

# Multi-omics network mining in Genestack for agri-research and beyond



To keep up with rapid global development, agri-producers have to breed or engineer crop varieties with ever higher yields, resistance to abiotic and biotic stress, and better adapted to their environments. This discovery process promises to become more fruitful thanks to rapid progress of omics technologies. We can now generate heterogeneous, complementary new insights into the complex stages between genotypes and phenotypes under various conditions.



However, the accumulated information is scattered across databases and literature in myriad forms: effects of genetic variations, gene regulations, protein interactions, pathways, homologues and others.

To make informed and effective decisions, these knowledge pieces need to be examined together: establishing chains of functional associations and interrelations between distant traits and causal genes. Networks provide a suitable data structure to capture such heterogeneous, complex and interconnected relations and provide a unified structure for deep relationship mining that's simply not achievable when dealing with the native data in isolation or pairwise. Unfortunately, building and mining a large biological knowledge networks is not a trivial task.

Supported by the Innovate UK, Genestack joined forces with the [Hassani-Pak lab](#) at Rothamsted Research to integrate the KnetMiner tool suite for evidence-based gene discovery into Genestack. The Genestack platform now provides a new environment for building, mining and distributing large-scale context- and species- specific knowledge networks. The underlying tools, [Ondex](#) and [KnetMiner](#), are made open-source, so you always have the option to contribute and use these tools outside Genestack, but remember that it will take a [steep learning curve](#), laborious data management, and dedicated servers. In Genestack, the process is much simpler and you can do much more by utilising the readily-available public data and other bioinformatics applications. Though originated in agri-research, our network mining solution is generic in principle and we've designed the system as such. This means, if you're working on any kind of data integration, whether it's for toxicology or drug development, you can tailor-make a network that suits your purpose. You have the flexibility to operate via a graphical user interface or interact programmatically, on- or off- the cloud. Everyone now has a new opportunity to compose meanings from the vastly evolving omics data.

Genestack now hosts over 40 plant and crop networks, as well as a prototype human disease network. You can see how these networks were built and mined by reading the user guide below. Nothing is stopping you from modifying them or creating many more, bringing your own data and research interest into play. All these data sources, built networks, and applications are immediately available: if you're an existing Genestack user, ask us for access; if you don't yet have a Genestack account, let us know and we'll provide a tester account for you. This is a proof of concept project and we'd very much welcome your feedback and ideas.



Please drop us a line at [info@genestack.com](mailto:info@genestack.com) to gain access to KnetMiner tester account

# User guide

This guide covers the following use cases:

## Mining species-specific plant networks..... 5

You'll learn how to use the KnetBuilder and KnetMiner applications to build and mine species-specific plant networks, by using the model species *Arabidopsis thaliana* as an example.

## Mining multi-species networks..... 17

You'll learn how to use homology to combine networks across species. As an example, we'll see how a network for *Brassica oleracea* becomes more useful when extended by the *Arabidopsis thaliana* network that's built earlier.

## Mining a human neurodegenerative network.....20

You'll learn how to apply the techniques earlier beyond the world of plant research, by looking into a prototype human network connecting drugs and neurodegenerative diseases.

## Sharing, reproducing, and updating networks..... 23

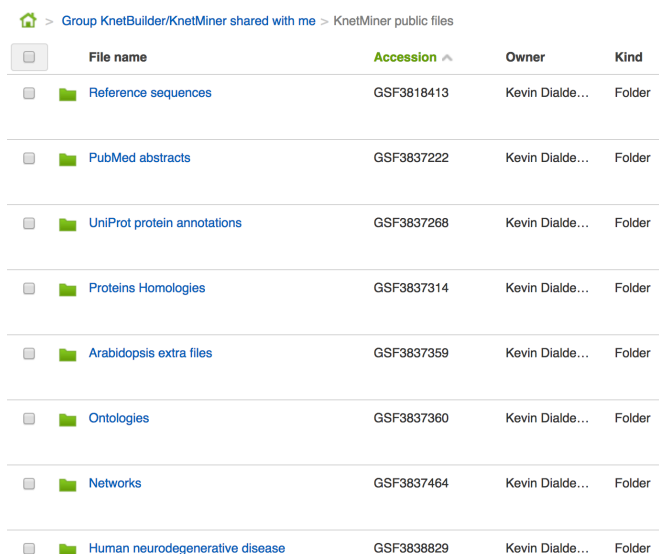
You'll learn how to collaborate and maintain your networks.

## Importing networks built outside Genestack.....24

You'll learn how to combine networks produced within and outside Genestack.

All the data sources and networks built in this guide are available in the shared folder [KnetMiner public files](#).

This means, you don't have to do all the intermediate steps in the guide; in fact, you should try different things and see what happens!



File name	Accession	Owner	Kind
Reference sequences	GSF3818413	Kevin Dialde...	Folder
PubMed abstracts	GSF3837222	Kevin Dialde...	Folder
UniProt protein annotations	GSF3837268	Kevin Dialde...	Folder
Proteins Homologies	GSF3837314	Kevin Dialde...	Folder
Arabidopsis extra files	GSF3837359	Kevin Dialde...	Folder
Ontologies	GSF3837360	Kevin Dialde...	Folder
Networks	GSF3837464	Kevin Dialde...	Folder
Human neurodegenerative disease	GSF3838829	Kevin Dialde...	Folder

## Mining species-specific plant networks

This section describes the entire process needed to build and mine a species-specific plant network:

1. Collecting the data sources and importing them into Genestack
2. Integrating them into a network using KnetBuilder
3. Mining and visualizing the network using KnetMiner

We'll demonstrate this on the model plant *Arabidopsis thaliana*. More research results are available for it compared to any other plant species, so this will provide a nice reference to the breadth of data types we can integrate and what kind of exploration is possible.

