OmicsConnect: flexible multi-omics data capture and integration tools for high-throughput biology

K. Joeri van der Velde, Morris Swertz, members of the Genomics Coordination Center, & many others

www.bioshare.eu
(Inter)national bioinformatics hub of ~15 on a mission to speed up rare and complex disease research and improve patient care via databases, integration tools and analysis pipelines.

Looking for colleague(s) 😊

Human and model organism research: genotype 2 phenotype
MOLGENIS: Motivation – building many apps

Researcher needs

NextGenSeq data

Mutation data

Model organisms data

Work very hard

Use

Solexa Sequencer LIMS

database of COL7A1 mutations

Animal Observatory
Instead: design blueprint of data model & GUI

What comes where?
What dimensions?
E.g.
- Phenotype reports?
- Genotype reports?
- Mutation reports?
- News?
- Submissions?
- Literature?
- Clinician contacts?
- …
MOLGENIS: Solution - generate the software

- Model in DSL
- NextGenSeq
- Mutation database
- Model organisms

Use generated software

Solexa Sequencer LIMS

Generator

database of COL7A1 mutations

Animal Observatory

http://www.molgenis.org
### Example of a basic application

**BBMRI-NL Biobank Registry**

<table>
<thead>
<tr>
<th>id</th>
<th>name</th>
<th>Address</th>
<th>Phone</th>
<th>Email</th>
<th>Fax</th>
<th>tollFreePhone</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>All UMCs</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2</td>
<td>AMC</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>3</td>
<td>BOOG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>4</td>
<td>DDHK</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>5</td>
<td>DCCG</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>6</td>
<td>ErasmusMC</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>7</td>
<td>EUR</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>8</td>
<td>GGD</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>9</td>
<td>HIV Monitoring Foundation</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>10</td>
<td>ICC consortium (Parelsnoer)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

* = this record is read only.

This database was generated using the open source **MOLGENIS database generator** version 3.3.3. Please cite **Swertz et al (2004)** or **Swertz & Jansen (2007)** on use.
Migrated from SVN to GitHub

- ~15 active devs
- ~25 projects
- [github.com/molgenis]
Migrated from Ant builds to Maven modules

- **MOLGENIS collection of repositories**
  - **molgenis**: rich application toolbox
  - **sdk**: bare bones development
  - **…others**

<table>
<thead>
<tr>
<th>Repository</th>
<th>Description</th>
<th>Date</th>
</tr>
</thead>
<tbody>
<tr>
<td>molgenis-app-compute-db</td>
<td>added extra parameter to specify backend credentials; make it run f...</td>
<td>10 days ago</td>
</tr>
<tr>
<td>molgenis-app-lifelines</td>
<td>add .gitignore files</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-app-ngs</td>
<td>update spring 3.2.2 --&gt; 3.2.3</td>
<td>15 days ago</td>
</tr>
<tr>
<td>molgenis-app-omx</td>
<td>update spring 3.2.2 --&gt; 3.2.3</td>
<td>15 days ago</td>
</tr>
<tr>
<td>molgenis-compute-core</td>
<td>fixed build; removed wrong testing</td>
<td>2 hours ago</td>
</tr>
<tr>
<td>molgenis-core-ui</td>
<td>fixed the bug that RestApi throws an error when the value of expanded...</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-core</td>
<td>improve entity importer performance</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-omx-auth</td>
<td>update spring 3.2.2 --&gt; 3.2.3</td>
<td>15 days ago</td>
</tr>
<tr>
<td>molgenis-omx-core</td>
<td>update spring 3.2.2 --&gt; 3.2.3</td>
<td>15 days ago</td>
</tr>
<tr>
<td>molgenis-omx-dataexplorer</td>
<td>add .gitignore files</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-omx-filemanager</td>
<td>removed jqgrid + removed dataviewer</td>
<td>22 days ago</td>
</tr>
<tr>
<td>molgenis-omx-importer</td>
<td>improve dataset importer performance</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-omx-protocolmanager</td>
<td>add .gitignore files</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-omx-protocolviewer</td>
<td>fixed a major in catalogue that protocol might be duplicated twice w...</td>
<td>21 days ago</td>
</tr>
<tr>
<td>molgenis-search-elasticsearch</td>
<td>add .gitignore files</td>
<td>14 days ago</td>
</tr>
<tr>
<td>molgenis-search</td>
<td>add .gitignore files</td>
<td>14 days ago</td>
</tr>
</tbody>
</table>
Continuous integration & automated deploy

