



## BIONUMERICS Tutorial:

# ***Salmonella* functional genotyping: predicting phenotypic traits from whole genome sequences**

## 1 Aim

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In this tutorial we will screen whole genome sequences of *Salmonella* samples for phenotypic traits such as serotype, virulence and antibiotic resistance using the *Salmonella functional genotyping plugin*. The plugin also allows you to detect phages.

The different steps are illustrated using the whole genome demonstration database of *Salmonella*. This database is available for download on our website (see [2](#)) and contains 62 publicly available sequence read sets of *Salmonella* with already calculated de novo assemblies.

## 2 Preparing the database

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### 2.1 Introduction to the demonstration database

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We provide a **WGS demo database** for *Salmonella* containing sequence read set data links for 62 samples, calculated de novo assemblies and wgMLST results (allele calls and quality information).



The wgMLST workflow and results will not be discussed in this tutorial.

The **WGS demo database** for *Salmonella* can be downloaded directly from the *BIONUMERICS Startup* window (see [2.2](#)), or restored from the back-up file available on our website (see [2.3](#)).

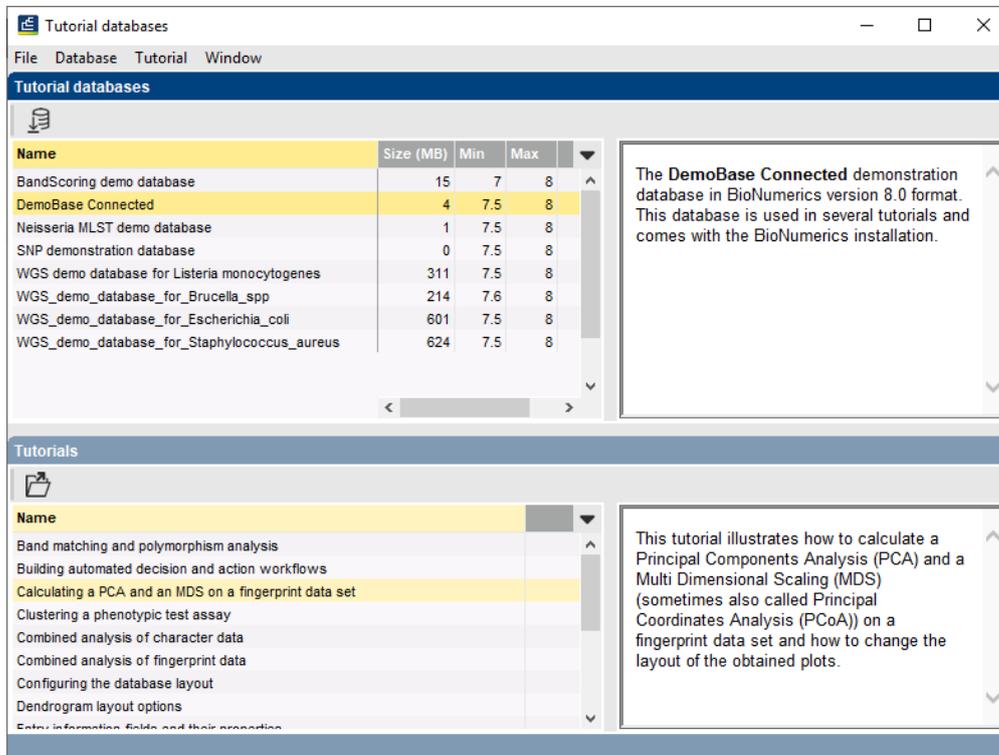
Installation of the *Salmonella functional genotyping plugin* is only possible when no spaces are present in the BIONUMERICS home directory and in the name of the database. Before downloading or restoring the **WGS demo database** for *Salmonella*, please check if your BIONUMERICS home directory does not contain any spaces:

1. Click the  button, located in the toolbar in the *BIONUMERICS Startup* window and select **Change home directory...** to call the *Home directory* dialog box.
2. In case the currently specified home directory contains spaces, update the path to a path containing no spaces and close the *Home directory* dialog box.

## 2.2 Option 1: Download demo database from the Startup Screen

3. Click the  button, located in the toolbar in the *BIONUMERICS Startup* window.

This calls the *Tutorial databases* window (see Figure 1).



**Figure 1:** The *Tutorial databases* window, used to download the demonstration database.

4. Select **WGS\_demo\_database\_for\_Salmonella** from the list and select **Database > Download** (.
5. Confirm the installation of the database and press **<OK>** after successful installation of the database.
6. Close the *Tutorial databases* window with **File > Exit**.

The **WGS\_demo\_database\_for\_Salmonella** appears in the *BIONUMERICS Startup* window.

7. Double-click the **WGS\_demo\_database\_for\_Salmonella** in the *BIONUMERICS Startup* window to open the database.

## 2.3 Option 2: Restore demo database from back-up file

A BIONUMERICS back-up file of the demo database for *Salmonella* is also available on our website. This backup can be restored to a functional database in BIONUMERICS.

8. Download the file `WGS_Sal1m.bnbk` file from <https://www.applied-maths.com/download/sample-data>, under 'WGS\_demo\_database\_for\_Salmonella'.



In contrast to other browsers, some versions of Internet Explorer rename the WGS\_Salm.bnbk database backup file into WGS\_Salm.zip. If this happens, you should manually remove the .zip file extension and replace with .bnbk. A warning will appear ("If you change a file name extension, the file might become unusable."), but you can safely confirm this action. Keep in mind that Windows might not display the .zip file extension if the option "Hide extensions for known file types" is checked in your Windows folder options.