## Importing data sources

The steps below describe how to get the various plant data, using *Arabidopsis thaliana* as an example. Manually, this process is laborious, so we've imported them programmatically instead. Public data for various plants are now available in the Genestack folder KnetMiner public files:

1. Reference genome
  - Go to [Ensembl genomes](#)
  - Navigate to the latest release release-x and plants directory
  - Continue navigating to *Arabidopsis thaliana* [DNA fasta file](#) and [annotation gtf file](#)
2. Protein sequence
  - Go to [Ensembl genomes](#)
  - Navigate to the latest release release-x and plants directory
  - Continue navigating to *Arabidopsis thaliana* [protein fasta file](#)
3. UniProt protein annotation
  - Go to [UniProt](#)
  - Press advanced search
  - Select the Organism[OS] filter and enter "Arabidopsis thaliana"
  - Download as XML file

Or, get the exact same file used in this guide [here](#)

4. PubMed abstracts
  - Go to [PubMed](#)
  - Search "Arabidopsis thaliana"
  - Press Send to, choosing File and XML

Or, get the exact same file used in this guide [here](#)

5. Protein-protein interaction



- Go to [BioGRID](#)
- Select the current release
- Download interactions collection by organism with Tab 2.0 format
- Select the file corresponding to Arabidopsis thaliana

Or, get the exact same file used in this guide [here](#)

#### 6. Pathway

- Go to [Plant Metabolic Network](#)
- Go to Download > Data Sets
- Fill the license agreement form
- Once you've been granted permission, download biopax-level2.owl for AraCyc

Or, get the exact same file used in this guide [here](#)

#### 7. GWAS

- Go to [Ensembl Plants](#)
- Choose plant variation mart
- Choose Arabidopsis thaliana variations
- Set filter distance to transcript <= 1000
- Set attributes variation ID, p-value, associated variant risk allele, distance to transcript, chromosome name, position on chromosome (bp), gene stable id, consequence to transcript, phenotype name, phenotype description
- Download result as TSV

Or, get the exact same file used in this guide [here](#)

#### 8. GO Annotation

- Go to [Gene Ontology Consortium](#)
- Get the [GO annotation for Arabidopsis thaliana](#)

#### 9. Gene ontology:

- Go to [Gene Ontology Consortium](#)
- Get the [GO obo file](#)

#### 10. Trait ontology:

- Go to [Planteome](#)
- Get the [Plant Trait Ontology obo file](#)

How to import them into Genestack:

1. Open Dock by clicking on the Genestack logo in the top left

2. Click on Import Data
3. Either drag and drop your local files or specify the file URLs
4. Click on Import files
5. Check that the file kinds were detected correctly
6. Click on Create files
7. You have imported your files
8. For the Reference Genome file, it's important for you to set the organism metainfo; it's *Arabidopsis thaliana* in this example.

To find out more about data and metadata import in Genestack, read our guide [here](#).

## Building the network

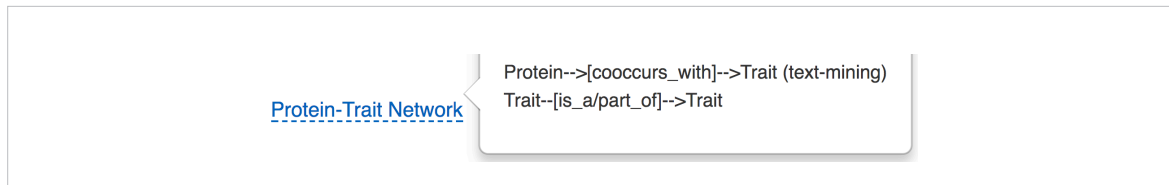
1. Select the files that you want to integrate: for example, go to the Reference sequence > *Arabidopsis thaliana* folder, and select the checkboxes next to the Reference Genome and Protein Sequence files.
2. Open the KnetBuilder application: right-click on your selection, and choose the KnetBuilder application under Analyse. This will take you to the KnetBuilder interface and creates a new file "Knowledge network for ... file".



3. Understand how the KnetBuilder interface works:
  - The Role entries list the different network pieces you can build. Pressing an entry will reveal what nodes and relationships a particular network piece would have. Network pieces that share the same node types will automatically be combined into a larger network. This is basically how the data integration works.
  - The Type entries map various data types into the network pieces. For example, reference genome and protein sequence are used to build a Gene-Protein network. Pressing an entry will reveal details about supported data formats, where/how to get the files, and how it's being transformed into a network.

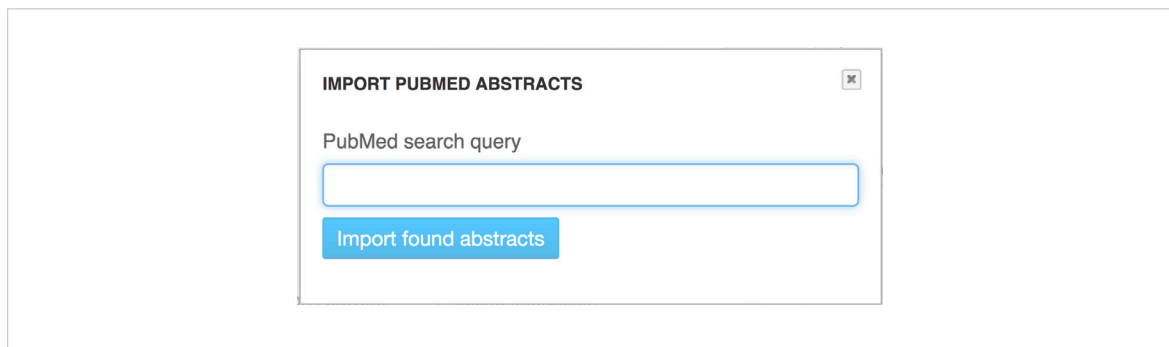
- The File entries show your selected input files for the network.

**Note:** text-mining is an automatic process whenever you supplied a Trait Ontology file. It will go through publication abstracts in the network (those cited in the UniProt Protein Annotation file, or supplied manually as PubMed Abstracts file) and creates co-occurrence relationships for gene-trait pairs that occur frequently in abstracts sentences.














#### 4. Add more data sources to integrate:

- Use the Add file button to bring up a File Chooser. It shows compatible files in the platform that you can use.
- There's also an Import from ... button to download the latest data from frequently-updated databases (such as UniProt and PubMed) with a specified query.

