Installing SynteView

There are two main ways using SynteView. In the Web service mode, SynteView is retrieving computed data from our database SynteBase. Alternatively, to visualize your home made synteny data from a local synteny database, you will use the local access mode.

Using SynteView Web service

There is nothing to install if your operating system contains Java (version >= 1.5),. Clicking on the Java Web Start link will launch SynteView by linking on the SynteView Web site.

Using SynteView in local access mode

1. Setting up the Database

A PostgreSQL database has to be built to contain your home-made synteny data. Your are free to design your schema but the database must contain mandatory data about

Proteins (identifier, coding strand, sequence, function, and length),

genomes (species name, species name abbreviation, strain name, taxonomy), and

synteny blocks (id, and pairs of orthologous proteins belonging to this block).

2. Configuring SynteView

Once the database is operational, several mandatory queries must be introduced that are required for visualizing gene order and conserved synteny blocks.

1. retrieving information on all genomes listed in the database:

   ```
   SELECT abbreviation,taxonomy,speciesname,nbprotein
   FROM ...
   WHERE ...
   ```

   Here, the abbreviation field stands for a short name of the species. It will be displayed in the synteny panel for visualization purpose. The taxonomy must be in the form of a list of node names, separated by a ";". The speciesname field describes the full name of the species, including the strain name if any. The nbprotein field specifies the number of proteins encoded by the genome of the species.

2. retrieving information on proteins:

   ```
   SELECT pid, chromosome, species, function, start, stop, genename, length
   FROM ...
   WHERE ...pid=%pid
   ```

   Here, the condition pid=%pid is mandatory. SynteView will replace, when necessary, %pid by the identifier of the protein under analysis. The pid field stands for the identifier of the protein, which has to be an integer. The chromosome field stands for the name of the replicon in which the gene encoding the protein under analysis is located. The species field stands for the short name of the species related to the protein. "function" is a string field representing a text description of the functional annotation of the protein. Start, stop, genename, are fields describing properties of the gene encoding the protein under analysis, respectively, and length is the amino acids length of the protein.

3. retrieving information on a genome:

```
SELECT pid, genename, strand, start, chromosome, function
FROM ...
WHERE ... abbreviation='%spabrv'
```

The condition abbreviation='%spabrv' is mandatory. SynteView will replace %spabrv by the corresponding species abbreviation when necessary. The definition of the different fields is as previously described.

4. retrieving information on syntenic blocks:

```
SELECT blockid, pid1, strand1, start1, stop1, genename1, pid2, strand2,
genename2
FROM ...
WHERE ... abbreviation1= %spabrv and abbreviation2 in (%sptab)
```

Here, the pid1, strand1, start1, and abbreviation1 stand for information about the reference genome "%spabrv", and the pid2, etc. for information about the compared genomes "%sptab".

Instruction manual

Initializing SynteView before use

To use the local acces mode, please fill in the database connection fields on the settings panel as follows: database server name, port, login, and password. Note that these fields are filled in by default in the web service mode.

Tool bar

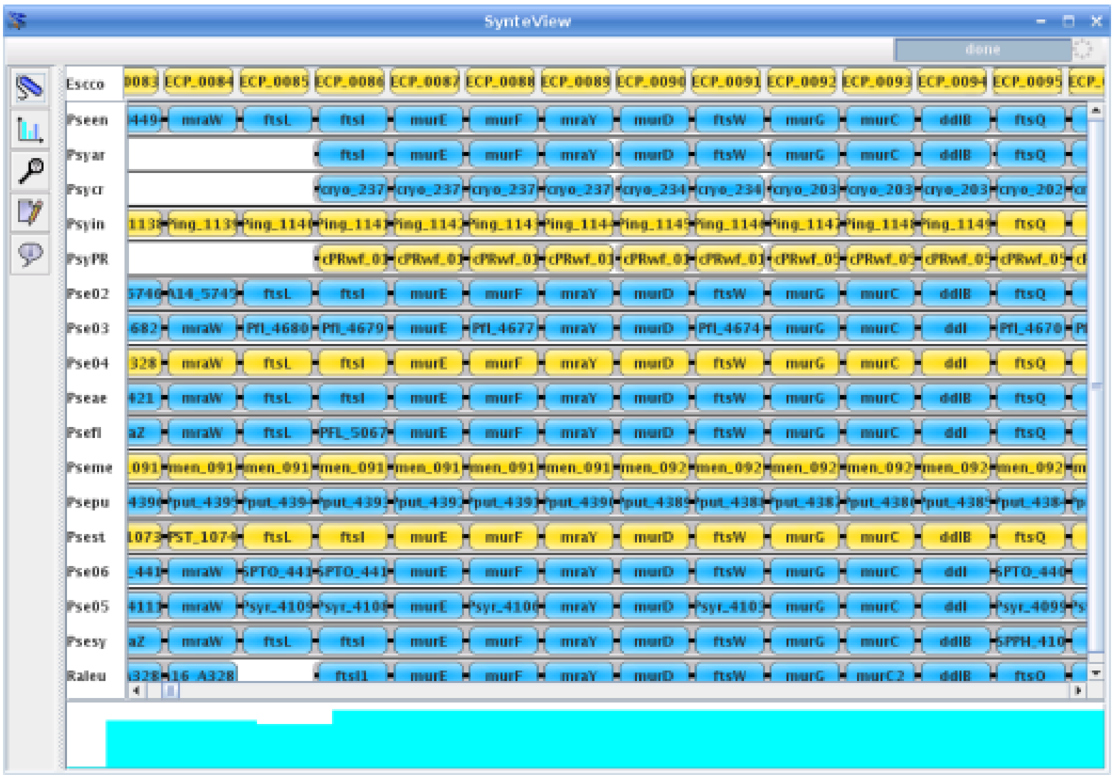
All the actions that can be performed with SynteView are accessible via the toolbar on the left hand side of the graphical user interface. Various buttons allow to display the following panels:

🖌	Choosing the reference species and the set of compared species
📊	Building histograms representing the size distribution of the synteny blocks
🔍	Showing and searching proteins information
✎	Opening the preferences dialog
💬	Opening the about panel
💾	Saving synteny data as CSV

The buttons accessible on the ToolBar

The central panel

It displays the strict conservation of gene order, in comparing to a reference species (first line), chosen by the user, all other available species which are automatically sorted by taxonomy. Each gene present in the genome of the reference species is depicted by a rectangle with a color code: blue (positive strand) or yellow (negative strand). Grey rectangles are genes without orthologs belonging to a synteny block in another species.

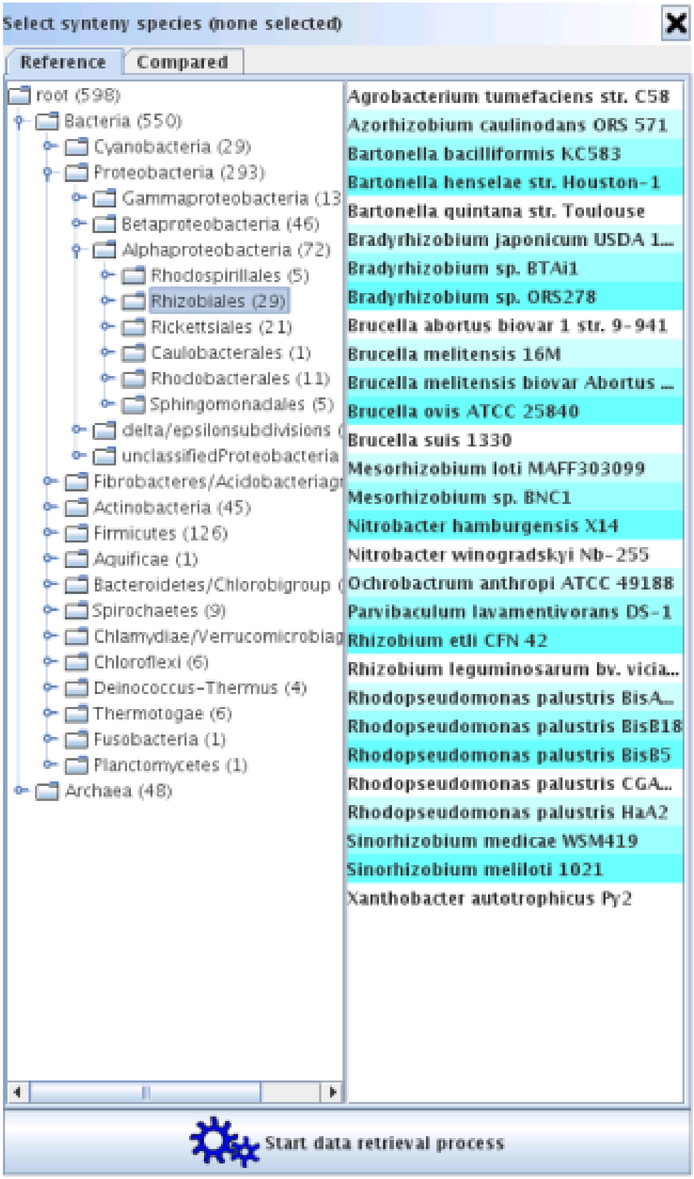


Conserved gene neighbouring in the compared species are exhibited in the next lines using the same colour code. Please remember that blocks which appear as adjacent in compared genomes are not necessarily physically neighbouring in the actual genome.

