Analyzing whole genome sequencing data of *Haemophilus* isolates

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🡪 Please let me know if you need any help or if you find any errors! 😊

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# Overall workflow

**Note1**: some steps are only relevant for *H. influenzae* (e.g. MLST and in silico serotyping).

**Note2**: so far it is unclear how to properly correct for recombination in *Haemophilus* phylogenies without losing too much resolution (Howell et al. 2014; Pinto et al. 2019).  
**Note3**: Mutational resistance is not included in this scheme because no proper tools exist yet (to the best of my knowledge) to determine this type of resistance.

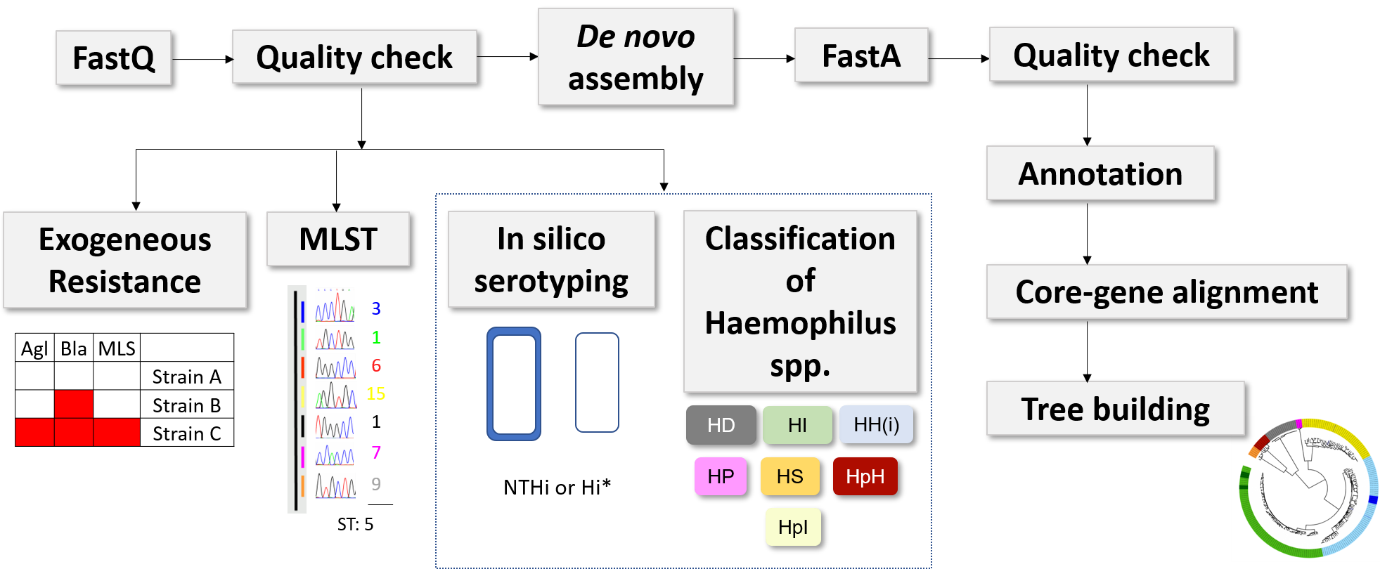


Figure 1 Example workflow for the analysis of whole genome sequencing data from Haemophilus isolates. MLST: multi-locus sequence typing. HI: Haemophilus influenzae; HI\*: serotypeable HI; NTHi: non-typeable HI; HH(i): Haemophilus haemolyticus (subsp. intermedius); HpH: Haemophilus parahaemolyticus; HpI: Haemophilus parainfluenzae; HP: Haemophilus pittmaniae; HS: Haemophilus sputorum; HD: Haemophilus ducreyi.