9. In the *BIONUMERIC*S Startup window, press the  button. From the menu that appears, select **Restore database...**
10. Browse for the downloaded file and select **Create copy**. Note that, if **Overwrite** is selected, an existing database will be overwritten.
11. Specify a new name for this demonstration database, e.g. "WGS\_Salmonella\_demobase".
12. Click <OK> to start restoring the database from the backup file.
13. Once the process is complete, click <Yes> to open the database.

The *Main* window is displayed (see Figure 2).

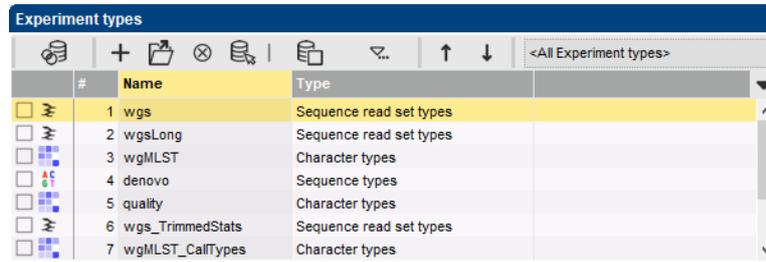
Key	Modified date	Organism	Serovar	NCBI	Resistance genes	NDARO	Run_accession
SRR3724530	2020-07-15 20:50:11	Salmonella enterica	29 e.h.				SRR3724530
SRR4119785	2020-07-15 20:50:11	Salmonella enterica	Aberdeen				SRR4119785
SRR1752879	2020-07-15 20:50:11	Salmonella enterica	Agona	aph(3)-b, fxaA7, suz2, tet(A)			SRR1752879
SRR1642091	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Ajobbo				SRR1642091
SRR1427104	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Amsterdam				SRR1427104
SRR3402078	2020-07-15 20:50:11	Salmonella enterica	Anatum	blaCMY-2, tet(C)			SRR3402078
SRR2855567	2020-07-15 20:50:11	Salmonella enterica	Bangkok				SRR2855567
SRR1653383	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Bardo				SRR1653383
SRR4842191	2020-07-15 20:50:11	Salmonella enterica	Braenderup				SRR4842191
SRR3049577	2020-07-15 20:50:11	Salmonella enterica	Brun				SRR3049577
SRR2421532	2020-07-15 20:50:11	Salmonella enterica	Cerro				SRR2421532
SRR1220728	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Chicago				SRR1220728
SRR3194585	2020-07-15 20:50:11	Salmonella enterica	derby	aac(3)-VIIa, aadA1, fxaA7, d...			SRR3194585
SRR1030845	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Dublin				SRR1030845
SRR1183899	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Enteritidis				SRR1183899
SRR1646564	2020-07-15 20:50:11	Salmonella enterica	Hadler	aph(3)-b, aph(6)-II, tet(A)			SRR1646564
SRR1105667	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Heidelberg				SRR1105667
SRR3289809	2020-07-15 20:50:11	Salmonella enterica	Heidelberg	aac(3)-VIIa, aadA1, blaHER-3...			SRR3289809
SRR1574295	2020-07-15 20:50:11	Salmonella enterica	Illa 18:24:z23-	aac(3)-VIIa, aadA1, qacEΔ6E...			SRR1574295
SRR1534041	2020-07-15 20:50:11	Salmonella enterica	Kentucky	aph(3)-b, aph(6)-II, tet(B)			SRR1534041
SRR3473955	2020-07-15 20:50:11	Salmonella enterica	Manhattan				SRR3473955
SRR1783160	2020-07-15 20:50:11	Salmonella enterica	Montevideo	aac(6)-b, aadA1, aph(3)-b...			SRR1783160
SRR1203019	2020-07-15 20:50:11	Salmonella enterica	Newport	aph(3)-b, aph(6)-II, blaCM...			SRR1203019
SRR3098689	2020-07-15 20:50:11	Salmonella enterica	Saipaul	blaTEM-1			SRR3098689
SRR1574259	2020-07-15 20:50:11	Salmonella enterica	Schwarzengrund	aph(3)-b, aph(6)-II, blaTEM...			SRR1574259
SRR1167400	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Thompson				SRR1167400
ERR340757	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	Typhi				ERR340757
SRR3376793	2020-07-15 20:50:11	Salmonella enterica	Typhimurium				SRR3376793
SRR330219	2020-07-15 20:50:11	Salmonella enterica	Typhimurium var. O:5-	blaCMY-2, suz2, tet(A)			SRR330219
SRR3098686	2020-07-15 20:50:11	Salmonella enterica	Waycross				SRR3098686
SRR6128335	2020-08-10 10:11:06	Salmonella enterica subsp. enterica	Typhimurium				SRR6128335
SRR6128336	2020-08-10 10:11:06	Salmonella enterica subsp. enterica	Typhimurium				SRR6128336
SRR6128337	2020-08-10 10:11:10	Salmonella enterica subsp. enterica	Typhimurium				SRR6128337
SRR6128338	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128338
SRR6128339	2020-08-10 10:11:14	Salmonella enterica subsp. enterica	Typhimurium				SRR6128339
SRR6128340	2020-08-10 10:11:18	Salmonella enterica subsp. enterica	Typhimurium				SRR6128340
SRR6128341	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128341
SRR6128342	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128342
SRR6128343	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128343
SRR6128344	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128344
SRR6128345	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128345
SRR6128346	2020-07-15 20:50:11	Salmonella enterica subsp. enterica	1,4,(5),12:-				SRR6128346

Figure 2: The *Salmonella* demonstration database: the *Main* window.

