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Quality control assessment for microbial genomes: GalaxyTrakr MicroRunQC workflow V.4

In 5 collections

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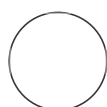
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GenomeTrakr

Vet LIRN



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We use this protocol and it's working

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ABSTRACT

PURPOSE: Step-by-step instructions for checking WGS sequence quality for bacterial pathogens. The MicroRunQC workflow, implemented in a custom Galaxy instance, will produce quality assessments for raw reads (Illumina paired-end fastq files) and draft de novo assemblies, along with reporting the sequence type for each isolate. This workflow will work on most microbial pathogens, so we advise laboratories to upload their entire MiSeq/NextSeq run through this workflow.

SCOPE: This protocol covers the following tasks:

1. set up an account in GalaxyTrakr
2. Create a new history/workspace
3. Upload data
4. Execute the MicroRunQC workflow
5. Interpret the results

Version updates:

V3: updated with *Cronobacter* thresholds

V4: MicroRunQC updated to V1.1 Includes updates to skeza and mlst methods, as well as adjusted assembly QC thresholds for E.coli. Added *Enterobacter* QC thresholds to threshold table.

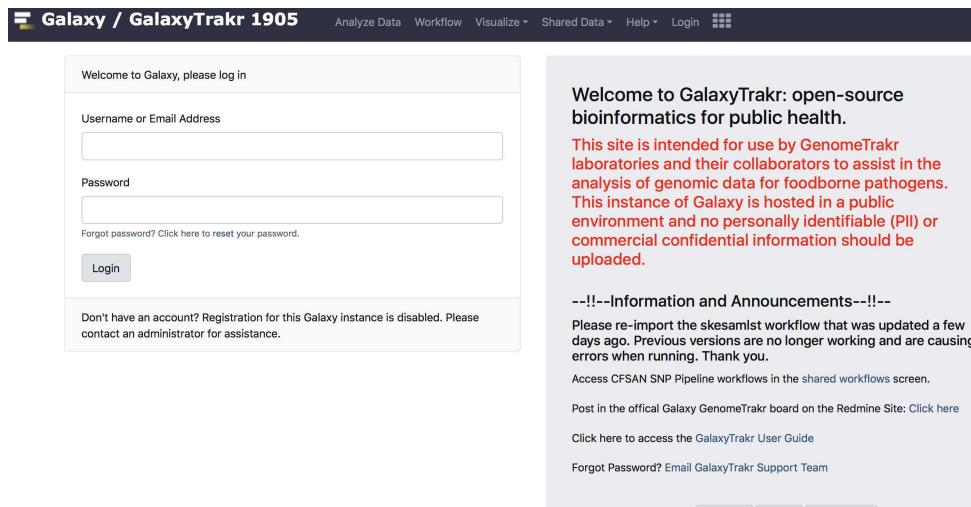
Account set up

1. Create a GalaxyTrakr account here: <https://account.galaxytrakr.org/Account/Register>

User Registration Form

Location	<input type="text" value="California Department of Public Health - Food and Drug Laboratory Branch"/> Add New Location
First Name	<input type="text" value="Enter First Name, Do not use characters: ^[]{}: '\"/>
Last Name	<input type="text" value="Enter First Name, Do not use characters: ^[]{}: '\"/>
Email	<input type="text"/> Email will be used for automated messages to include registration information!
Primary Phone	<input type="text" value="Please enter number with country code, without dashes, for example +17035456789"/> If possible please use a mobile number than can accept text messages, only used for support
Title	<input type="text"/>
Requirements	<input type="text" value="Please annotate intended use of Galaxy and Analysis tools. List specific tools you would like to see deployed in Galaxy."/> <div></div>
<input type="button" value="Register"/>	

1.1 Log into your GalaxyTrakr account: <https://galaxytrakr.org>



Create a new history

2 Create a new history.

We recommend creating a new history for each new MiSeq Run and including the flow-cell ID and date in the history name.

Save your MicroRunQC output here and any other relevant analyses, like serotyping, or AMR detection.

After all the analysis output from this run is saved to your internal data network or computer, older history's should be purged/deleted so as not to occupy the limited storage space in your account. In some cases it may be useful to save, for a limited time, multiple histories or to run analyses concurrently in multiple histories. In these cases you need to pay attention to your % usage bar (shows % used of allocated storage space) in the upper right corner of the GalaxyTrakr page. If you need additional space you can contact galaxytrakrsupport@fda.hhs.gov and request additional storage.