Choosing the reference species and the set of compared species

The figure below shows the species choosing panel. It contains two tabs. The first one is dedicated to choose the reference species, and the second one to choose the set of compared species. All these process are guided with the species taxonomy (according to the NCBI).

Selecting the reference species



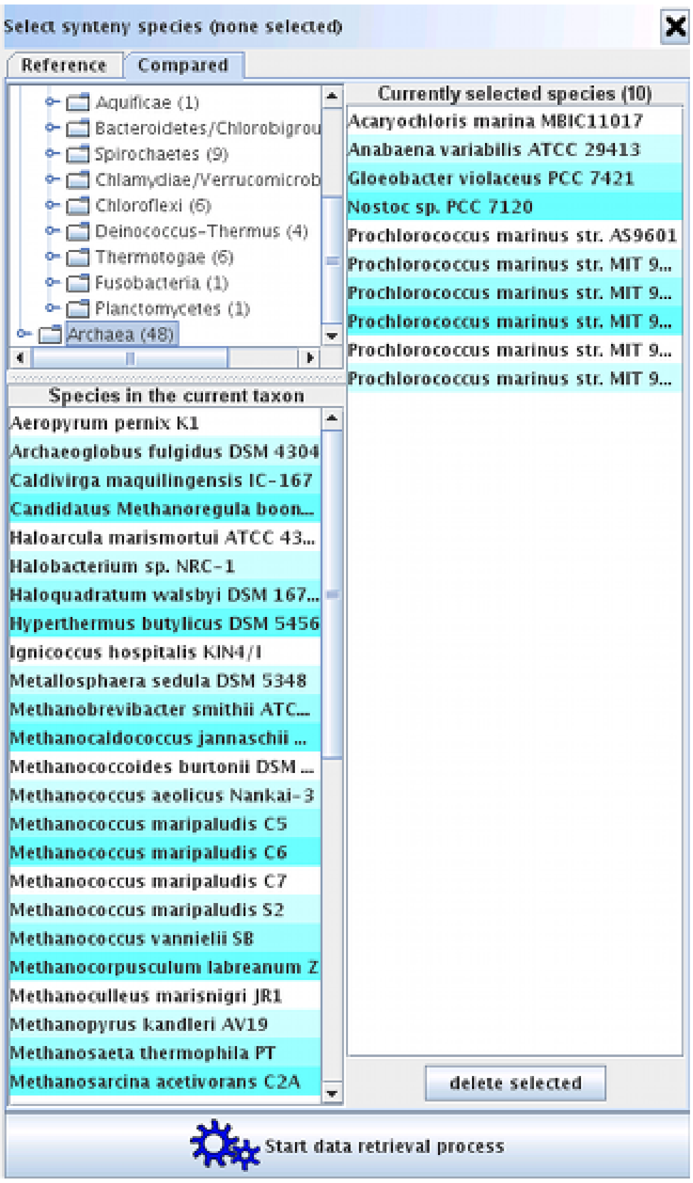
- root (598)
  - Bacteria (550)
    - Cyanobacteria (29)
    - Proteobacteria (293)
      - Gammaproteobacteria (13
      - Betaproteobacteria (46)
      - Alphaproteobacteria (72)
        - Rhodospirillales (5)
        - Rhizobiales (29)
        - Rickettsiales (21)
        - Caulobacterales (1)
        - Rhodobacterales (11)
        - Sphingomonadales (5)
      - delta/epsilonsubdivisions (
      - unclassifiedProteobacteria
    - Fibrobacteres/Acidobacteriagr
    - Actinobacteria (45)
    - Firmicutes (126)
    - Aquificae (1)
    - Bacteroidetes/Chlorobigroup (
    - Spirochaetes (9)
    - Chlamydiae/Verrucomicrobiag
    - Chloroflexi (6)
    - Deinococcus-Thermus (4)
    - Thermotogae (6)
    - Fusobacteria (1)
    - Planctomycetes (1)
  - Archaea (48)