### 3 About the demonstration database

The WGS demo database contains links to sequence read set data on NCBI's sequence read archive (SRA) for 62 publicly available sequencing runs. Additional information (in entry info fields Organism, Serovar etc.) was collected from the corresponding publications and added to the demonstration database.

Seven experiments are present in the demo database and are listed in the *Experiment types* panel (see Figure 3).



#	Name	Type
1	wgs	Sequence read set types
2	wgsLong	Sequence read set types
3	wgMLST	Character types
4	denovo	Sequence types
5	quality	Character types
6	wgs_TrimmedStats	Sequence read set types
7	wgMLST_CallTypes	Character types

**Figure 3:** The *Experiment types* panel in the *Main* window.

1. Click on the green colored dot for one of the entries in the first column in the *Experiment presence* panel. Column 1 corresponds to the first experiment type listed in the *Experiment types* panel, which is **wgs** in the default configuration.

In the *Sequence read set experiment* window, the link to the sequence read set data on NCBI (SRA) with a summary of the characteristics of the sequence read set is displayed: *Read set size*, *Sequence length statistics*, *Quality statistics*, *Base statistics* (see Figure 4).

2. Close the *Sequence read set experiment* window.
3. Click on the green colored dot for one of the entries in the fourth column in the *Experiment presence* panel. Column 4 corresponds to the fourth experiment type listed in the *Experiment types* panel, which is **denovo** in the default configuration.

The *Sequence editor* window opens, containing the results from the de novo assembly algorithm, i.e. concatenated de novo contig sequences (see Figure 5).

4. Close the *Sequence editor* window.

The sequence read set experiment type **wgs\_TrimmedStats** contains some data statistics about the reads retained after trimming, used for the de novo assembly.

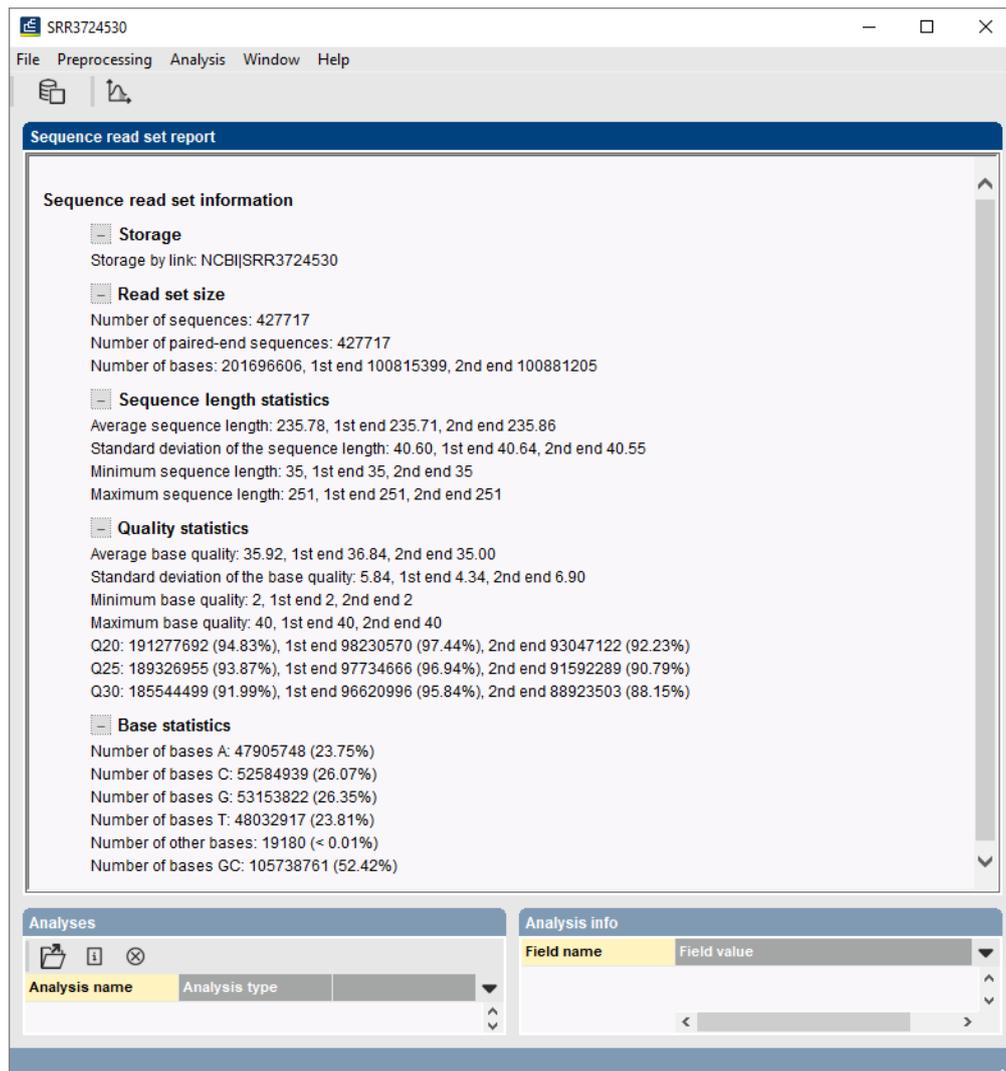
The sequence read set experiment type **wgsLong** contains the links to long read sequence read data (typically PacBio or MinION datasets). In this demo database, no links are defined for this experiment.

The other three experiments contain data related to the wgMLST analysis performed on the samples:

- Character experiment type **wgMLST** contains the allele calls for detected loci in each sample, where the consensus from assembly-based and assembly-free calling resulted in a single allele ID.
- Character experiment type **quality** contains quality statistics for the raw data, the de novo assembly and the different allele identification algorithms.
- Character experiment type **wgMLST\_CallTypes**: contains details on the call types.