2.1 Click on the + icon in the upper right History panel



- 2.2 Name your new History by clicking on the “Unnamed history”, type in desired name and hit enter. We recommend including the run cell ID and the date the run was started.



Upload data

- 3 This section will describe the process for uploading raw fastq files into your active History panel. After the files have been uploaded they will stay in your account until they are deleted.

- 3.1 Click on the Upload Data icon on the top of the left web page to start an upload process.























3.2



Select "Type (set all):auto-detect." Choose local file button and navigate to the desired fastq files, then click "start" to upload files. These files should be paired (two per sample/isolate).




Download from web or upload from disk


Regular Composite Collection Rule-based

You added 4 file(s) to the queue. Add more files or click 'Start' to proceed.

Name	Size	Type	Genome	Settings	Status
 CFSAN074382_S15_L	151.8 MB	Auto-det... 	unspecified (?) 		0% 
 CFSAN074382_S15_L	152.5 MB	Auto-det... 	unspecified (?) 		0% 
 CFSAN074384_S20_I	172.6 MB	Auto-det... 	unspecified (?) 		0% 
 CFSAN074384_S20_I	181.2 MB	Auto-det... 	unspecified (?) 		0% 

1. Type (set all): Auto-detect  Genome (set all): unspecified (?) 

2.  Choose local file  Choose FTP file  Paste/Fetch data Pause Reset Start Close

3. 

As the file uploads complete, each row will turn green. Samples in yellow are still in process.

3.3

You have just upload a set of forward and reverse reads. For further analysis these files need to be paired properly so the platform knows which R1 and R2 files go with each sample/isolate. GalaxyTrakr does this by creating a **List of Dataset Pairs**.

Within your newly created History panel, click the "check box," then select all the files you just uploaded by clicking "All" or by individually selecting the ones you want to pair.



Screenshot of History panel showing recently uploaded files. Note the way the files are named, using R1 and R2 to identify the paired reads. This will be important in the next step. Some naming conventions can be slightly different.

3.4 Click "For all selected" and choose "Build List of Dataset Pairs"



3.5 A new window will open to help you pair the fastq files properly. Note how your paired reads

are named.

Select **Clear filters**, then click **Auto-pair**.

Create a collection of paired datasets

Could not automatically create any pairs from the given dataset names. You may want to choose or enter different filters and try auto- pairing again. Close this message using the X on the right to view more help.

0 unpaired forward - (4 filtered out) Choose filters Clear filters 1 0 unpaired reverse - (4 filtered out)

_1 Auto-pair 2 _2

(no datasets were found matching the current filters)

If auto-pairing does not work, you can click "choose filters" and select the appropriate filter for the pairing:

e.g. choose "_R1 "and "_R2 "

0 unpaired forward - (4 filtered out) Choose filters Clear filters 0 unpaired reverse - (4 filtered out)

_1

Choose from the following filters to change which unpaired reads are shown in the display:

Forward: _1, Reverse: _2

Forward: _R1, Reverse: _R2

3.6 Paired reads will pair in the middle column and turn green.

Name your dataset: Example, "pairedSet-<FlowCell>-<date>"

Click **Create list**.

Create a collection of paired datasets

2 pairs created: all datasets have been successfully paired

0 unpaired forward - (0 filtered out)

Choose filters Clear filters

0 unpaired reverse - (0 filtered out)

Filter this list

Filter this list

2 paired

Unpair all

CFSAN074382_S15_L001_R1_001.fastq.gz	→	CFSAN074382_S15_L001_R_001.fastq	←	CFSAN074382_S15_L001_R2_001.fastq.g	
CFSAN074384_S20_L001_R1_001.fastq.gz	→	CFSAN074384_S20_L001_R_001.fast	←	CFSAN074384_S20_L001_R2_001.fastq.g	