1. Perform a **quality check** of your WGS data (illumina paired-end fastQ files) e.g. with FastQC (general quality check of coverage, read length,...) and kraken2 (to check for contamination).
2. Determine in silico resistance, MLST, serotype and (sub)species (see below)
3. If you have multiple samples you can build a **phylogenetic** tree (e.g. with FastTree) using an assembly-based core-gene-alignment (e.g. generated by Roary) or mapping-based SNP aligment (e.g. generated by adjusted MTBseq pipeline). Visualize the tree (e.g. with iTOL). Plot presence/absence of marker genes and the final decision (e.g. serotype or species) on your tree using the itol annotation files that are automatically generated by the scripts described below.

# Installation of required packages/tools

Packages/tools can be installed in several ways. I like to use e.g. miniconda (<https://docs.conda.io/en/latest/miniconda.html>).

An example if you need to start from scratch:

1. Make sure you have access to a linux environment e.g. using a virtual machine or the Windows subsystem for linux (see Supplementary materials section). My scripts were tested using ubuntu 20.04 LTS.
2. Install (mini)conda (only needs to be done once)
3. Create a conda environment in which you will install your tool (e.g. SRST2) (only needs to be done once) and activate the environment (has to be done each time you want to use the tool/environment)

$conda create --name Analysis\_Haemophilus

$ conda activate Analysis\_Haemophilus

1. Install **SRST2** (https://github.com/katholt/srst2) (only needs to be done once)

$ conda install -c bioconda srst2

*This tool detects genes directly from raw sequencing data*

*Note: the scripts were tested with SRST2 v0.2.0.*

1. Install **GNU parallel** (https://www.gnu.org/software/parallel/parallel\_tutorial.html) e.g. using conda (only needs to be done once)

$ conda install -c conda-forge parallel

*This tool allows you to analyze multiple samples in parallel (decreases the computational time)*

*Note: the scripts were tested with GNU parallel v.20200722.*

1. Install other tools (e.g. shovill, prokka, roary,…)

conda install -c conda-forge -c bioconda -c defaults shovill

shovill –check

…

# Scripts and reference databases

## How to use

Please copy/download the scripts/reference databases from github to a folder on your computer!  
Please install the required tools/packages (see above). If you have used conda to install tools, don´t forget to activate the environment before running my scripts!

Margo`s scripts are typically run using the bash command:

$bash /PathToScripts/script\_name.sh

## Input and output files

Save your input files (typically fastQ files and reference databases) in a folder and specify the paths to these folders in the script you want to use (see below).

The output files depend on the script. However, if the script uses SRST2, following files are automatically generated:

1. Files per sample:

* \*.Log: log file that contains the user-defined parameters and info regarding the steps of the algorithm.
* \*\_\_fullgenes\_\_\*.txt: this file contains all hits with a horizontal coverage > user-defined minimum coverage threshold. Note that this file also contain hits with divergence > user-defined maximum divergence cutoff.
* \*\_\_genes\_\_\*.txt: this file contains for each loci one hit. All hits meet the criteria set by the user, i.e. horizontal coverage > user-defined minimum coverage threshold and divergence <= user-defined maximum divergence cutoff. Important note: if there are multiple hits meeting the criteria per loci, the last hit as listed in the \_\_fullgenes\_\_ file is used in the \_\_genes\_\_file. This is rather unexpected as one would expect the best hit (highest coverage + lowest divergence towards the reference allele) to be reported. This is highly likely a bug and was reported to the developer(s) in November 2020.
* SAM/BAM files and mpilup files (my scripts often contain commands to automatically remove these files as they can take up quite some space)

1. Combined file for all samples:

* \*\_\_compiledResults\_\_\*.txt: this file combines the information from \*\_\_genes\_\_\* files into one summary file.

## Parameters

Always check if ALL parameters of the script are correct (everything before the actual code starts, so before the \*######\*), using e.g. notepad++.  
  
Typical parameters that need to be changed are:

1. **PATH\_input**: Directory where you stored the (raw) paired-end illumina fastQ files e.g. "$HOME/FastQ"
2. **PATH\_output**: Directory where the final files will be stored e.g. "$HOME/Results"
3. **Threads/cpus**: Amount of threads/cpus that can be used to perform calculations. This depends on the performance of your computer/server (e.g. a laptop with a 4-core processor that runs two threads per core, has 8 logical processors 🡪 set threads ≤ 8). Typically, if you put this number on 0, you use all available resources.