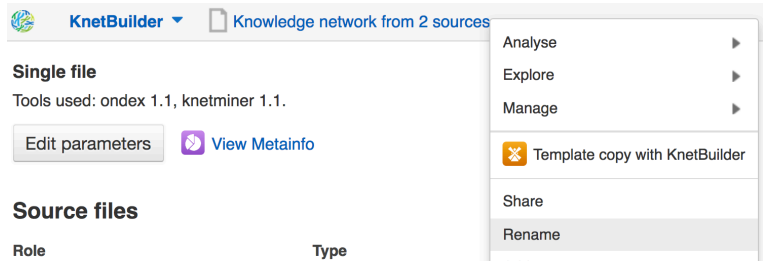


Try adding the Arabidopsis data sources described in the previous section (they're already available in Genestack); this is what you should get in the end:



Role	Type	File	Actions
<a href="#">Gene-Protein Network</a>	<a href="#">Reference Genome</a>	 <a href="#">Arabidopsis thaliana / TAIR10 release 36 (toplevel, unmasked, DNA)</a>	Select another... x
	<a href="#">Protein Sequence</a>	 <a href="#">Arabidopsis thaliana / TAIR10 release 36</a>	Select another... x
<a href="#">Protein Annotation Network</a>	<a href="#">UniProt Protein Annotation</a>	 <a href="#">UniProt protein annotation for Arabidopsis thaliana</a>	Select another... x
	<a href="#">Gene Ontology</a>	 <a href="#">Gene ontology</a>	Select another... x
<a href="#">Publication Abstracts</a>	<a href="#">PubMed Abstracts</a>	 <a href="#">PubMed abstracts for Arabidopsis thaliana</a>	Select another... x
<a href="#">Protein-Trait Network</a>	<a href="#">Trait Ontology</a>	 <a href="#">Trait ontology</a>	Select another... x
<a href="#">Protein-Protein Interaction Network</a>	<a href="#">Proteins Interaction</a>	 <a href="#">Arabidopsis proteins interaction</a>	Select another... x
<a href="#">Pathway</a>	<a href="#">Pathway</a>	 <a href="#">Arabidopsis pathway</a>	Select another... x
<a href="#">SNP-Gene-Trait Network</a>	<a href="#">GWAS</a>	 <a href="#">Arabidopsis GWAS</a>	Select another... x
<a href="#">Gene-GO Network</a>	<a href="#">GO Annotation</a>	 <a href="#">Arabidopsis GO annotation</a>	Select another... x
<a href="#">Drug-Protein Network</a>	<a href="#">DrugBank Data</a>	Add file...	
<a href="#">Protein-Disease Network</a>	<a href="#">OMIM Data</a>	Add file...	
<a href="#">Protein-Protein Homology Network</a>	<a href="#">Proteins Homology</a>	Add file...	
<a href="#">Ondex Network</a>	<a href="#">Ondex Networks</a>	Add file...	
Reference Genome (required for KnetMiner)	<a href="#">Reference Genome</a>	 <a href="#">Arabidopsis thaliana / TAIR10 release 36 (toplevel, unmasked, DNA)</a>	Select another... x

- Name your network file: right-click on the file link to open its file menu, and choose Rename.



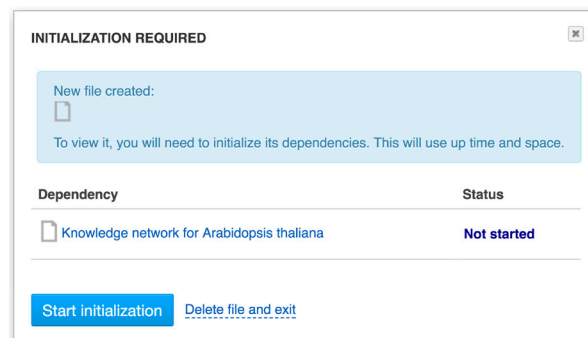
The screenshot shows the KnetBuilder interface. At the top, there is a header with the KnetBuilder logo and a dropdown menu. Below the header, there is a section titled 'Single file' with the text 'Tools used: ondex 1.1, knetminer 1.1.' and two buttons: 'Edit parameters' and 'View Metainfo'. Below this is a section titled 'Source files' with a table header showing 'Role' and 'Type'. A context menu is open over the 'Knowledge network from 2 sources' file, listing actions: 'Analyse', 'Explore', 'Manage', 'Template copy with KnetBuilder', 'Share', and 'Rename'.

6. Open the KnetMiner application: press the KnetMiner link located under Explore Results at the bottom of the page. This will take you to the KnetMiner application, but you will be informed to first “initialize” the file before being able to view it: it’s a computational process to import, transform and integrate individual datasets into a unified knowledge network (find out more about initialization in our general guide [here](#)).

## Explore Results

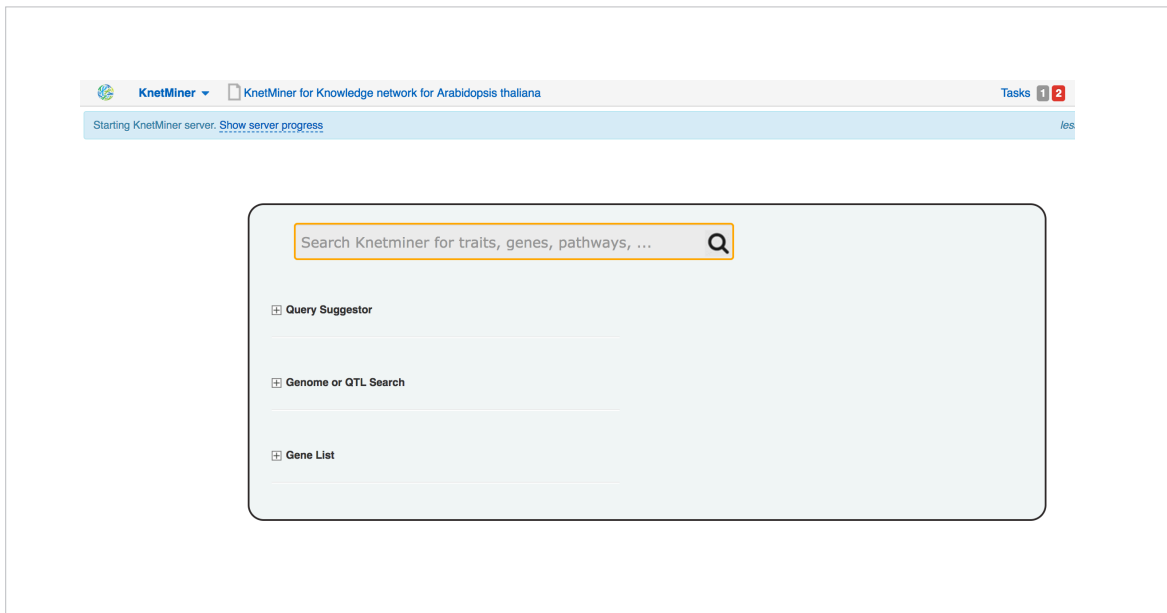


7. Start initialization: press the big blue Start initialization button. This will take about an hour or two, depending on the size of your network. You can just wait for now, or monitor the initialization progress by going to the Task Manager (the link is at the top-right corner of the toolbar).