<table>
<thead>
<tr>
<th>Job</th>
<th>Last Success</th>
<th>Last Failure</th>
<th>Last Duration</th>
<th>Console</th>
</tr>
</thead>
<tbody>
<tr>
<td>molgenis-app-compute-db</td>
<td>11 days (#2)</td>
<td>N/A</td>
<td>3 min 23 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-app-lifelines</td>
<td>6 hr 14 min (#46)</td>
<td>8 days 6 hr (#31)</td>
<td>6 min 6 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-app-ngs</td>
<td>6 hr 18 min (#30)</td>
<td>N/A</td>
<td>4 min 0 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-app-omx</td>
<td>6 hr 25 min (#30)</td>
<td>11 days (#6)</td>
<td>3 min 42 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-compute-core</td>
<td>6 hr 31 min (#30)</td>
<td>9 hr 24 min (#29)</td>
<td>1 min 30 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-core</td>
<td>6 hr 33 min (#32)</td>
<td>11 days (#1)</td>
<td>2 min 11 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-core-ui</td>
<td>6 hr 31 min (#30)</td>
<td>N/A</td>
<td>23 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-genotype-reader2</td>
<td>7 days 9 hr (#9)</td>
<td>11 days (#1)</td>
<td>2 min 32 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-auth</td>
<td>6 hr 28 min (#32)</td>
<td>11 days (#6)</td>
<td>1 min 56 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-core</td>
<td>6 hr 31 min (#29)</td>
<td>N/A</td>
<td>2 min 23 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-dataexplorer</td>
<td>6 hr 28 min (#52)</td>
<td>11 days (#7)</td>
<td>1 min 10 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-filenmanager</td>
<td>6 hr 28 min (#30)</td>
<td>11 days (#4)</td>
<td>57 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-importer</td>
<td>6 hr 28 min (#30)</td>
<td>11 days (#4)</td>
<td>58 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-protocolmanager</td>
<td>9 days 10 hr (#23)</td>
<td>N/A</td>
<td>48 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-omx-protocolviewer</td>
<td>6 hr 26 min (#30)</td>
<td>N/A</td>
<td>1 min 20 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-sck</td>
<td>6 hr 25 min (#69)</td>
<td>11 days (#33)</td>
<td>58 sec</td>
<td></td>
</tr>
<tr>
<td>molgenis-search</td>
<td>6 hr 31 min (#27)</td>
<td>N/A</td>
<td>52 sec</td>
<td></td>
</tr>
</tbody>
</table>
Motivation: Understanding geno-to-pheno
Situation: Many types and flavours of data

Genomic features, individuals, ontologies ...

Metadata for phenotypes, datasets, samples, panels ...

Biomolecular measurements, association results ...

Genotypes, conditions ...
Challenge: Building a ‘team’ database

Data model
Bigger challenge: Building many databases
MOLGENIS: Many unique apps is not optimal

What data models to use? Can we have a model that rules them all? One application > Many applications

Model in DSL
NextGenSeq
Mutation database
Model organisms

Use generated software
Solexa Sequencer LIMS
Generator

What data models to use? Can we have a model that rules them all? One application > Many applications

http://www.molgenis.org
What are we dealing with?

Annotations of concepts used in data sets, mostly static content

Stable?

Experimental data sets, usually flexible and volatile content

Dynamic?
Example: eQTL data

**Probe (annotation)**

<table>
<thead>
<tr>
<th>name</th>
<th>mismatch</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>WSU1</td>
<td>true</td>
<td>NA / SpotReport / blast_match_NA / n</td>
</tr>
<tr>
<td>WSU2</td>
<td>false</td>
<td>C25A1.8 / cea2.c.000914 / blast_match</td>
</tr>
<tr>
<td>WSU3</td>
<td>false</td>
<td>F21F3.6 / cea2.c.02677 / blast_match</td>
</tr>
<tr>
<td>WSU4</td>
<td>false</td>
<td>F25H2.9 / cea2.c.02801 / blast_match</td>
</tr>
<tr>
<td>WSU5</td>
<td>false</td>
<td>F56H1.4 / cea2.c.04344 / blast_match</td>
</tr>
</tbody>
</table>