Typical parameters that need to be changed unless your file name follows this convention „SampleName\_R1.fastq.gz” are:

* **FastqType:** Extension of your fastq file e.g. ".fastq.gz"
* **Fw**: Forward read notation e.g. "\_R1"
* **Rv:** Reverse read notation e.g. "\_R2"

Specific parameters for SRST2 are:

* **geneDB**: Path to nucleotide reference database e.g. "$HOME/Database/Refdatabase.fasta"
* **GeneMaxMis** (only if you don´t want to use default values): M
* **MaxDiv** (only if you don´t want to use default values): D
* **MinCov** (only if you don´t want to use default values): C

For *Haemophilus*, I use by default use 50M-15D-90C (instead of default SRST2 values 10M-10D-90C). However, if you want to detect very small contaminations or truncated genes, one can e.g. use 200M-80D-40C. Note that decision rules defined in the scripts do not necesserily apply anymore using these relaxed conditions.

* Additional parameters (see bottom of script) can also be added (e.g. minimum depth,…).

Specific parameters for GNU parallel are:

1. **Jobs:** Amount of samples to be analyzed in parallel. Similar to threads/cpus. Jobs=0 means you will run as many jobs in parallel as possible (depends on your computational resources, but sometimes leads to problems, so better set manually).

**IMPORTANT**: If it is the first time you use the script/database, you need to run this script ones with jobs=1. This is necessary because the first time, fai and bt2 files of the reference database still need to be created (errors occur when you analyze multiple samples in parallel during this step). Afterwards, you can set it to the value that best matches your computers` performance.

1. **PATH\_temp**: path were temporary files are stored (can be important to change if there is not enough space)

## Resistance determination

**starter\_Resistome\_SRST2.sh**

Determines the presence/absence of resistance genes (exogeneously acquired resistome) included in a resistance database using SRST2. A resistance database needs to be downloaded/uploaded for this script (see <https://github.com/katholt/srst2>).

INPUT:

* Raw paired-end illumina fastQ files (\*\_R1 and \*\_R2.fastq.gz)
* Resistance database (\*.fasta)

OUTPUT:

* SRST2 output files

## MLST analysis

**starter\_MLST\_SRST2.sh**

Determines the MLST type starting from raw sequencing data with SRST2. A MLST reference database needs to be downloaded/uploaded for this script (see e.g. <https://github.com/katholt/srst2>).

INPUT:

* Raw paired-end illumina fastQ files (\*\_R1 and \*\_R2.fastq.gz)
* MLST database (\*.fasta)
* ST definition file (\*.txt)

OUTPUT:

* SRST2 output files

## Classification and in silico serotyping

**starter\_Classification\_Of\_Haemophilus\_And\_Serotyping\_SRST2.sh**

This script can be used to detect and differentiate between all relevant human-related *Haemophilus* species: *Haemophilus parahaemolyticus* (HpH), *Haemophilus ducreyi* (HD), *Haemophilus parainfluenzae* (HpI), *Haemophilus sputorum* (HS), *Haemophilus pittmaniae*, typeable and non-typeable *Haemophilus influenzae* (HI), putative X-factor dependent and independent *Haemophilus haemolyticus* (HH). It cannot be used to classify “fuzzy” species with aberrant marker patterns. Although it can detect samples with multiple *Haemophilus* species to a certain extent, it cannot detect the presence of multiple strains from same species.