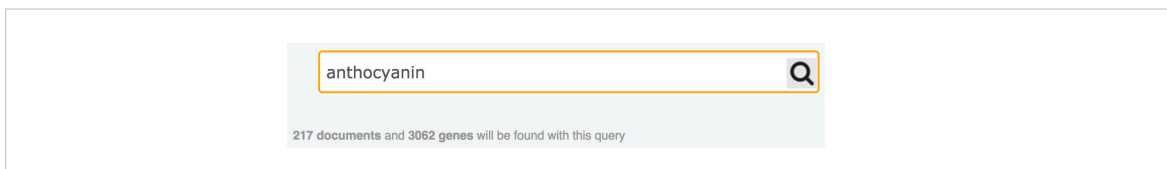
## Exploring the network

1. Open your network using KnetMiner: in case you didn’t try the previous section on building a network, select a pre-built Arabidopsis network in the folder Networks, and open it using KnetMiner.
2. Wait for the KnetMiner server to be ready: when you land on the KnetMiner page, you’ll be welcomed by a notification that a KnetMiner server is being started. This is a special application requiring a running server to handle your large network. Please be patient, it will take a couple of minutes.



3. Performing basic search: use the Google-like search box to enter anything that your network may contain, e.g. phenotype term, pathway term, etc. For example, let's type "anthocyanin", a powerful antioxidant and a type of flavonoid that provides the bright color of many vegetables and fruits. As you type a search term, you'll get a real-time feedback of how many documents and genes will be found.

**Note:** The found documents refer to any nodes in the network that are related to your query, e.g. a biological process involved in anthocyanin formation, or a publication abstract about anthocyanin. The found genes are those genes that are connected to the found documents, either directly or indirectly via other nodes, e.g. a gene encodes an enzyme catalyzed by a reaction in a pathway.

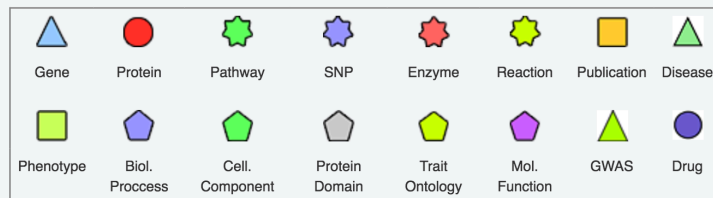


4. Exploring results: when you press the search button, you will get four kinds of results:

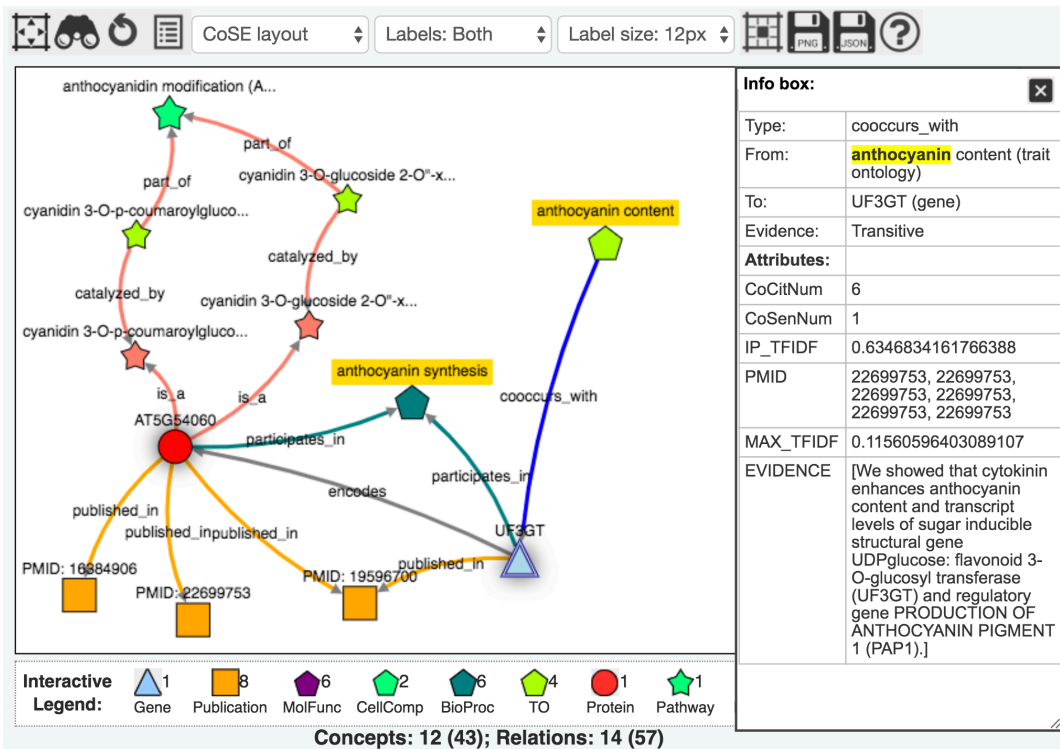
**Gene View** shows a list of genes ranked by relevancy to your search query. The relevancy (quantified by the Score entry) is determined by the number and specificity of the evidence. Evidence is synonymous to what we called documents earlier; here it's grouped by the different genes they're connected with (again, either directly or indirectly). The icons with different shapes and colors correspond to different types of evidence, and the numbers inside them show how many there are.