Remove file extensions from pair names? ☒

Hide original elements? ☐

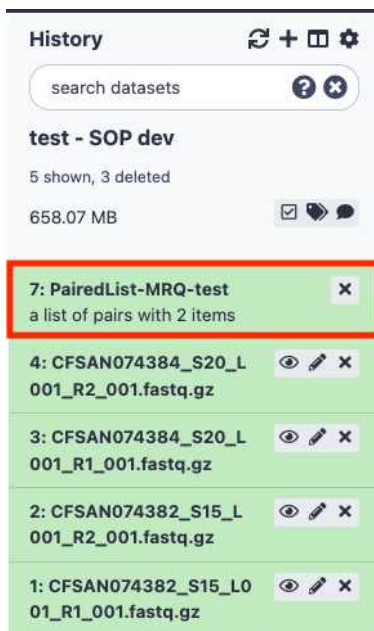
Name: test

Cancel

Create list

3.7 This paired dataset will now be available for analysis in your history panel. You can run multiple analyses on the same dataset in a history rather than upload the same sequence data to a new history to perform additional analyses. This will help you use your allocated storage space efficiently.

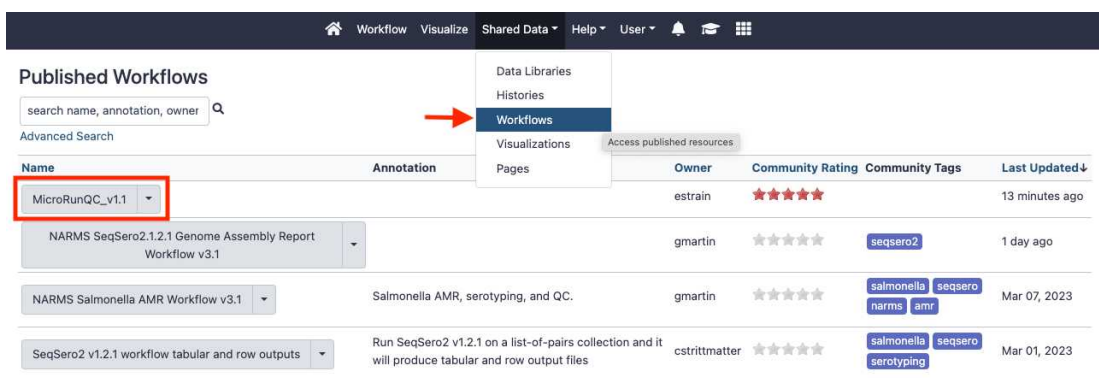
You can re-name this PairedList by clicking on the name.



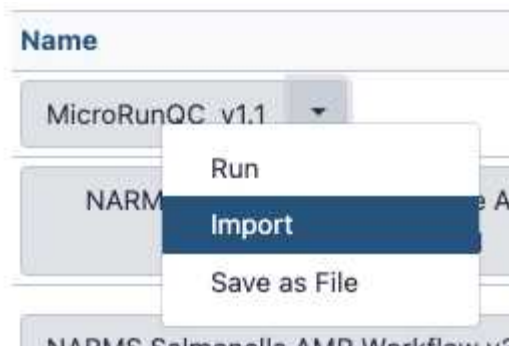
Run the MicroRunQC workflow

- 4 Add the MicroRunQC workflow to your own "workflows" panel. You only have to do this step once for each new workflow you need.

- 4.1 Navigate to the "Shared Data" drop down menu, choose workflows and locate MicroRunQC_v1.1

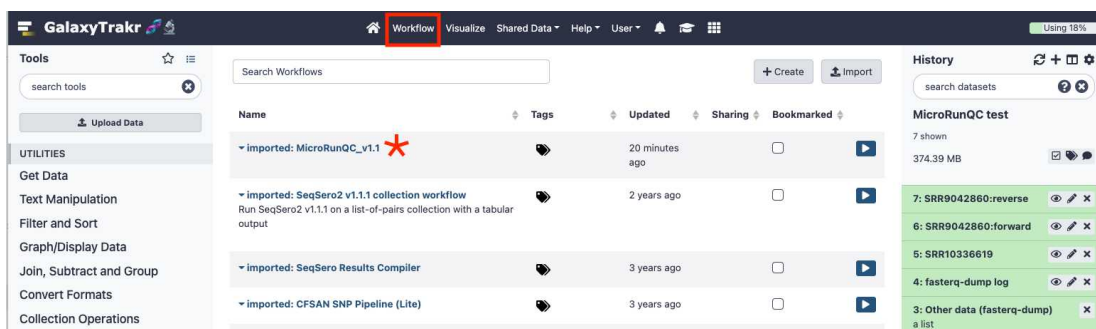


From Dropdown, select "Import"