INPUT:

* Raw paired-end illumina fastQ files (\*\_R1 and \*\_R2.fastq.gz)
* Reference database (Class\_Haemophilus\_and\_Serotyping.fasta)

OUTPUT:

* SRST2 output files
* Classification\_Serotyping\_SRST2\_itol\_Decision\_Species.txt (this file can be dragged and dropped over an itol tree to visualize the species detected)
* Classification\_Serotyping\_SRST2\_itol\_Binary.txt (this file can be dragged and dropped over an itol tree to visualize the presence/absence of the genes)
* Classification\_Serotyping\_finalDecision.txt (contains the species and serotype of your strain in a simple text file)
* Classification\_Serotyping\_SRST2\_itol\_Decision\_Serotype.txt (this file can be dragged and dropped over an itol tree to visualize the serotype of *H. influenzae* strains)
* Classification\_Serotyping\_SRST2\_itol\_Decision\_Subspecies.txt (this file can be dragged and dropped over an itol tree to visualize the *H. haemolyticus* subsp. *intermedius* strains = presumptive haemin/X-factor-independent)

## Analysis of fuc operon

**Starter\_FucOperon\_SRST2.sh**

This script determines the presence/absence of the six fucose genes (fucK, fucR, fucI, fucA, fucU and fucP) using SRST2.

INPUT:

* Raw paired-end illumina fastQ files (\*\_R1 and \*\_R2.fastq.gz)
* Reference database (fuc\_operon.fasta)

OUTPUT:

* SRST2 output files
* Failed.txt (lists the samples for which an unexpected error occurred)
* OK.txt (lists the samples for which no unexpected error occurred)
* Fuc\_SRST2\_itol\_Binary.txt (this file can be dragged and dropped over an itol tree to visualize the presence/absence of the genes)

## De novo assembly

**starter\_assemble\_Shovill.sh**

This script allows you to make assemblies using the Shovill tool (https://github.com/tseemann/shovill).

Tip: Start with spades as assembler and change it to skesa if this is not working.

Note: If you use the function trimming, you trim with following trimmomatic parameters: LEADING:3 TRAILING:3 MINLEN:30 TOPHRED33. This will remove Illumina adapters, remove leading and trailing low quality or N bases (below quality 3) and will drop reads which are less than 30 bases long after these steps.

INPUT:

* Raw paired-end illumina fastQ files (\*\_R1 and \*\_R2.fastq.gz)

OUTPUT:

* Per sample: Shovill output files (e.g. log files and final assemblies in fasta format)
* For all samples: shovillOutput\_summary.txt (which can be used as a first quality check)

## Annotation

**starter\_Annotate\_Prokka.sh**

This script performs genome annotation using prokka (<https://github.com/tseemann/prokka>).

INPUT:

* Genome (.fasta)

OUTPUT:

* Annotated genome (.gff)

## Pan-genome and phylogenetic analysis

**starter\_Pan-genomeAnalysis-Phylogeny\_Roary-FastTree.sh**

This script calculates a pan and core-genome with Roary and creates a phylogenetic tree file using FastTree.

Note: To prevent over-splitting (Bayliss et al. 2019) of homologues genes into different clusters and thus to increase the size of the core (gene alignment), one can do two things:

* You can turn of paralogue splitting using the -s parameter
* Using a reduced blastP identity of e.g. 60% instead of 95%.

# References

Bayliss SC, Thorpe HA, Coyle NM, Sheppard SK, Feil EJ. 2019. PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. *Gigascience* **8**: 1–9.