ACCESSION	CHRO	START	SCORE	USER	QTL	EVIDENCE	Select
5MAT	3	11398592	37.32	no	0		<input type="checkbox"/>
AT1G56650	1	21233555	36.43	no	0		<input type="checkbox"/>
UF3GT	5	21936746	28.13	no	0		<input type="checkbox"/>
LDOX	4	12004726	22.08	no	0		<input type="checkbox"/>
AT5G17220	5	5658416	21.18	no	0		<input type="checkbox"/>
AT4G14090	4	8122188	13.35	no	0		<input type="checkbox"/>
AT1G12910	1	4394897	11.68	no	0		<input type="checkbox"/>

[View Network](#)



**Network View** lets you dig deeper and explore the relationships between the found genes and their evidence by network visualisation. For example, select the gene UF3GT and press the view network button. The visualisation is scalable and interactive: you can filter, expand, and re-layout the network, as well as reveal detailed information about the nodes and edges (right-click on it and press Show info). The info includes references to external databases and publication abstracts. This is particularly interesting for text-mined relationships, where you can access the abstracts that support the gene-trait co-occurrences, e.g. press the blue edge for co\_occurs relation.



**Map View** shows the distribution of the found genes genome-wide. It's highly-scalable and becomes especially interesting when you supply GWAS data (as we do here): SNPs from the GWAS study that are relevant to the search query will be super-imposed on the genome. Moreover, you can filter the SNPs by their strength of association (go to the advanced option in the menu).





**Evidence View** simply provides a summary of all the evidence, and rank them based on the number of connected genes.

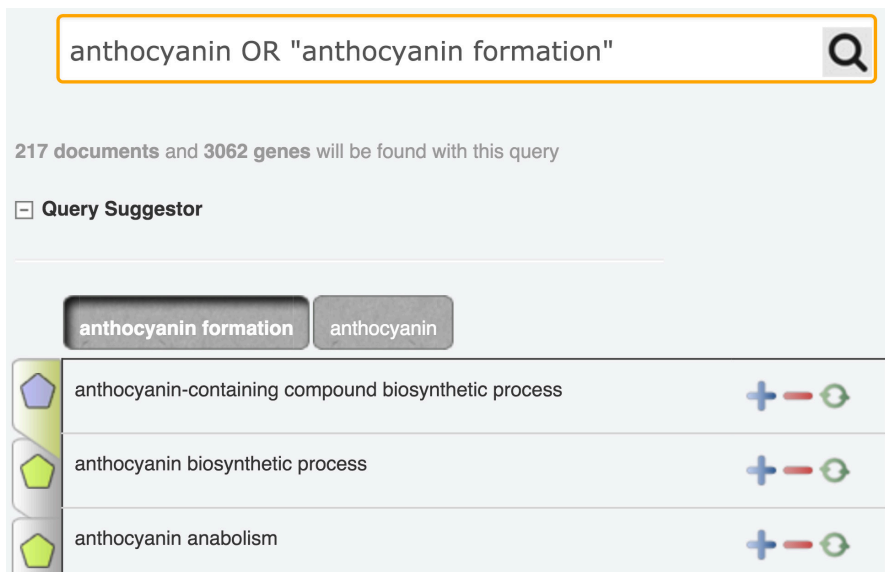
153 42 6 9 3 1 1 1 1

Exclude	TYPE	NAME	SCORE	GENES	USER GENES	QTLs
<input type="checkbox"/>		Results expressed as binary d...	6.39	945	0	0
<input type="checkbox"/>		Results expressed as binary d...	6.39	1015	0	0
<input type="checkbox"/>		Results expressed as binary d...	6.39	931	0	0
<input type="checkbox"/>		Q9LVW3	5.61	1	0	0
<input type="checkbox"/>		anthocyanin anabolism	5.48	19	0	0
<input type="checkbox"/>		anthocyanin content	5.11	51	0	0
<input type="checkbox"/>		regulation of anthocyanin bre...	4.47	1	0	0

Gene	Protein	Pathway	SNP	Enzyme	Reaction	Publication	Disease
Phenotype	Biol. Process	Cell. Component	Protein Domain	Trait Ontology	Mol. Function	GWAS	Drug

5. Performing advanced search: there are three ways to refine your results:

**Query Suggestor** scans the network to identify terms related to your search query. These different terms can be composed together via logical operators ("OR", "AND") to increase the specificity of your search.



The screenshot shows a search interface with a search bar containing the query "anthocyanin OR 'anthocyanin formation'". Below the search bar, it indicates that 217 documents and 3062 genes will be found. A section titled "Query Suggestor" is expanded, showing two buttons for "anthocyanin formation" and "anthocyanin". Below these buttons is a list of three suggested terms, each with a plus, minus, and refresh icon.

Term	Actions
anthocyanin-containing compound biosynthetic process	+ - ↻
anthocyanin biosynthetic process	+ - ↻
anthocyanin anabolism	+ - ↻

**Genome or QTL Search** visualises specified regions in the Map View as prior QTL or limits your search to specific regions (by selecting within region option).

Chromosome	Start	End	Label	Genes
4	9920000	10180000	Seed size	63

[Add or remove region.](#)

whole-genome  within region

**Gene List** highlights user-specified genes (marked on User entries in Gene View) and lets you filter them. You can manually supply this list or by selecting genes from available differential expression analysis results on the platform (use the Select genes from file button).

**Gene List**

- UF3GT
- LDOX








Select genes from file

## Mining multi-species networks


While plant genomes become increasingly available and easy to obtain, it's still expensive and laborious to perform the associated functional studies. This results in a vague and incomplete understanding of their genetics. To help linking their genetics with biological processes and pathways, we therefore take a computational route of inferring functions based on comparative genomics. We'll demonstrate this by using proteins homologies to extend a limited Brassica oleracea network with the information-rich Arabidopsis thaliana network. Using this technique, we've produced over 40 crop networks in the platform, ranging from rice to kale and cabbages.

To build a Brassica oleracea network extended with Arabidopsis thaliana network:

1. Add some Brassica oleracea data to KnetBuilder: for example, let's add reference genome, protein sequence, UniProt protein sequence, PubMed abstracts, as well as gene ontology and trait ontology. You should get something like this:

Role	Type	File	Actions
<a href="#">Gene-Protein Network</a>	<a href="#">Reference Genome</a>	 Brassica oleracea / v2.1 release 36 (toplevel, unmasked, DNA)	Select another... x
	<a href="#">Protein Sequence</a>	 Brassica oleracea / v2.1 release 36	Select another... x
<a href="#">Protein Annotation Network</a>	<a href="#">UniProt Protein Annotation</a>	 UniProt protein annotation for Brassica oleracea	Select another... x
	<a href="#">Gene Ontology</a>	 Gene ontology	Select another... x
<a href="#">Publication Abstracts</a>	<a href="#">PubMed Abstracts</a>	 PubMed abstracts for Brassica oleracea	Select another... x
<a href="#">Protein-Trait Network</a>	<a href="#">Trait Ontology</a>	 Trait ontology	Select another... x
<a href="#">Protein-Protein Interaction Network</a>	<a href="#">Proteins Interaction</a>	Add file...	
<a href="#">Pathway</a>	<a href="#">Pathway</a>	Add file...	
<a href="#">SNP-Gene-Trait Network</a>	<a href="#">GWAS</a>	Add file...	
<a href="#">Gene-GO Network</a>	<a href="#">GO Annotation</a>	Add file...	
<a href="#">Drug-Protein Network</a>	<a href="#">DrugBank Data</a>	Add file...	
<a href="#">Protein-Disease Network</a>	<a href="#">OMIM Data</a>	Add file...	
<a href="#">Protein-Protein Homology Network</a>	<a href="#">Proteins Homology</a>	Add file...	
Ondex Network	<a href="#">Ondex Networks</a>	Add file...	
Reference Genome (required for KnetMiner)	<a href="#">Reference Genome</a>	 Brassica oleracea / v2.1 release 36 (toplevel, unmasked, DNA)	Select another... x

2. Add an Arabidopsis thaliana network to KnetBuilder:

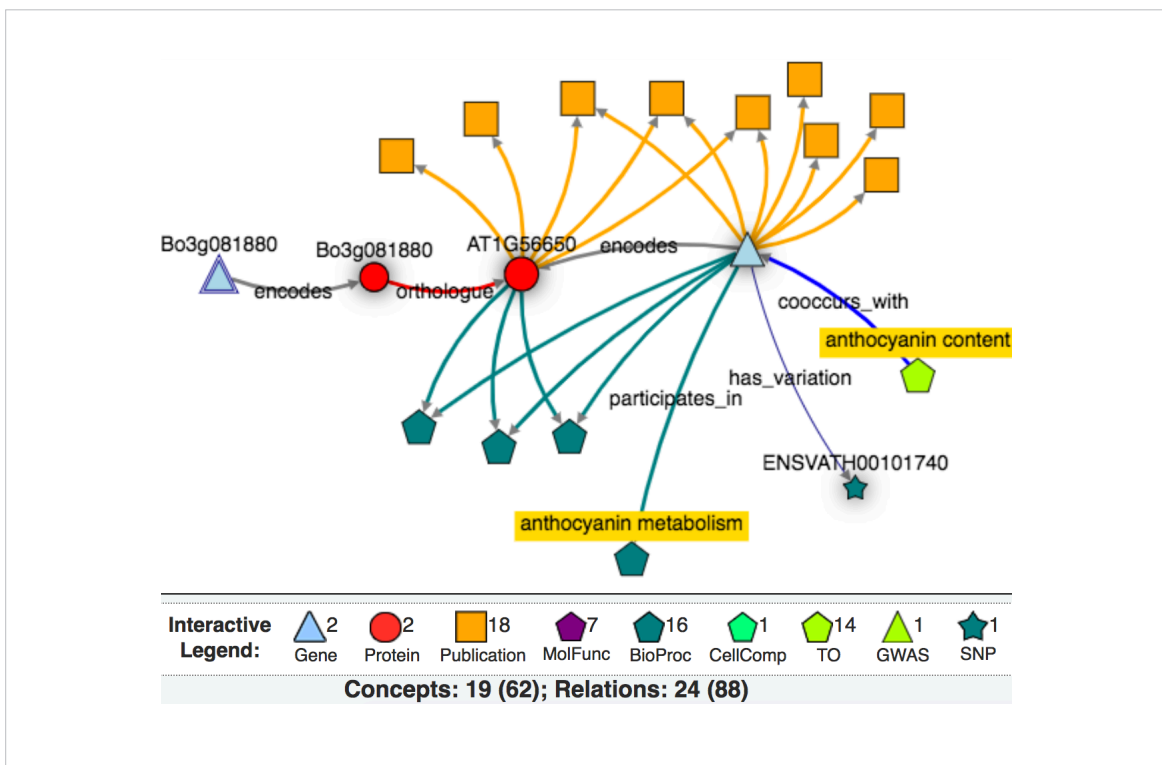
Ondex Network	<a href="#">Ondex Networks</a>	 Knowledge network for Arabidopsis thaliana
---------------	--------------------------------	--

3. Add a homology file to Knetbuilder: this is used to link the Brassica Oleracea proteins with the Arabidopsis thaliana proteins, and thus combining the two networks. There are two ways to provide a homology file:
  - By importing a two-column text file where each row is a pair homologous proteins between two species.
  - By producing it in the platform using Infer Homology application. This application takes protein sequences from two species as input and runs the OMA tool to produce a homology file.

Homology files between Arabidopsis thaliana and several organisms have been imported from Ensembl, and are available in the folder Proteins Homologies. Let's use the one between Arabidopsis thaliana and Brassica Oleracea:

[Protein-Protein Homology Network](#)
[Proteins Homology](#)
 [Proteins homology for Arabidopsis thaliana and Brassica oleracea](#)

When you search the network, you will find Brassica oleracea genes supported by evidence from Arabidopsis thaliana. For example, if you search "anthocyanin" again on the Brassica oleracea network in the networks folder, and view the network for gene Bo3g081880, you should see some orthologue relations:



## Mining a human neurodegenerative network

The Genestack-KnetMiner module is readily applicable to any organism and research subject. To illustrate, we'll go beyond the world of plants, and explore a network of neurodegenerative diseases for a subset of human proteins that are known to be relevant for Alzheimer, Parkinson, and Huntington diseases. We'll draw data from OMIM, DrugBank, and literature, to pick up interesting (co-)relationships between drugs, proteins and diseases.

### Importing data sources










We'll be using the following data sources. They have been imported into Genestack and available in the folder Human neurodegenerative disease.