**Marker (annotation)**

<table>
<thead>
<tr>
<th>name</th>
<th>chromosome bpstart</th>
<th>cm</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pkP1050</td>
<td>169018</td>
<td>-18.26</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>pkP1101</td>
<td>992189</td>
<td>-17.28</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>pkP1103</td>
<td>1881116</td>
<td>-11.96</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>pkP1052</td>
<td>2818974</td>
<td>-6.1</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>egPE107</td>
<td>3502476</td>
<td>-3.55</td>
<td>PCR_non_cu</td>
</tr>
</tbody>
</table>

**eQTL profiles (data set)**

<table>
<thead>
<tr>
<th></th>
<th>pkP1050</th>
<th>pkP1101</th>
<th>pkP1103</th>
<th>pkP1052</th>
<th>egPE107</th>
</tr>
</thead>
<tbody>
<tr>
<td>WSU1</td>
<td>0.5036565</td>
<td>0.4603331</td>
<td>0.3544101</td>
<td>0.9123223</td>
<td>0.4157701</td>
</tr>
<tr>
<td>WSU2</td>
<td>0.1365825</td>
<td>0.1037847</td>
<td>0.6608989</td>
<td>0.1241076</td>
<td>0.1672075</td>
</tr>
<tr>
<td>WSU3</td>
<td>0.5837218</td>
<td>0.5611695</td>
<td>0.1708836</td>
<td>1.439448</td>
<td>1.94431</td>
</tr>
<tr>
<td>WSU4</td>
<td>0.5558796</td>
<td>0.7246171</td>
<td>0.1777933</td>
<td>0.1937225</td>
<td>0.4413371</td>
</tr>
<tr>
<td>WSU5</td>
<td>0.3393896</td>
<td>0.4705863</td>
<td>0.224066</td>
<td>0.7713159</td>
<td>0.01334126</td>
</tr>
</tbody>
</table>
Stable = good for code generation

Annotations: Column-oriented data

1. model
2. generate
3. import

Attributes

- name
- chromosome_bpstart
- cm
- description

<table>
<thead>
<tr>
<th>name</th>
<th>chromosome_bpstart</th>
<th>cm</th>
<th>description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pkP1050</td>
<td>169018</td>
<td>-18.26</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>pkP1101</td>
<td>992189</td>
<td>-17.28</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>pkP1103</td>
<td>188116</td>
<td>-11.96</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>pkP1052</td>
<td>2818974</td>
<td>6.1</td>
<td>PCR_non_cu</td>
</tr>
<tr>
<td>egPE107</td>
<td>3502476</td>
<td>-3.55</td>
<td>PCR_non_cu</td>
</tr>
</tbody>
</table>
Challenge: Data sets can be variable combinations

Panel
- N2
- CB
- ...

Marker
- pkP1050
- pkP1101
- pkP1103
- pkP1052
- ...

Genotype

Sample
- GSM588088
- GSM588089
- GSM588090
- GSM588091
- ...

Probe
- AGIUSA45211
- AGIUSA45212
- AGIUSA45213
- AGIUSA45214
- ...

Sample

Microarray

Masspeak
- MSP0015
- MSP0023
- ...

Individual
- ewlR001
- ewlR002
- ewlR003
- ewlR004
- ...

LC/MS
XGAP model: <any trait> X <any subject>

Extensible core model for homogen. datasets

Probe
- Name
- Gene
- Chromosome
- Locus

Marker
- Name
- Allele
- Chromosome
- Locus

MassPeak
- Name
- MZ
- RetentionTime

And so on

Individual
- Name
- Strain
- Mother
- Father
- Sex

Sample
- Name
- Individual
- Tissue

Panel
- Name
- Type: CSS, RIL...
- Parent Panels

And so on...

Subject

Dimension Element

Data Element

Row

Column
Observ-OM model for flexible columns/prov.

Observ-OM data example

**Observation**
Dr. Smith examines cohort patients, June 12th 1949

**Value**
140.1

**Protocol**
FRAMINGHAM Clinic Exam, Original Cohort, Exam 10

**Feature**
BLOOD PRESSURE, SYSTOLIC, FIRST READING TAKEN BY PHYSICIAN [unit: mmHg, dataType: decimal]

**Ontology**
MeSH: Blood Pressure

“PRESSURE of the BLOOD on the ARTERIES and other BLOOD VESSELS.”

