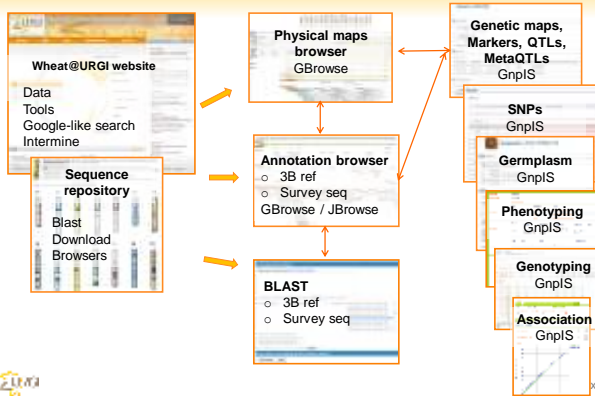
<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

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Wheat dataflow overview



Acknowledgments



Alaux M.
Letellier T.
Couderc L.
Alfama F.
Jamilloux V.
Flores R.
Guerche C.
Loaec M.
Steinbach D.
Quesneville H.



Choulet F.
Paux E.



Rogers J.
Eversole K.

All data providers



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Questions

Sequence Repository

<http://wheat-urgi.versailles.inra.fr/Seq-Repository>

BLAST (public)

<https://urgi.versailles.inra.fr/blast/>

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