1. Reference genome, protein sequence, and UniProt protein annotation
  - We will use Ensembl's [DNA fasta file](#) and [annotation gtf file](#)
  - We will use Ensembl's [protein sequence fasta file](#), but subsetted to 33 proteins. You can find the subsetted version [here](#)
  - We will use [UniProt](#) protein annotation on these 33 proteins. You can find the subsetted version [here](#)
2. OMIM phenotype terms for Alzheimer, Parkinson, and Huntington diseases
  - Go to [OMIM](#)
  - Type "alzheimer parkinson huntington" in the search bar
  - Select "Title" in Search in option
  - Select "# phenotype description" in MIM Number Prefix
  - Download as tab-delimited file
3. Drug-target interactions
  - Go to [DrugBank](#)
  - Add Search Condition: "target uniprot" & "is present"
  - Add Display Fields: DrugBankID, Name, Smallmolecule, Biotech, Target uniprot, Target name
  - Press search and then export results
4. Protein-protein interaction related to Alzheimer and Parkinson
  - Go to [IntAct](#)
  - Open advanced field and choose Dataset = "Alzheimers" (and also repeat this for "Parkinson")
  - Download as MI-TAB 2.7 format
5. Human GWAS catalogue
  - Get it from Ensembl [here](#)



## Building the network

Select all these files and open them in KnetBuilder:

Role	Type	File	Actions
<a href="#">Gene-Protein Network</a>	<a href="#">Reference Genome</a>	 Homo sapiens / GRCh38 release 85 (primary assembly, unmasked, DNA)	Select another... x
	<a href="#">Protein Sequence</a>	 33 Human protein sequences	Select another... x
<a href="#">Protein Annotation Network</a>	<a href="#">UniProt Protein Annotation</a>	 UniProt protein annotation for 33 human proteins	Select another... x
	<a href="#">Gene Ontology</a>	 Gene ontology	Select another... x
<a href="#">Publication Abstracts</a>	<a href="#">PubMed Abstracts</a>	Add file... Import from PubMed...	
<a href="#">Protein-Trait Network</a>	<a href="#">Trait Ontology</a>	Add file...	
<a href="#">Protein-Protein Interaction Network</a>	<a href="#">Proteins Interaction</a>	 IntAct proteins interactions for Alzheimer and Parkinson	Select another... x
<a href="#">Pathway</a>	<a href="#">Pathway</a>	Add file...	
<a href="#">SNP-Gene-Trait Network</a>	<a href="#">GWAS</a>	 GWAS for human	Select another... x
<a href="#">Gene-GO Network</a>	<a href="#">GO Annotation</a>	Add file...	
<a href="#">Drug-Protein Network</a>	<a href="#">DrugBank Data</a>	 DrugBank data	Select another... x
<a href="#">Protein-Disease Network</a>	<a href="#">OMIM Data</a>	 OMIM data	Select another... x
<a href="#">Protein-Protein Homology Network</a>	<a href="#">Proteins Homology</a>	Add file...	
Ondex Network	<a href="#">Ondex Networks</a>	Add file...	
Reference Genome (required for KnetMiner)	<a href="#">Reference Genome</a>	 Homo sapiens / GRCh38 release 85 (primary assembly, unmasked, DNA)	Select another... x

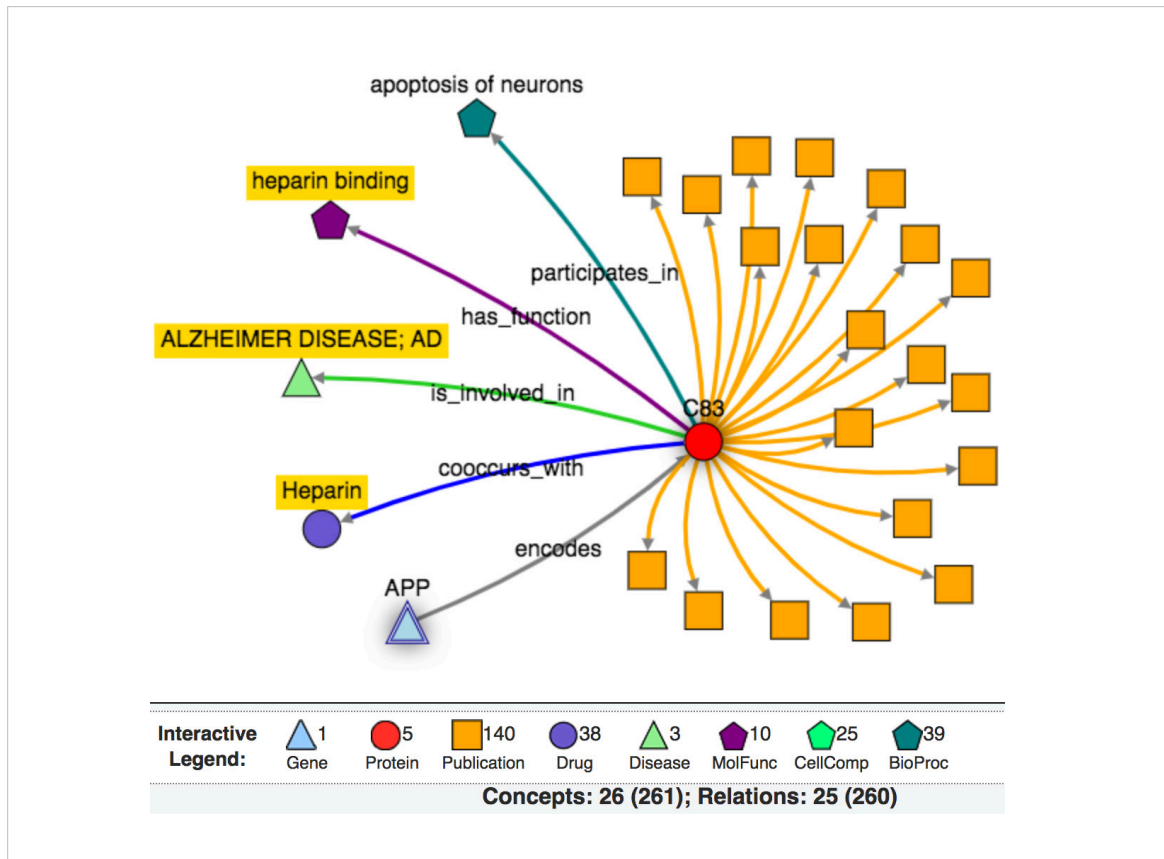
The main difference between this example and the plants example is the use of OMIM and Drug-Bank data:

1. The OMIM data is used to build a protein-disease network. Publications cited in the UniProt protein annotation are mined for which proteins are associated with which diseases.
2. The DrugBank data is used to build a drug-protein network: which drugs target which proteins.

Thus, these two data are integrated to infer indirect relationships: which drugs are associated with which diseases.