4.2 To see the new imported workflow, click “Workflow” tab on the top panel.

Click "Bookmarked" box to make it available in the left panel under "Workflows"



4.3 From the Workflow menu on the left panel, select **MicroRunQC_v1.1**

GalaxyTrakr

Tools ☆ ☰

search tools ✕

⬆ Upload Data

metagenomics:Functional Profiling

Metagenomics:Assembly

Metagenomics:Rpackages

Metagenomics:Metaphlan

Metagenomics:CPIPES

test:tools

tes

blast_to_scaffold Generate DNA scaffold from blastn or tblastx alignment of Contigs

small_rna_maps

Clip adapter

Normalize By Median Filter reads using digital normalization via k-mer abundances

Bowtie2 - map reads against reference genome

Trim sequences

NCBI EFetch fetch records from NCBI

Unique occurrences of each record

QIIME

kraken2

QualiMap BamQC Tool to to facilitate the quality control of alignment sequencing data and its derivatives like feature counts.

NGS:Simulator

WORKFLOWS

All workflows

imported: MicroRunQC_v1.1 →

4.4 Select paired list dataset you created earlier.

Click **Run Workflow**. This can take some time depending on the number of samples you are analyzing. If you choose to you can log out of GalaxyTrakr and log back in at a later time to see if the job is completed.



4.5 Upon completion of the pipeline all tiles in the history bar will be green.

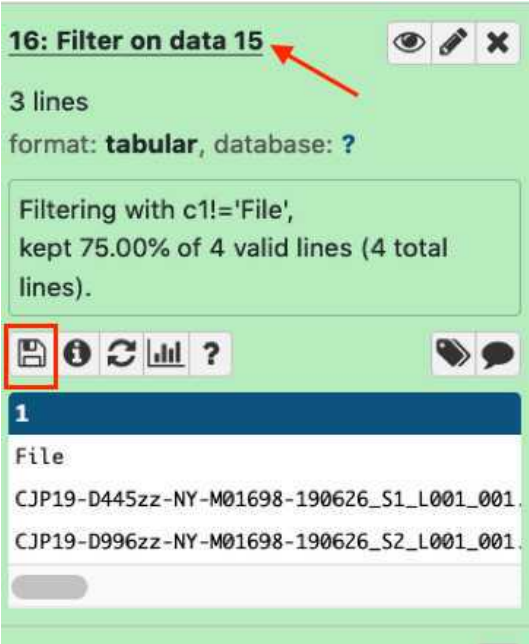
In the “**Filter on Data ##**”, click on the “Eye” icon to view the output table in the GalaxyTrakr window.



Interpret the results

5 Download and interpret the results:

- 5.1 Click “**Filter on data ##**” and then the floppy disc icon. The tabular file can be opened in a text reader or converted to a format (.txt) that can be opened in excel.



- 5.2 The MicroRunQC output file includes the following columns:

A	B	C
<i>Parameter</i>	<i>Input</i>	<i>Description</i>
Contigs	Assembly	Number of contigs in the de-novo SKESA assembly. Contigs smaller than 200 base-pairs (bp) are not counted.
Length	Assembly	Total length of all contigs > 200bp. This should approximate the size of the genome for the target organism.
EstCov	Assembly	Mean coverage for contigs in the SKESA assembly.
N50	Assembly	Sequence length of the shortest contig at 50% of the total genome length
MedianInsert	Read	Distance between forward and reverse reads. Calculated by mapping reads to SKESA assembly using bwa.
MeanLength_R1	Read	Mean length of forward read
MeanLength_R2	Read	Mean length of reverse read
MeanQ_R1	Read	Mean Q-score of forward read
MeanQ_R2	Read	Mean Q-score of reverse read

A	B	C
Scheme	Assembly	PubMLST scheme name (output from mlst application that scans contig files against traditional PubMLST typing schemes).
ST	Assembly	Sequence Type
Loci	Assembly	gene (allele number) – for example aroC(118)

MicroRunQC output table headers. This table lists the summary metrics for sequence quality, number of contigs, and estimated genome size, along with other common metrics for reads (Median Insert Size and Mean Length) and assemblies (N50). Additionally, if the Multi-Locus Sequence Type (MLST) for the isolate is available from pubmlst, the workflow also reports Sequence Type (ST) and the associated alleles.