## 4 Installing the *Salmonella* functional genotyping plugin

1. Call the *Plugins* dialog box from the *Main* window by selecting **File > Install / remove plugins...** (⚙).



**Figure 4:** The sequence read set experiment card for an entry.

2. Select the *Salmonella* functional genotyping plugin in the *Application* tab and press the <Activate> button (see Figure 6).
3. Confirm the installation of the plugin.
4. Click <Yes> to review the settings.

The *Settings* dialog box pops up, consisting of 7 tabs (see Figure 7).

In the *General* tab following general settings need to be specified (see Figure 7):

- The **Information fields** that will appear in the report (see 6).
  - The **Exports directory** for the export of the reports (see 6).
  - The **Input Sequence experiment** that holds the (whole) genome sequences that will be screened.
5. In our demonstration database, the assembled sequences are stored in the **denovo** sequence experiment. Make sure this experiment is selected from the drop-down list and optionally check the **Isolate** to include in the report (see Figure 7).

The screenshot displays the SRR3724530 (Sequence Viewer) interface. The top section is the Sequence Editor, showing a DNA sequence with a red vertical line indicating the current position. Below this is the Sequence Viewer, which includes a genomic map with features like SALM\_5050, SALM\_7089, SALM\_11208, and SALM\_110415. The bottom section is the Annotation table, which lists features with their start and end coordinates.

Feature key	Start	End
10	12076	14247
11	15253	16122
12	18389	18991
13	21151	22005
14	22074	23615

The annotation table also includes a 'Feature list' column with icons for each feature. The right side of the annotation window shows the details for feature 11, including its locus tag (SALM\_5050), evidence score (100.0), and a partial translation of the protein sequence.

Figure 5: The Sequence editor window.

The screenshot shows the Plugins dialog box with the 'Salmonella functional genotyping' plugin selected. The dialog has tabs for Applications, Utilities, Custom, and Database Functionality. The 'Applications' tab is active, and the 'Salmonella functional genotyping' plugin is highlighted in blue. A description of the plugin is provided on the right side of the dialog.

Activate functionality for specific applications.

- Antibiotics susceptibility
- BandScoring
- E. coli functional genotyping
- Listeria functional genotyping
- MTBC functional genotyping
- Salmonella functional genotyping
- S. aureus functional genotyping
- HIV Resistance
- MIRU-VNTR
- MLST online
- QIAxcel
- RDP
- RiboPrinter
- SNP calling

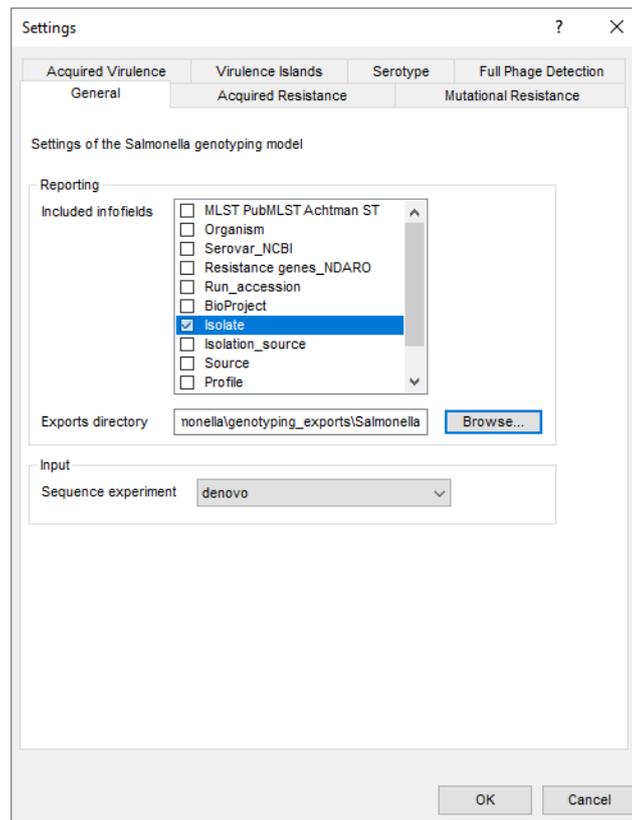
This plugin allows functional prediction of phenotypic traits of Salmonella bacteria, that is: virulence prediction, resistance prediction.

Show only activated

Show Manual

Activate Exit

Figure 6: Install plugin.



**Figure 7:** The *Settings* dialog box: *General* tab.

The *Acquired Resistance*, *Acquired Virulence*, *Virulence Islands*, and *Full Phage Detection* tabs all consist of three separate panels:

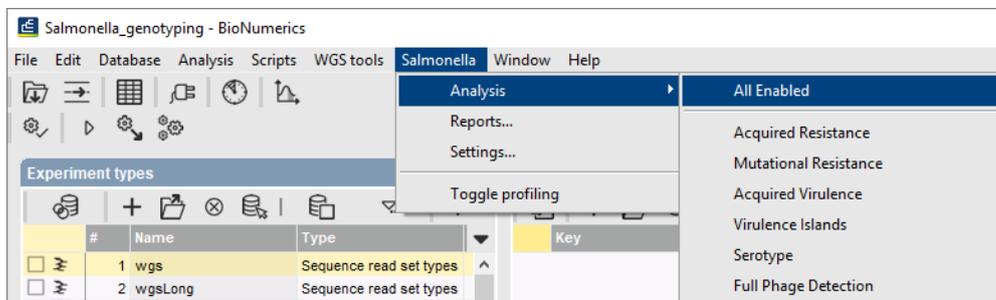
1. *Knowledgebase*: in this panel the knowledgebase against which you want to screen can be specified.
2. *Blast*: in this panel two settings for the BLAST algorithm can be specified; the **Minimum percent identity (%)** and the **Minimum coverage (%)** of your query sequence against the knowledgebase's reference sequences. If the option **Combine fragments** is checked, genes that occur fragmented in the genome (i.e. split over two contigs) can still be detected.
3. *Results*: in this panel the output database information fields and experiments to which the screening results will be written can be dictated. Use the drop-down menu to choose an existing experiment type or field, or the **<Create>** option to create new experiments and fields. A default name for the experiment or information field is suggested, but you can adjust this if you want to. In the *Virulence Islands* tab you can specify the minimum percentage of virulence island loci that needs to be detected (**Minimum loci (%)**) before the presence of the virulence island is shown in the results.