Agrobacterium tumefaciens str. C58
Azorhizobium caulinodans ORS 571
Bartonella bacilliformis KC583
Bartonella henselae str. Houston-1
Bartonella quintana str. Toulouse
Bradyrhizobium japonicum USDA 1...
Bradyrhizobium sp. BTAi1
Bradyrhizobium sp. ORS278
Brucella abortus biovar 1 str. 9-941
Brucella melitensis 16M
Brucella melitensis biovar Abortus ...
Brucella ovis ATCC 25840
Brucella suis 1330
Mesorhizobium loti MAFF303099
Mesorhizobium sp. BNC1
Nitrobacter hamburgensis X14
Nitrobacter winogradskyi Nb-255
Ochrobactrum anthropi ATCC 49188
Parvibaculum lavamentivorans DS-1
Rhizobium etli CFN 42
Rhizobium leguminosarum bv. vicia...
Rhodopseudomonas palustris BisA...
Rhodopseudomonas palustris BisB18
Rhodopseudomonas palustris BisB5
Rhodopseudomonas palustris CGA...
Rhodopseudomonas palustris HaA2
Sinorhizobium medicae WSM419
Sinorhizobium meliloti 1021
Xanthobacter autotrophicus Py2

When browsing the taxonomy, please select a particular taxon (for instance, Rhizobiales). Once selected (on the left hand side of the panel), all the species contained in this taxon are displayed on the right hand side of the panel. Clicking on a particular species will select it as a reference species.

Selecting the compared species

When browsing the species tree and selecting a particular taxon as described above, its species are displayed and can be drag and drop to the right panel. This can be repeated. For instance, in the screenshot below, several cyanobacteria have been selected and it is now possible to add various archaeal species.



Currently selected species (10)

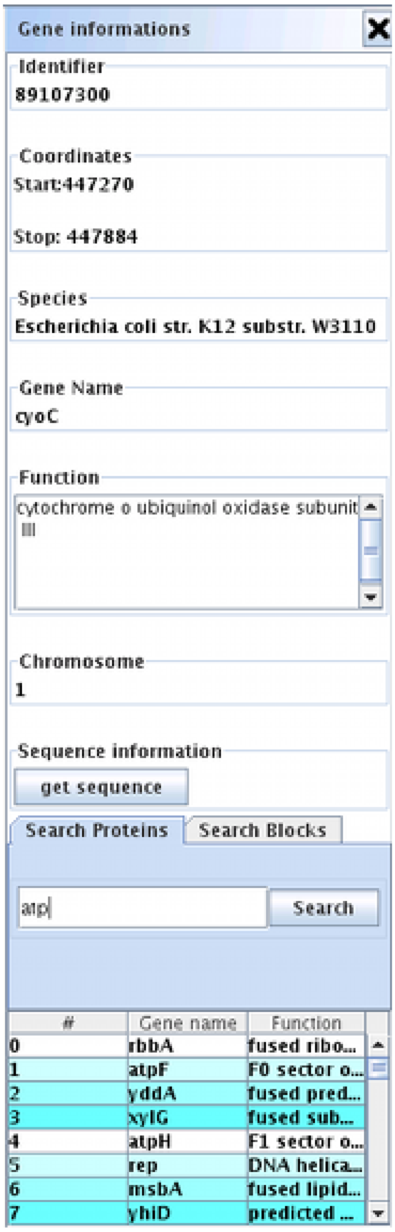
- Acaryochloris marina MBIC11017
- Anabaena variabilis ATCC 29413
- Gloeobacter violaceus PCC 7421
- Nostoc sp. PCC 7120
- Prochlorococcus marinus str. AS9601
- Prochlorococcus marinus str. MIT 9...
- Prochlorococcus marinus str. MIT 9...
- Prochlorococcus marinus str. MIT 9...
- Prochlorococcus marinus str. MIT 9...
- Prochlorococcus marinus str. MIT 9...