Evolution

MOLGENIS software
http://www.molgenis.org

XGAP model
Swertz et al, Genome Biology (2010)
http://www.xgap.org

Observ-OM model
Adamusiak et al, Human Mutation (2012)
http://www.observ-om.org

xQTL workbench
Arends & van der Velde et al, Bioinformatics (2012)
http://www.xqtl.org

EB Registry
Van den Akker et al, Human Mutation (2011)
http://www.deb-central.org

tubular eb

AnimalDB
Track and trace of animal life events in research laboratories
http://www.animaldb.org

WormQTL
• Panacea project, C. elegans data
• ~300 million measurements
http://www.wormqtl.org

CropQTL
Learning From Nature project, arabidopsis thaliana data
• 1400 plants
• SNP genotypes (~70 million values)
• Classical traits, e.g. flowering time

LifeLines Research Portal

EURATRANS xQTL workbench

umcg
university of groningen

Parel IBD
Pareo IBD

TIF FOOD NUTRITION

molgenis
One to rule all? Observ-OMX

Catalogue
Find data item and sample collections

Data
Filter individual data sets and download to Excel & SPSS

Compute
Run analysis workflows on big data compute infrastructure

GWAS Central
Explore summary level GWAS data

Protocol
CRFs, Questionnaires, Lab protocols, and assays

NGS
Next-Generation Sequencing

xQTL
Multi-omics association & visualization tools

XGAP
Multi-omics genotypes and phenotypes

Share
Friends, Groups and Permission management

Mutation
Explore genetic mutations and pathogenicity effects

Organization
Institutes, Departments, People, Locations & Containers

File
File storage and drivers for images and data

molgenis
Outcome: working applications (e.g. xQTL)

Micro-array probes blasted against WS220 and linked to the genes, used for gene expression phenotypes and eQTLs.

Click on to plot an item, and on to return to this list.
<table>
<thead>
<tr>
<th>Patient ID</th>
<th>Phenotype</th>
<th>cDNA change 1</th>
<th>Protein change 1</th>
<th>Exon/Intron 1</th>
<th>Consequence 1</th>
<th>cDNA change 2</th>
<th>Protein change 2</th>
<th>Exon/Intron 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>P37</td>
<td>RDEB, severe generalized</td>
<td>c.3G&gt;T</td>
<td>p.0</td>
<td>Exon 1</td>
<td>pathogenic</td>
<td>c.3G&gt;T</td>
<td>p.0</td>
<td>Exon</td>
</tr>
<tr>
<td>P292</td>
<td>RDEB, severe generalized</td>
<td>c.3G&gt;A</td>
<td>p.0</td>
<td>Exon 1</td>
<td>pathogenic</td>
<td>c.353delGinsCCCCTTGCAAA</td>
<td>p.Arg118ProfsX14</td>
<td>Exon</td>
</tr>
<tr>
<td>P172</td>
<td>RDEB, unknown</td>
<td>c.3G&gt;T</td>
<td>p.0</td>
<td>Exon 1</td>
<td>pathogenic</td>
<td>c.448G&gt;A</td>
<td>p.Gly150Arg</td>
<td>Exon</td>
</tr>
<tr>
<td>P34</td>
<td>RDEB, severe generalized</td>
<td>c.3G&gt;T</td>
<td>p.0</td>
<td>Exon 1</td>
<td>pathogenic</td>
<td>c.4997dupG</td>
<td>p.Pro1688AalsFX4</td>
<td>Exon</td>
</tr>
<tr>
<td>P367</td>
<td>RDEB, generalized other</td>
<td>c.112G&gt;T</td>
<td>p.Asp38Tyr</td>
<td>Exon 2</td>
<td>pathogenic</td>
<td>c.2157G&gt;A</td>
<td>p.Trp719Ter</td>
<td>Exon</td>
</tr>
<tr>
<td>P213</td>
<td>RDEB, severe generalized</td>
<td>c.143C&gt;T</td>
<td>p.Ser48Phe</td>
<td>Exon 2</td>
<td>pathogenic</td>
<td>c.3625_3635del</td>
<td>p.Ser1209LeufsX6</td>
<td>Exon</td>
</tr>
<tr>
<td>P1</td>
<td>RDEB, pruriginosa</td>
<td>c.151C&gt;G</td>
<td>p.Arg51Gly</td>
<td>Exon 2</td>
<td>pathogenic</td>
<td>c.7474C&gt;T</td>
<td>p.Arg2492Ter</td>
<td>Exon</td>
</tr>
<tr>
<td>P2</td>
<td>RDEB, severe generalized</td>
<td>c.238G&gt;C</td>
<td>p.Ala80Pro</td>
<td>Exon 2</td>
<td>pathogenic</td>
<td>c.3631C&gt;T</td>
<td>p.Gln1211Ter</td>
<td>Exon</td>
</tr>
<tr>
<td>P435</td>
<td>RDEB, severe generalized</td>
<td>c.267-3C&gt;G</td>
<td>p.267-3G&gt;C</td>
<td>IVS2</td>
<td>pathogenic</td>
<td>p.267-3C&gt;G</td>
<td>IVS2</td>
<td></td>
</tr>
<tr>
<td>P110</td>
<td>RDEB, severe generalized</td>
<td>c.313dupC</td>
<td>p.Arg105ProfsX5</td>
<td>Exon 3</td>
<td>pathogenic</td>
<td>c.5047C&gt;T</td>
<td>p.Arg1683Ter</td>
<td>Exon</td>
</tr>
<tr>
<td>P267</td>
<td>RDEB, severe generalized</td>
<td>c.325_326insCG</td>
<td>p.Glu109AalsFX39</td>
<td>Exon 3</td>
<td>pathogenic</td>
<td>c.3277-1G&gt;C</td>
<td>IVS2</td>
<td></td>
</tr>
<tr>
<td>P268</td>
<td>RDEB, severe generalized</td>
<td>c.325_326insCG</td>
<td>p.Glu109AalsFX39</td>
<td>Exon 3</td>
<td>pathogenic</td>
<td>c.3277-1G&gt;C</td>
<td>IVS2</td>
<td></td>
</tr>
</tbody>
</table>