In the *Mutational resistance* tab only the *Knowledgebase* and *Results* panels are present, as no BLAST settings can be specified for this analysis. In the *Serotype* tab, the input experiment as well as the type of input data for the SeqSero job needs to be defined in the *Input* panel: **Assembly**, **Paired end reads** or **Single end reads**. In the *Results* panel the output database information

fields and experiments to which the screening results will be written can be dictated.

6. In this tutorial, specify the experiment types and information fields in all tabs by selecting the **<Create>** option in the drop-down lists and accepting the default names. In the *Serotype* tab select **denovo** as input experiment and **Assembly** as input data. Leave the other settings unaltered.
7. Click **<OK>** in the *Settings* dialog box.
8. When the *Salmonella functional genotyping plugin* is successfully installed, a confirmation message pops up. Press **<OK>**.
9. Press **<Exit>** to close the *Plugins* dialog box.
10. Close and reopen the database to activate the features of the *Salmonella functional genotyping plugin*.

The *Salmonella functional genotyping plugin* installs menu items in the main menu of the software under **Salmonella** (see Figure 8).



**Figure 8:** New menu-items after installation of the *Salmonella functional genotyping plugin*.



The settings specified during installation of the plugin can be called again at any time with **Salmonella > Settings....**

## 5 Screening of entries

The screening can be done on any selection of entries in the database.

1. Select a single entry in the *Database entries* panel by holding the **Ctrl**-key and left-clicking on the entry. Alternatively, use the **space bar** to select a highlighted entry or click the ballot box next to the entry.

Selected entries are marked by a checked ballot box () and can be unselected in the same way.

2. In order to select a group of entries, hold the **Shift**-key and click on another entry.

A group of entries can be unselected the same way.

3. Make sure a few entries are selected in the *Database entries* panel of the demonstration database.

### 5.1 Serotype prediction using the WGS tools plugin

SeqSero jobs need to be submitted to the calculation engine first. The Calculation engine option requires credits for running jobs on the Applied Maths cloud calculation engine. Credits are linked

to credentials that you need to enter when installing the WGS tools plugin. In our demo database the WGS tools plugin is installed but no credits are assigned to the demo project so no SeqSero jobs can be performed on the external calculation engine. Please contact Applied Maths to obtain more information.

To perform SeqSero serotype prediction you need to submit a job to the CE:

4. Select **WGS tools** > **Submit jobs...** (▶) to open the *Submit jobs* dialog box (see Figure 9).

From the *Submit jobs* dialog box, one can define which algorithms need to be run on the selected samples and as such, define and launch the related jobs on the calculation engine.

5. Select the **Calculation Engine** option.
6. Check the box next to **Serotype prediction (SeqSero)**. Note that this option is only available after successful installation of the plugin.

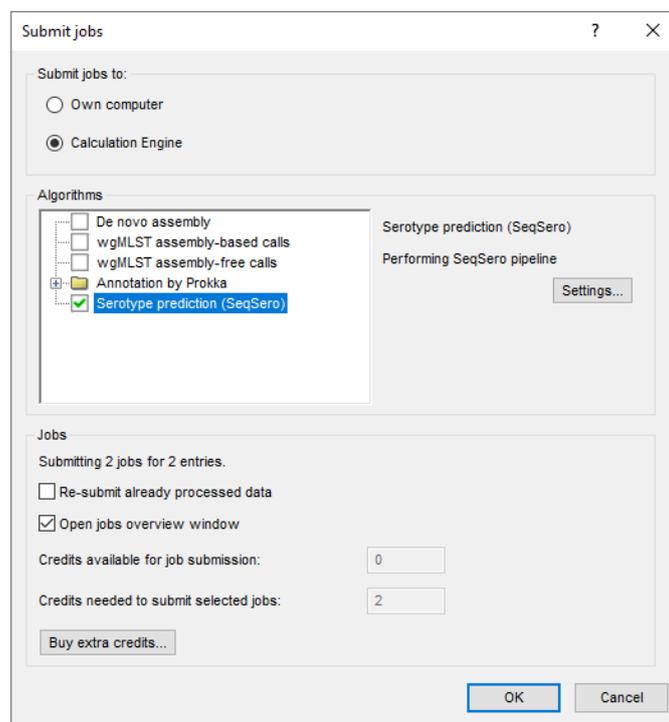


Figure 9: Submit jobs.