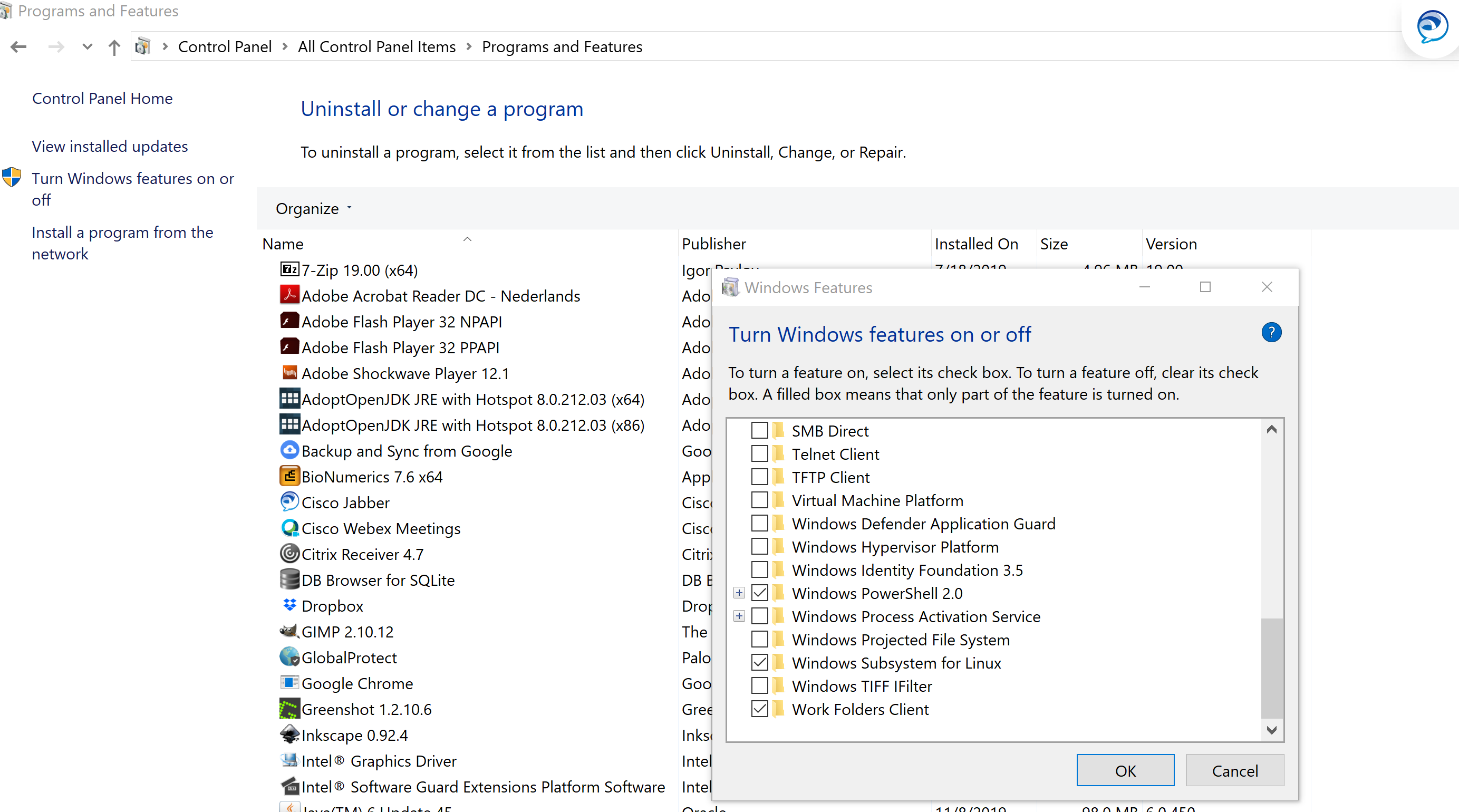
Howell KJ, Weinert LA, Chaudhuri RR, Luan SL, Peters SE, Corander J, Harris D, Angen Ø, Aragon V, Bensaid A, et al. 2014. The use of genome wide association methods to investigate pathogenicity, population structure and serovar in Haemophilus parasuis. *BMC Genomics* **15**: 1179.

Pinto M, González-Díaz A, Machado MP, Duarte S, Vieira L, Carriço JA, Marti S, Bajanca-Lavado MP, Gomes JP. 2019. Insights into the population structure and pan-genome of Haemophilus influenzae. *Infect Genet Evol* **67**: 126–135.

# Supplementary materials

## Workflow to install and run linux programs on a windows (desktop) PC

1. Activate Windows subsystem for linux in control panel > Programs and features > Turn Windows features on or off (only once)



1. Install latest version ubuntu (linux environment) on your PC from microsoft store (sometimes only works when VPN is disabled): e.g. Ubuntu 20.04 LTS
2. Open Ubuntu (you can search for it in start or make a desktop icon), install some basic packages (only once)

$ sudo apt update  
$ sudo apt install python  
$ sudo apt install python-pip  
$ pip install biopython