3156 data items found
Dystrophic EB Register (COL7A1)

### Phenotypic details for patient 'P10'

**Characteristics**

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<th>Characteristics</th>
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<td>Gender</td>
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<td>Cause of death</td>
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<tr>
<td>MMP1 allele 1</td>
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<td>MMP1 allele 2</td>
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**Cutaneous**

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<td>Blistering</td>
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<td>Location</td>
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<td>Feet</td>
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<td>Legs</td>
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<td>Proximal body flexures</td>
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<tr>
<td>Trunk</td>
<td>unknown</td>
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<tr>
<td>Mucous membranes</td>
<td>yes</td>
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<tr>
<td>Skin atrophy</td>
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<tr>
<td>Milia</td>
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<tr>
<td>Nail dystrophy</td>
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WormQTL – Public archive and analysis web portal for natural variation data in Caenorhabditis spp.

WormQTL is an online scalable system for QTL exploration to service the worm community. WormQTL provides many publicly available datasets and welcomes submissions from other worm researchers.

What can you do?

- I want to search (e)QTLs for my trait or gene
  1. Go to Find QTLs
  2. Type the name or identifier of your trait or gene and press Search
  3. Put any relevant hits in the shopping cart
  4. Click Plot cart now and explore the results

- I want to know which genes have a QTL on my favourite position
  1. Go to Genome browser
  2. Add tracks from experiments of interest
  3. Navigate to your favourite location (tip: use open in new window)
  4. Collect significant probe identifiers from that region
  5. Use the identifiers to a q-q search with Find QTLs
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<th>Phenotypes</th>
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<th>Sample size</th>
<th>Parental strains</th>
<th>Reference</th>
<th>Pubmed link</th>
<th>Growing temperature</th>
<th>Stage</th>
<th>Food</th>
<th>Medium</th>
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<td>Gene expression</td>
<td>Washington State University</td>
<td>2x40 RILs</td>
<td>N2, N2</td>
<td>Li et al. 2006; Mapping determinants of gene expression plasticity by genetic genomics in C. elegans.</td>
<td>17196041</td>
<td>16oC and 24oC</td>
<td>(72h at 16 and 40h at 24); L4</td>
<td>OP50</td>
<td>NGM Plate</td>
<td>37, 38</td>
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<td>Gene expression</td>
<td>Affymatrix tiling array</td>
<td>60 RILs</td>
<td>N2, N2</td>
<td>Li et al. 2010; Global genetic robustness of the alternative splicing machinery in Caenorhabditis elegans.</td>
<td>20610403</td>
<td>24oC</td>
<td>(40h) L4</td>
<td>OP50</td>
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<td>36x3 RILs</td>
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<td>Vinuela &amp; Snoek et al. 2010; Genome-wide gene expression regulation as a function of genotype and age in C. elegans.</td>
<td>20488933</td>
<td>24oC</td>
<td>(40h, 96h and 214h) L4, Adult, Old</td>
<td>OP50</td>
<td>NGM Plate</td>
<td>3, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21</td>
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<td>Gene expression</td>
<td>Agilent 4x44k microarrays</td>
<td>208 RIALs</td>
<td>N2, N2</td>
<td>Rockman et al. 2010; Selection at linked sites shapes heritable phenotypic variation in C. elegans.</td>