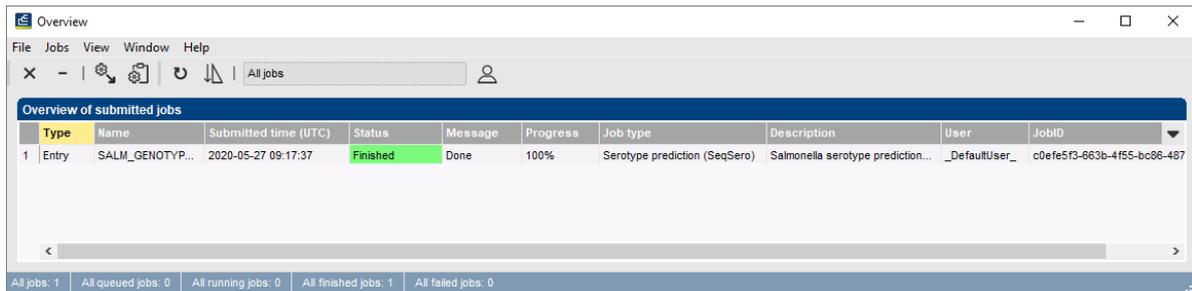
7. Uncheck all other boxes if you do not want to perform any additional analyses (e.g. wgMLST).

Jobs that already have been submitted and have been imported successfully, will not be re-launched for analysis, unless the check box in front of **Re-submit already processed data** in the **Jobs** part is checked.

By default, the *Job overview* window will be opened after submission of the jobs. However, this can be changed by unchecking the option **Open jobs overview window**. The *Job overview* window can always be opened later by selecting **wgMLST** > **Job overview...** in the *Main* window.

The cost to analyze one sample with SeqSero is 1 credit. The number of credits required to run the selected jobs for the selected entries and the number of credits that are available for job submission on your project can be consulted in the *Jobs* panel of the *Submit jobs* dialog box (see Figure 9).

8. Click <OK> to launch the SeqSero jobs and open the *Job overview* window for the calculation engine (see Figure 10).



Type	Name	Submitted time (UTC)	Status	Message	Progress	Job type	Description	User	JobID	
1	Entry	SALM_GENOTYP...	2020-05-27 09:17:37	Finished	Done	100%	Serotype prediction (SeqSero)	Salmonella serotype prediction...	_DefaultUser_	c0defe5f3-663b-4f55-bc86-487

Summary: All jobs: 1 | All queued jobs: 0 | All running jobs: 0 | All finished jobs: 1 | All failed jobs: 0

**Figure 10:** Job overview.

In the *Job overview* window you can see the status of the submitted jobs. SeqSero jobs that were executed starting from a (de novo) assembly will go faster than those starting from raw reads (fastq files). However, the results of the latter might be more complete. The input experiment type can be redefined at any point in the *Serotype* tab of the *Settings* dialog box. Once the input experiment was changed in the settings a job needs to be re-submitted to the CE to have the serotype recalculated.

Once the SeqSero job has been finished, the message **Finished** is displayed in the **Status** column.

- Finished jobs can be imported with a manual action (**Jobs** > **Get results** (🔧)) or through an automatic update: select **File** > **Settings**, check both options and specify an interval (e.g. 10 min).

The job results can also be imported starting from the entry selection in the *Main* window:

- Make an entry selection in the *Database entries* panel and select **WGS tools** > **Get results** (🔧).



The job log files are saved in the *Job log* panel of the *Entry* window. Double-click on an entry in the *Database entries* panel to open the *Entry* window and to consult this information.

Once the results are imported, the corresponding jobs and their underlying data sets are automatically deleted from the calculation engine and as such, from the *Job overview* window.

## 5.2 Screening for phenotypic traits using the *Salmonella* plugin

Screening for the phenotypic traits can be done for all tools checked in the *Settings* dialog box (using **Salmonella** > **Analysis** > **All Enabled**) or for each tool separately with the corresponding command (**Salmonella** > **Analysis...**).

Clicking **Salmonella** > **Analysis** > **All Enabled** or **Salmonella** > **Analysis** > **Serotype** will only reprocess the WGS tools SeqSero job results (e.g. if you have changed the settings to import the result in a different information field).

- Select **Salmonella** > **Analysis** > **All Enabled** to screen the selected entries for all enabled traits.

A progress bar appears. The analysis time depends on the number of selected entries. When the analysis is finished, the progress bar disappears. The detected traits for the screened entries are stored in the database.



An error message pops up when no SeqSero results are available (see 5.1).

### 5.3 Results

The antigenic profile (**Profile**), serotype (**Serotype**) and virulence islands results (**Total Islands**) are written to the information fields in the *Database entries* panel (see Figure 11). Please note that the shown names of the information fields are those created per default, but can be different in your case depending whether you choose an alternative name during installation.



Key	Level	Modified date	Profile	Serotype	Total Islands
<input type="checkbox"/> SRR1427104		2020-05-27 11:32:41	3,10:g,m,s,-	Amsterdam	11
<input type="checkbox"/> SRR3402078		2020-05-27 13:11:56	3,10:e,h:1,6	Anatum	13

**Figure 11:** Example output of the Profile, Serotype and Total Islands information fields.

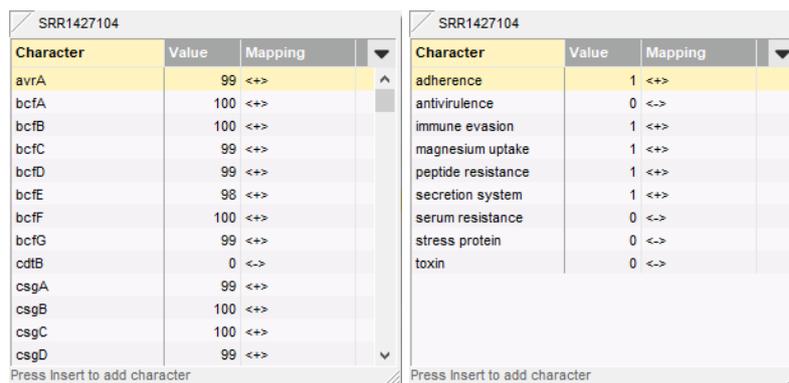
The character experiment types for **Acquired Virulence**, **Virulence Islands**, **Acquired Resistance**, **Mutational Resistance** and **Full Phage detection** are created and updated with the predicted traits. Please note that the shown names of the experiment types are those created per default, but can be different in your case depending whether you choose an alternative name during installation.