Species in the current taxon

- Aeropyrum pernix K1
- Archaeoglobus fulgidus DSM 4304
- Caldivirga maquilingensis IC-167
- Candidatus Methanoregula boon...
- Haloarcula marismortui ATCC 43...
- Halobacterium sp. NRC-1
- Haloquadratum walsbyi DSM 167...
- Hyperthermus butylicus DSM 5456
- Ignicoccus hospitalis KIN4/I
- Metallosphaera sedula DSM 5348
- Methanobrevibacter smithii ATC...
- Methanocaldococcus jannaschii ...
- Methanococcoides burtonii DSM ...
- Methanococcus aeolicus Nankai-3
- Methanococcus maripaludis C5
- Methanococcus maripaludis C6
- Methanococcus maripaludis C7
- Methanococcus maripaludis S2
- Methanococcus vannielii SB
- Methanocorpusculum labreanum Z
- Methanoculleus marisnigri JR1
- Methanopyrus kandleri AV19
- Methanosaeta thermophila PT
- Methanosarcina acetivorans C2A

Gene information Panel

Clicking on either a specific gene or on the button (3) opens an information panel (located on the left hand side) that shows several data such as its gi number (identifier), the name of its species (Species), its location (Chromosome, Start, Stop), its name (Gene name), and its function (Function) as described in GenBank.



Identifier
89107300

Coordinates
Start:447270

Stop: 447884

Species
Escherichia coli str. K12 substr. W3110

Gene Name
cyoC

Function
cytochrome o ubiquinol oxidase subunit III

Chromosome
1

Sequence information

atp

#	Gene name	Function
0	rbbA	fused ribo...
1	atpF	F0 sector o...
2	yddA	fused pred...
3	xylG	fused sub...
4	atpH	F1 sector o...
5	rep	DNA helica...
6	msbA	fused lipid...
7	yhiD	predicted ...

Moreover, the frame "Sequence information" allows getting the amino acid sequence (in Fasta format) encoded by the selected gene, as well as the amino acid sequence of its orthologues in other species.

In the "Search proteins" tab, a text field allows the user to query the database. For example, searching "atp" will open a window listing all related genes. Clicking on these genes allow to look at their conservation in the selected species.

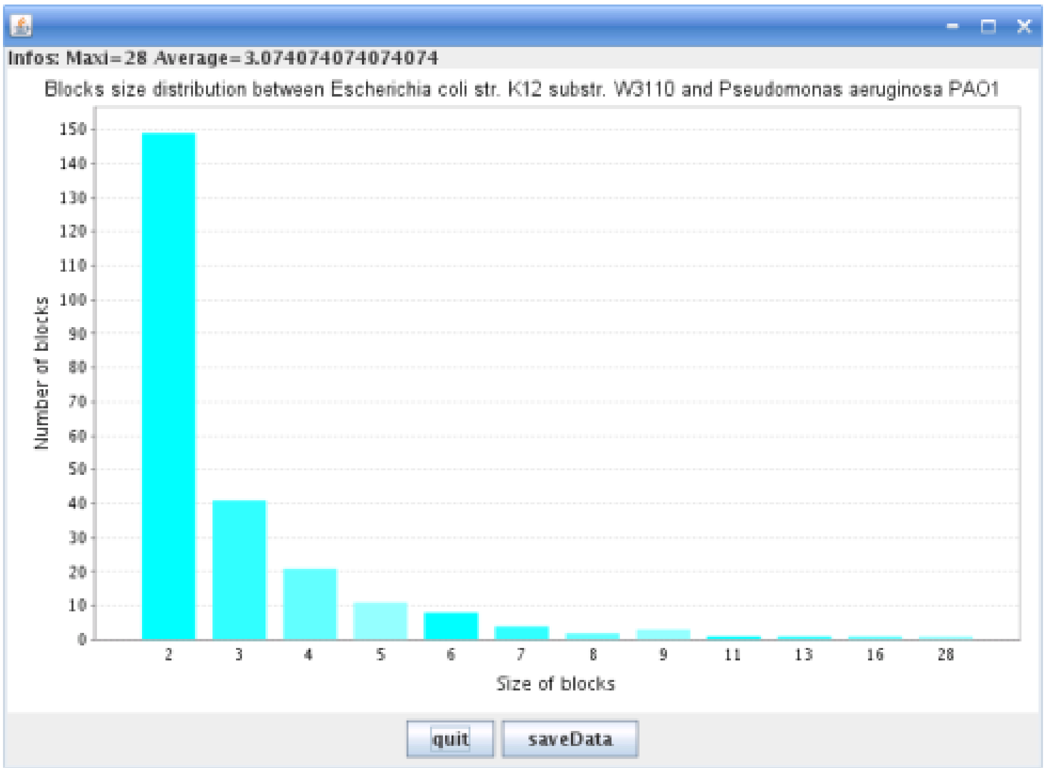
Finally, in the "Search blocks" tab, one can search synteny blocks containing at least x adjacent genes and having orthologous genes in at least y species. x and y can be parametrized with sliders.