<td>20947766</td>
<td>20oC</td>
<td>YA</td>
<td>OP50</td>
<td>NGM Plate</td>
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<td>Feeding curves RNAi exposure</td>
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<td>56 RILs + 12 RNAi</td>
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<td>Elvin &amp; Snoek et al. 2011; A fitness assay for comparing RNAi effects across multiple C. elegans genotypes.</td>
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<td>Multi-generational</td>
<td>Liquid S-medium</td>
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<td>Life-history traits</td>
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<td>80 RILs</td>
<td>N2, N2</td>
<td>Cutteling et al. 2007; Mapping phenotypic plasticity and genotype-environment interactions affecting life-history traits in Caenorhabditis elegans.</td>
<td>16955112</td>
<td>12oC and 24oC</td>
<td>Egg, L4, YA</td>
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<td>Lifespan and pharyngeal-pumping</td>
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<td>90 NILS</td>
<td>N2, N2</td>
<td>Doroszuk et al. 2009; A genome-wide library of CB4856/N2 introgression lines of Caenorhabditis elegans.</td>
<td>19542186</td>
<td>20oC</td>
<td>All; synchronised</td>
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<td>Lifespan, Recovery and reproduction after heat-shock</td>
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<td>58 RILs</td>
<td>N2, N2</td>
<td>Rodriguez et al. 2012; Genetic variation for stress-response hormesis in C. elegans lifespan.</td>
<td>22613270</td>
<td>20oC and 35oC heat-shock</td>
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<td>Washington State University</td>
<td>CB4856 and N2</td>
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<td>Vinuela &amp; Snoek et al. 2012; Aging Uncouples Heritability and Expression–QTL in Caenorhabditis elegans.</td>
<td>22670229</td>
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WormQTL.org (C. Elegans)
Results for my selected hits:
(get a permanent link to these results)

Legend, click to enlarge:

More downloads:
- Get the Cytoscape network for this plot. (how-to import)
- Note: includes significant results only. (LOD > 3.5)
- Save both files. Import network (has LOD scores), then node attributes (chrom, bploc, dataset). Example visualization

- Get the generated source data for these plots.
- Get the generated multiplot plot R script.
- Get the generated cistrans R plot script.
- Get the generated profile R plot script.
WormQTL.org (C. Elegans)

More downloads:

- Get the [Cytoscape network](#) for...
- Get the [Cytoscape nodes](#) for...
- Note: includes significant results
- Save both files. Import network attributes (chrom, bploc, data)

- Get the generated [source data](#)
- Get the generated [multiplot](#)
- Get the generated [cistrans R plots](#)
- Get the generated [profile R plots](#)

/ daf-1 [explore deeper] - protein kinase [F29C4.1b] / F29C4.1b
/ daf-3 [explore deeper] - F25E2.5b.3 / F25E2.5 / wb[F25E2.5b.3]
/ sf-11 [explore deeper] - B02C4.3 / seq2 p 107079 / bla
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Hans Hillege
Ronald Stolk
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And more ...

NBIC/BioAssist consortium (bioinfo)
BBMRI–NL catalogue group (Hs)
CTMM/TraIT consortium (Hs)
EU–GEN2PHEN consortium (Hs)
EU–PANACEA consortium (Ce)
EU–BioSHARE consortium (Hs)
EU–CASIMIR consortium (Mm)
EU–BioMedBridges consortium (all)
NL Brassica Nutr. consortium (At)
Learning from Nature (At)
LifeLines (Hs)
TIFN (Hs)
BigGrid (info)
Target + CIT (info)
And more …
Wrap-up

Summary
- MOLGENIS software generator
- Exploiting bio data requires structure
- Best-of flexible and stable components
- OmicsConnect as modular platform of apps

Read more
- MOLGENIS: http://www/molgenis.org
- xQTL: http://www.xqtl.org
- Adamusiak et al (2011) BMC Bioinformatics
- Akker et al (2011) Human Mutation
- Brandsma et al, Norsk Epidemiologi 2012