12. Open a character card for one of the analyzed entries by clicking on the corresponding green colored dot in the *Experiment presence* panel.

Below, the interpretation of the results gathered in the character experiment types is given.

Acquired virulence (see Figure 12):

1. **Acquired\_Virulence\_loci\_identity**: contains the results for each virulence gene: 0 = not detected, when detected the % identity of the best hit is shown.
2. **Acquired\_Virulence\_traits\_identity**: contains the results for each virulence type: 0 = not detected, 1 = detected.



Character	Value	Mapping
avrA	99	<=>
bcfA	100	<=>
bcfB	100	<=>
bcfC	99	<=>
bcfD	99	<=>
bcfE	98	<=>
bcfF	100	<=>
bcfG	99	<=>
cdtB	0	<=>
csgA	99	<=>
csgB	100	<=>
csgC	100	<=>
csgD	99	<=>

Character	Value	Mapping
adherence	1	<=>
antivirulence	0	<=>
immune evasion	1	<=>
magnesium uptake	1	<=>
peptide resistance	1	<=>
secretion system	1	<=>
serum resistance	0	<=>
stress protein	0	<=>
toxin	0	<=>

**Figure 12:** Example output of the **Acquired\_Virulence\_loci\_identity** and the **Acquired\_Virulence\_traits\_identity** experiment types for sample SRR1427104.

Virulence islands (see Figure 13):

1. **Island\_Counts**: contains the number of detected loci associated to a pathogenicity island.
2. **Island\_Percentages**: contains the percentage of detected loci associated to a pathogenicity island.

Character	Value	Mapping
CSS4 island	3	<=>
SESS LEE	0	<->
SPI-1	39	<=>
SPI-10	0	<->
SPI-11	8	<=>
SPI-12	5	<=>
SPI-13	0	<->
SPI-14	0	<->
SPI-2	41	<=>
SPI-3	9	<=>
SPI-4	11	<=>
SPI-5	8	<=>
SPI-6	5	<=>

Character	Value	Mapping
CSS4 island	38	<=>
SESS LEE	0	<->
SPI-1	95	<=>
SPI-10	0	<->
SPI-11	89	<=>
SPI-12	71	<=>
SPI-13	0	<->
SPI-14	0	<->
SPI-2	93	<=>
SPI-3	53	<=>
SPI-4	100	<=>
SPI-5	100	<=>
SPI-6	33	<=>

**Figure 13:** Example output of the *Island Counts* and the *Island Percentages* experiment types for sample SRR1427104.

Acquired resistance (see Figure 14):

1. **Acquired\_Resistance\_loci\_identity:** contains the results for each resistance gene: 0 = not detected (sensitive), when detected (resistant) the % identity of the best hit is shown.
2. **Acquired\_Resistance\_traits\_identity:** contains the results for each antibiotic: 0 = not detected (sensitive), 1 = detected (resistant).

Character	Value	Mapping
aac(2)-Ia	0	<=>
aac(2)-Ib	0	<->
aac(2)-Ic	0	<->
aac(2)-Id	0	<->
aac(2)-Ie	0	<->
aac(2)-IIa	0	<->
aac(3)-I	0	<->
aac(3)-Ia	0	<->
aac(3)-Ib	0	<->
aac(3)-Ib-aac(6)-Ib'	0	<->
aac(3)-Ic	0	<->
aac(3)-Id	0	<->
aac(3)-If	0	<->

Character	Value	Mapping
ampicillin	0	<=>
azithromycin	0	<->
cefepime	0	<->
cefotaxime	0	<->
cefotaxime-clavulan...	0	<->
cefotaxin	0	<->
ceftazidime	0	<->
ceftazidime-clavulan...	0	<->
chloramphenicol	0	<->
ciprofloxacin	0	<->
clindamycin	0	<->
colistin	0	<->
dalfopristin	0	<->

**Figure 14:** Example output of the *Acquired\_Resistance\_loci\_identity* and the *Acquired\_Resistance\_traits\_identity* experiment types for sample SRR1427104.

Mutational resistance (see Figure 15):

1. **Mutational\_Resistance\_identifiers:** contains the results for each resistance mutation: -2 = partially indecisive, -1 = fully indecisive, 0 = not detected (sensitive), 1 = detected (resistant).
2. **Mutational\_Resistance\_traits:** contains the results for each antibiotic group: -2 = partially indecisive, -1 = fully indecisive, 0 = not detected (sensitive), 1 = detected (resistant).

Full phage detection (see Figure 16):

1. **Phage\_Full\_coverage:** contains the results of the full phages detection: 0 = not detected, when detected the % of the detected full phage is shown.

13. Close the character card(s).

Character	Value	Mapping
16S_rrsD_dC1065T	0	<->
16S_rrsD_dC1191T	0	<->
gyrA_pA119E	0	<->
gyrA_pA119S	0	<->
gyrA_pA119V	0	<->
gyrA_pA131G	0	<->
gyrA_pA67P	0	<->
gyrA_pD72G	0	<->
gyrA_pD82G	0	<->
gyrA_pD82N	0	<->
gyrA_pD87G	0	<->
gyrA_pD87K	0	<->
gyrA_pD87N	0	<->

Character	Value	Mapping
ciprofloxacin	1	<->
colistin	0	<->
nalidixic acid	1	<->
spectinomycin	0	<->

**Figure 15:** Example output of the *Mutational\_Resistance\_identifiers* and the *Mutational\_Resistance\_traits* experiment types for sample SRR1427104.