Histogram

In the bottom, a histogram shows for each gene the percentage of species in which this gene is belonging to a synteny block found in the reference species. Accordingly, one can see the width of large intervals where synteny is well conserved such as in operons for instance.

Statistical analysis

Besides visualizing gene order, SynteView can compute the size distribution of synteny blocks. Clicking the menu button (2) opens a new panel allowing choosing a species to be compared with the reference species. Once this species is chosen, the distribution of the size of synteny blocks between both species is automatically computed and shown as a histogram.



Infos: Maxi=28 Average=3.074074074074074

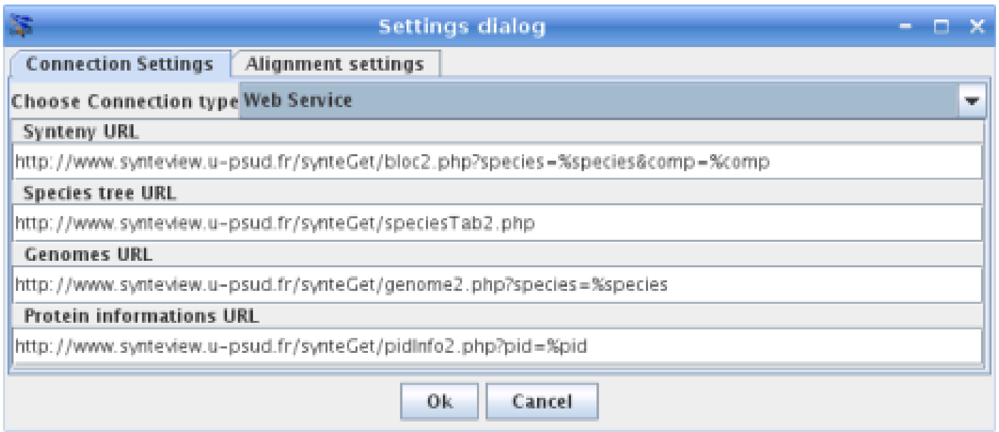
The example above shows the size distribution of synteny blocks that are conserved between the two gammaproteobacteria *Escherichia coli* and *Pseudomonas aeruginosa*.

Settings

First tab: Database access

This tab gathers several settings and the available information is dependent on the mode on which you want to use SynteView.

- If you use the Web service mode, SynteView needs the URLs from which it can retrieve the data. These URLs are filled by default.
- In the local acces mode, SynteView needs not only the database access information, but also the queries that are described in the section "Initializing SynteView before use".



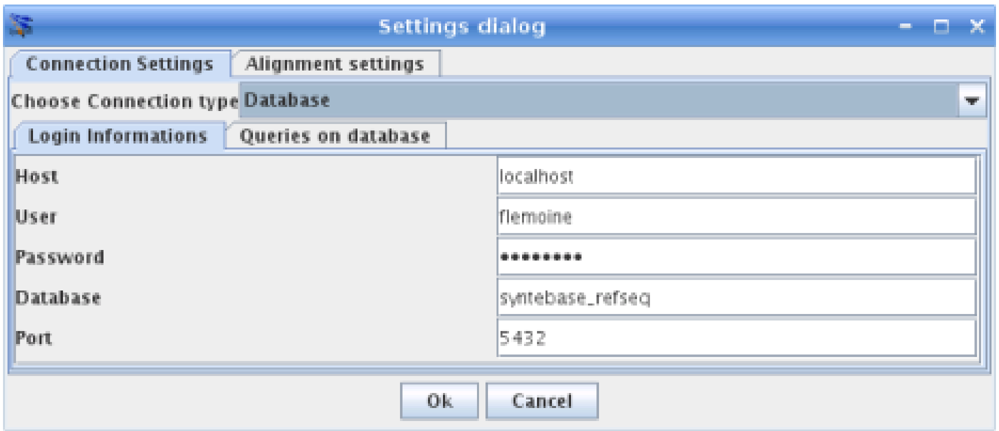
Choose Connection type: Web Service

Synteny URL: http://www.synteview.u-psud.fr/synteGet/bloc2.php?species=%species&comp=%comp

Species tree URL: http://www.synteview.u-psud.fr/synteGet/speciesTab2.php

Genomes URL: http://www.synteview.u-psud.fr/synteGet/genome2.php?species=%species

Protein informations URL: http://www.synteview.u-psud.fr/synteGet/pidInfo2.php?pid=%pid



Choose Connection type: Database

Host	localhost
User	flemoine
Password	•••••••••
Database	syntebase_refseq
Port	5432