Wheat3BMine
a data warehouse dedicated to wheat 3B chromosome data

Thomas LETELLIER

thomas.letellier@versailles.inra.fr

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URGI-GnpIS

URGI is a research unit in genomics and bioinformatics dedicated to plants and crop parasites.

    https://urgi.versailles.inra.fr/

GnpIS is the URGI information system dedicated to genetic and genomic data for plant and especially for wheat.

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

transPLANT

transPLANT is a European-Union funded e-infrastructure to support computational analysis of genomic data from crop and model plants.

http://www.transplantdb.eu/

➢ Wheat3BMine:robust data warehouse centered on wheat genomics

Why Intermine ?

➢ Open source data warehouse

➢ Dedicated to integration and analyse of complex biological data

➢ Fast, flexible and user friendly access to integrated data

http://intermine.github.io/intermine.org/

Data types

Wheat3BMine contains:

➤ Genomic annotation data (genes, mRNA, transposable elements…)

➤ Genetic mapping data (QTL, metaQTL)

➤ Polymorphisms data (markers)

➤ Phenotyping data (Germplasm, evaluation data)

Wheat3Bmine overview

You can get data using:

➢ A powerfull **QuickSearch** with wildcard and operators (AND, OR...)

➢ A **QueryBuilder** which allow you to make complex queries

➢ A **Region form** using genomic positions

➢ **Templates** which facilitates data querying

➢ A dedicated **API** (Java, Python...)

➢ Store and analyse your favourite features with **Lists**

Wheat3Bmine overview

Easy data querying:

- ✓ An **online documentation**
- ✓ A **dedicated account** to store your favourite queries/lists.

Wheat3BMine Documentation

Wheat3BMine is a data warehouse which contains wheat 3B chromosome data. It allows you to perform complex queries, making lists of your favorite features or search for features using a range of positions.
Wheat3bMine is developed using InterMine:

- – here a video presenting InterMine's features → http://intermine.github.io/intermine.org/
- – here the technical documentation → https://intermine.readthedocs.org/en/latest/

Wheat3BMine content

Wheat3bMine allows retrieving information/data from:

- – **Annotation** of the 3b chromosome (mrnas, genes and polypeptides)
- – **ontologies** like the Gene Ontology
- – **polymorphisms data** (transposable elements or markers)
- – **phenotyping data** (accessions, evaluation data)

Online demonstration

http://urgi.versailles.inra.fr/Wheat3BMine/

Use cases:

1. Search for a Dart marker in the **QuickSearch**

2. Find genes located on strand 1 with a function coverage > 80 thanks to the **QueryBuilder**

3. Get all features located on genomic regions of interest and export results in the **Region form**

Find more use cases into the online documentation.

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