Character	Value	Mapping
Salmonella virus ST64T	0	<->
Salmonella virus SP126	0	<->
Salmonella virus P22...	0	<->
Salmonella virus BTP1	0	<->
Salmonella phage v...	0	<->
Salmonella phage v...	0	<->
Salmonella phage v...	0	<->
Salmonella phage p...	0	<->
Salmonella phage f...	0	<->
Salmonella phage ep...	0	<->
Salmonella phage S13	0	<->
Salmonella phage Sh19	0	<->
Salmonella phage S...	0	<->

**Figure 16:** Example output of the *Phage\_Full\_coverage* experiment type for sample SRR1427104.

## 6 Reports

1. Open the genotype report for the selected entries with **Salmonella > Reports...**

The *Report* window contains a genotype report for each of the selected entries (see Figure 17).

2. Select another entry in the *Entries* panel to update the results in the *Genotype report* panel.

The creation date of the report (**Date**), the Key (**Name**), and information fields checked in the *Settings* dialog box are displayed in the *Genotype report* panel.

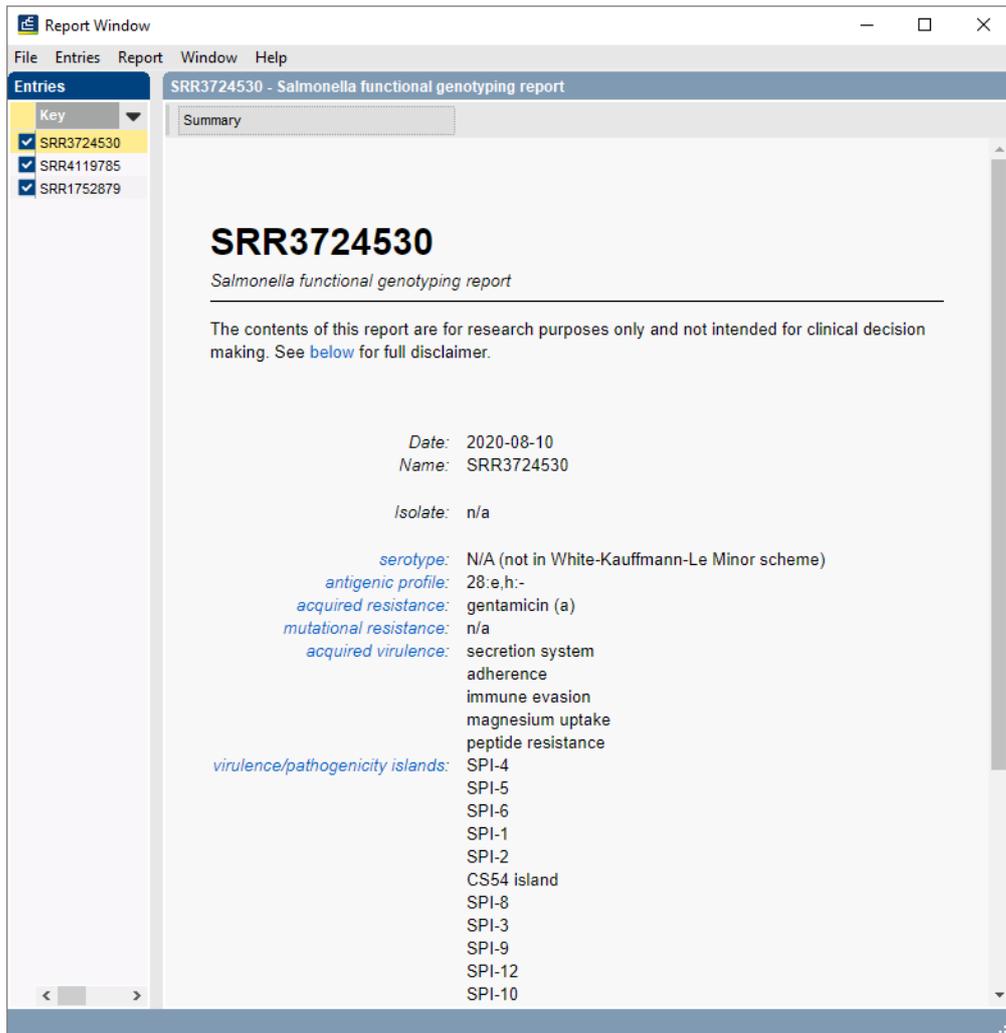
3. Select **Report > Report templates** in the *Report* window and make sure the option **Summary** is selected.

A summary of the results of all analyzed traits is displayed in the *Report* window.

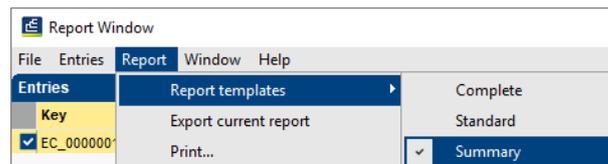
4. Select **Report > Report templates** in the *Report* window (see Figure 18) and select the option **Complete**.

In the **Complete** view, the summarized results as well as all details are shown, including the serotype antigens, descriptions of the detected genes, the detected mutations, the detected loci of the virulence islands and the genome positions of the full phages.

5. Click on a hyperlink of one of the predicted traits to display the detailed results in the *Genotype report* panel.



**Figure 17:** Example of a functional genotyping report.



**Figure 18:** Report templates in the *Report window*.

6. Select **File** > **Exit** to close the *Report window*.