**This output should be saved either to your LIMS or to a spreadsheet linked to the sequencing run and samples.

5.3 Example output for 1 *Salmonella* and 5 *Listeria* isolates.

A	B
Srain ID	Lab Confirmation
FDA1216271-C001-001	Listeria mono
FDA817806-S073-001	Listeria mono
FDA746634	Listeria mono
FDA1213377-C001-002	Listeria grayi
FDA933376-S060-005	Listeria innocua
FDA1213835-C001-001	Salmonella

Lab confirmed IDs for 6 isolates

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
File	C on ti gs	Le ng th	Es tC ov	N5 0	M ed ia n In se rt	Me an Le ngt h_ R1	Me an Le ngt h_ R2	M ea n Q_ R1	M ea n Q_ R2	Sch em e	S T							

A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S
FDA 1216 271- C00 1- 001	16	29 11 94 9	36 .7	47 62 10	32 1	148 .4	148 .4	36 .4	34 .6	liste ria_ 2	5	ab cZ(2)	bgl A(1)	cat (11)	da pE(3)	da t(3)	ldh (1)	lhk A(7)
FDA 8178 06- S073 -001	20	30 68 35 4	17 9. 6	52 54 38	32 9	234 .7	235 .2	36 .7	31 .9	liste ria_ 2	3 2 1	ab cZ(5)	bgl A(6)	cat (8)	da pE(62)	da t(6)	ldh (7)	lhk A(3 4)
FDA 7466 34	30	30 52 88 8	41 .4	29 39 47	32 0	148 .4	148 .4	36 .5	36	liste ria_ 2	-	ab cZ(2)	bgl A(1)	cat (11)	da pE(3)	da t(3)	ldh (1)	lhk A(~ 7)
FDA 1213 377- C00 1- 002	20	26 72 18 0	15 5. 1	47 31 81	27 0	147 .3	147 .3	37 .2	36 .1	-	-							
FDA 9333 76- S060 -005	9	28 81 86 9	21 3	14 98 79 0	30 3	232 .1	232 .2	37	36 .2	liste ria_ 2	1 4 8 9	ab cZ(25 0)	bgl A(21)	cat (83)	da pE(29 8)	da t(20)	ldh (4 58)	lhk A(2 16)
FDA 1213 835- C00 1- 001	37	48 32 36 5	34 .4	29 49 36	35 4	149	149	36 .6	35 .7	sent eric a_a cht man _2	2 1 4	aro C(14)	dn aN (7 2)	he mD (21)	his D(12)	pu rE (6)	su cA (1 9)	thr A(1 5)

MicroRunQC example report showing mlst ST results for different *Listeria* species.

The listeria database includes multiple species, including *Listeria monocytogenes* and *L. innocua*. If users want to investigate which Listeria DB corresponds to the resulting ST types, they can query the [Institut Pasteur](#) mlst database:

Example: query Listeria ST type here: https://bigsdbs.pasteur.fr/cgi-bin/bigsdbs/bigsdbs.pl?db=pubmlst_listeria_seqdef&page=query

5.4 Quality control threshold guidelines for the GenomeTrakr surveillance network. These are also relevant for NARMS and VetLIRN contributors.

*MicroRunQC users should follow QC threshold guidelines established by their respective surveillance coordinating body(s).

A	B	C	D	E	F	G	H	I	J

A	B	C	D	E	F	G	H	I	J
Quality metric	<i>Salmonella</i>	<i>Listeria</i>	<i>E. coli</i>	<i>Shigella</i>	<i>Campylobacter</i>	<i>Vibrio par.</i>	<i>Cronobacter</i>	<i>Enterococcus faecium</i>	<i>Enterococcus faecalis</i>
Average read quality Q score for R1 and R2	>=30	>=30	>=30	>=30	>=30	>=30	>=30	>=30	>=30
Average coverage	>=30X	>=20X	>=40X	>=40X	>=20X	>=40X	>=20X	>=50X	>=40X
<i>De novo</i> assembly: Seq. length (Mbp)	~4.3-5.2	~2.7-3.2	~4.5-5.9	~4.0-5.0	~1.5-1.9	~4.8-5.5	~4-5	~2.5-3.5	~2.5-3.25
<i>De novo</i> assembly: no. contigs	<=300	<=300	<=400	<=550	<=300	<=300	<=500	<=350	<=200