## Exploring the network

1. Open your network using KnetMiner: in case you didn't try the previous section on building a network, select a pre-built Human neurodegenerative network in the folder Human neurodegenerative disease > Networks, and open it using KnetMiner.
2. As an example query, search Heparin OR Alzheimer OR "cell death" to find a potential link between Heparin, Alzheimer and cell death.

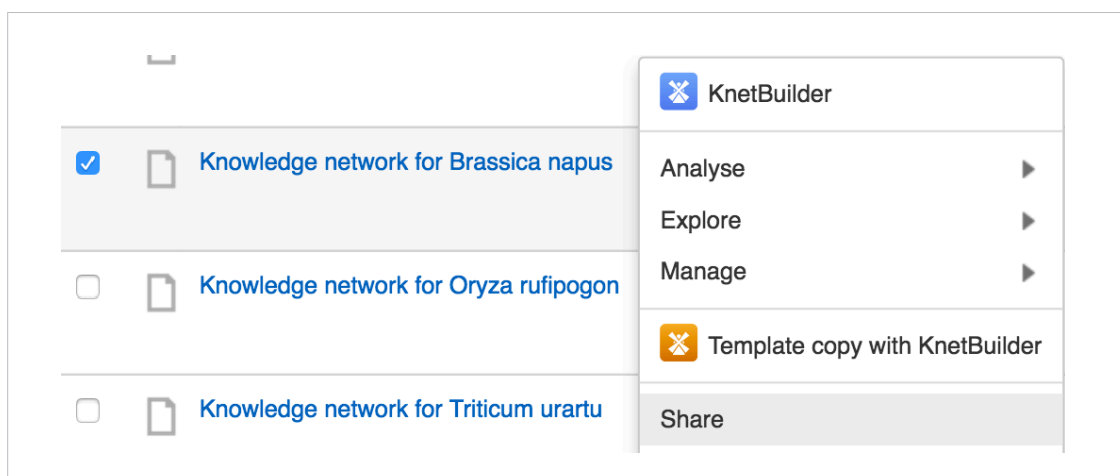


## Sharing, reproducing, and updating networks

### Sharing the entire knowledge network

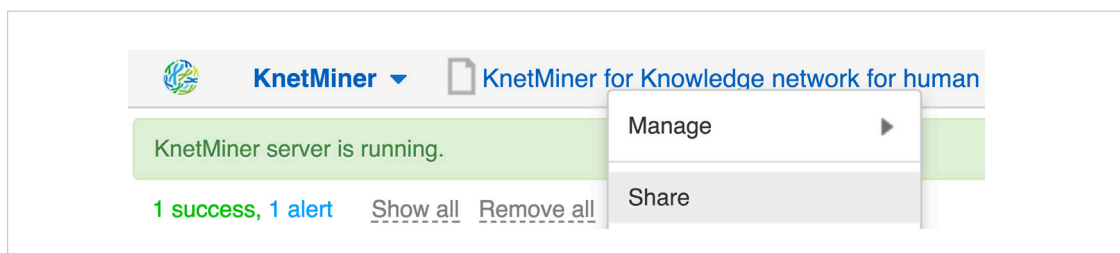
You can share the entire knowledge network by:

1. Opening its file menu
2. Press share
3. And choose the group to share it with



### Sharing KnetMiner results

You can also share your KnetMiner results. All your search query and results, including visualisation of subnetworks, are automatically saved and can be shared by sharing the KnetMiner page itself:



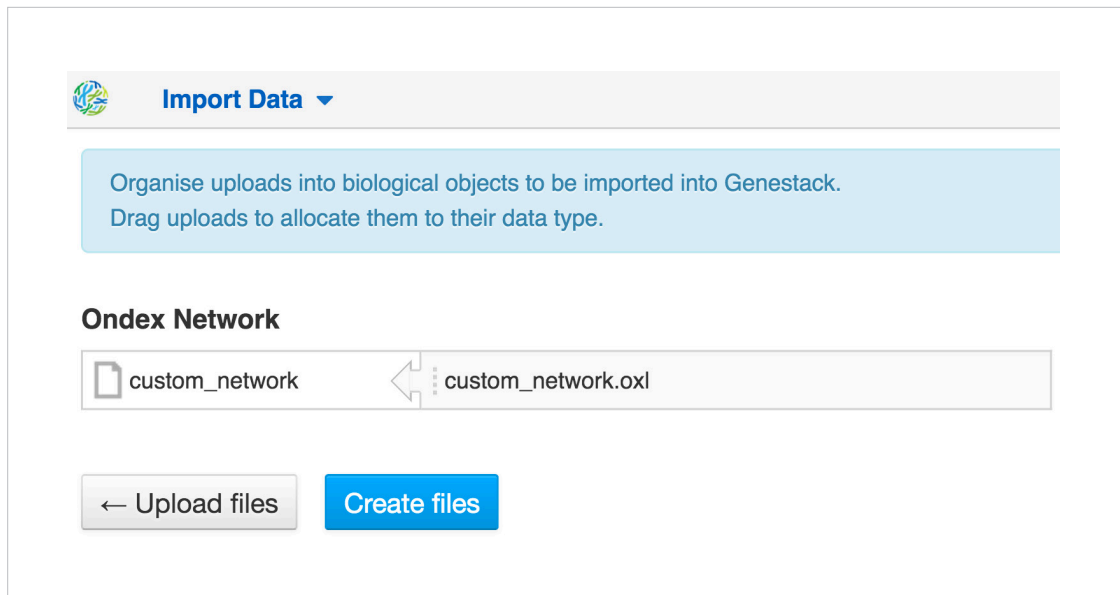
### Reproducing and updating your knowledge network

Like any other analysis done in Genestack, all the steps including inputs, applications, and parameters, are recorded and can be replayed or modified. See our general guide [here](#).

## Importing networks built outside Genestack

You could import and combine [Ondex](#) network in Genestack as follow:

1. Go to the importer and import your .oxl file.



2. Open the network in KnetBuilder:
  - To use it on its own, you need to additionally supply a reference genome, so KnetMiner can decide which genes should be target of the evidence-based search, as well displaying the right genome visualization.
  - Alternative, you can use it as an extension to another network, e.g. see the section on "Mining multi-species networks".
3. Once your imported .oxl file is processed in KnetBuilder, you can explore it as usual in KnetMiner.

