

JASEN debugging

0. Download/clone jasen from github repo `git@github.com:genomic-medicine-sweden/jasen.git`
1. make conda environment with `python=3.11`; `conda activate jasen`
2. `cd container && make`

```
git clone --recurse-submodules --single-branch --branch master \\
    git@github.com:genomic-medicine-sweden/jasen.git &&      \\
cd jasen

conda create -n jasen python=3.11
conda activate jasen

cd container
make # it will take upto ~4 hours to build all containers

cd ..
```

Download references and databases using singularity

```
#/mnt/SD2/Jyotirmoys/GMS-CGL/jasen --check directory PATH/TO/JASEN
ml singularity-3.8.6
make install
```

💡 Check before run `make install`

1. requires singularity module load `>=3.8`
2. requires `gzip /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/ShigaPass/Example/Input/*.fasta`

IMPORTANT

Would it be possible to use only one make instead two?

Load Singularity and update mlst database

```
#ml singularity-3.8.6
bash assets/mlst_db/update_mlst_db.sh
```

Check installation

```
make check
# (jasen-test) jyotirmoy@z6g4:jasen$ make check
# [] PASSED check for chewBBACA: Directories exist:
# - /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/cgmlst/staphylococcus_aureus/alleles_rereffed
# - /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/cgmlst/escherichia_coli/alleles_rereffed
# - /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/cgmlst/klebsiella_pneumoniae/alleles_rereffed
# [] PASSED check for bwa: Indexes exist in /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/genomes
# [] PASSED check for blast: Indexes exist in /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/mlst_
```

Get kraken standard database and untar

```
wget -O /mnt/WD1/ref/krakenstd.tar.gz https://genome-idx.s3.amazonaws.com/kraken/k2_standard.
tar xf /mnt/WD1/ref/krakenstd.tar.gz
```

Change Samplelist.csv file

modify the PATH/TO/JASEN in samplelist file

read1	read2
/mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/test_data/sequencing_data/SRR1011841.fastq.gz	/mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/test_data/sequencing_data/SRR1011841.fastq.gz
/mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/test_data/sequencing_data/SRR1011841.fastq.gz	/mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/test_data/sequencing_data/SRR1011841.fastq.gz

Change config/nextflow.base.config file

- Edit the root parameter in configs/nextflow.base.config - **provide absolute PATH/TO/JASEN**
 - root = "/mnt/SD2/Jyotirmoys/GMS-CGL/jasen"
- Edit the krakenDb, workDir and outdir parameters in configs/nextflow.base.config - **provide absolute PATH/TO/JASEN**
 - krakenDb = "/mnt/WD1/ref/krakenstd/" //edit if useKraken = true
 - workDir = "." //edit
 - outdir = "./outdir" //edit

- Edit the runOptions in configs/nextflow.base.config in order to mount directories to your run - *provide absolute PATH/TO/JASEN*

```
runOptions='--bind /mnt/SD2/Jyotirmoys/GMS-CGL/jasen/assets/test_data/sequencing_data/saureus
```

Run NextFlow command

```
ml nextflow-23.10.1
nextflow run main.nf \
  -profile staphylococcus_aureus \
  -config configs/nextflow.base.config \
  --csv assets/test_data/samplelist.csv
```

nextflow command output

```
(jasen-test) jyotirmoy@z6g4:jasen$ nextflow run main.nf -profile staphylococcus_aureus
Nextflow 24.04.4 is available - Please consider updating your version to it
N E X T F L O W ~ version 23.10.1
Launching `main.nf` [special_poitras] DSL2 - revision: 44c22f8cb2
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:assembly_trim_clean
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:assembly_trim_clean
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:save_analysis_metadata
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:assembly_trim_clean
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:save_analysis_metadata
executor > local (7)
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:assembly_trim_clean
[c6/c1b66a] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:save_analysis_metadata
executor > local (7)
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:assembly_trim_clean
[c6/c1b66a] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:save_analysis_metadata
executor > local (26)
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:assembly_trim_clean
[c6/c1b66a] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:save_analysis_metadata
[87/ea3ea4] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:skesa (p1000)
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:spades_illumina
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:spades_iontorrent
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:flye
[-] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:medaka
```

```

[68/c32b5e] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:quast (p1000)
[f2/fd354a] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:bwa_mem_ref (p1000)
[a4/e6ebeb] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:samtools_index_ref (p1000)
[13/72011b] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:post_align_qc (p1000)
[9a/afc991] process > CALL_STAPHYLOCOCCUS_AUREUS:CALL_BACTERIAL_BASE:sourmash (p1000)
[80/f168e1] process > CALL_STAPHYLOCOCCUS_AUREUS:bwa_index (p1000)
[2d/dc37d0] process > CALL_STAPHYLOCOCCUS_AUREUS:bwa_mem_dedup (p1000)
[a7/b6c4cf] process > CALL_STAPHYLOCOCCUS_AUREUS:samtools_index_assembly (p1000)
[82/a6e210] process > CALL_STAPHYLOCOCCUS_AUREUS:freebayes (p1000)
[a5/d3c2e7] process > CALL_STAPHYLOCOCCUS_AUREUS:mask_polymorph_assembly (p1000)
[49/d87ff1] process > CALL_STAPHYLOCOCCUS_AUREUS:mlst (p1000)
[97/31f33e] process > CALL_STAPHYLOCOCCUS_AUREUS:chewbbaca_create_batch_list
[0a/a9ab56] process > CALL_STAPHYLOCOCCUS_AUREUS:chewbbaca_allelecall (special_poitras)
[75/100127] process > CALL_STAPHYLOCOCCUS_AUREUS:chewbbaca_split_results (p1000)
[56/baaaaaf] process > CALL_STAPHYLOCOCCUS_AUREUS:amrfinderplus (p1000)
[17/ceff6c] process > CALL_STAPHYLOCOCCUS_AUREUS:resfinder (p1000)
[60/543d3a] process > CALL_STAPHYLOCOCCUS_AUREUS:serotypefinder (p1000)
[e0/1bb845] process > CALL_STAPHYLOCOCCUS_AUREUS:virulencefinder (p1000)
[84/c3b616] process > CALL_STAPHYLOCOCCUS_AUREUS:kraken (p1000)
[60/fafdb1] process > CALL_STAPHYLOCOCCUS_AUREUS:bracken (p1000)
[4b/b13e3a] process > CALL_STAPHYLOCOCCUS_AUREUS:create_analysis_result (p1000)
[b8/0b0cf7] process > CALL_STAPHYLOCOCCUS_AUREUS:create_yaml (p1000)
[56/ac3a83] process > CALL_STAPHYLOCOCCUS_AUREUS:create_cdm_input (p1000)
[d7/a16b6a] process > CALL_STAPHYLOCOCCUS_AUREUS:export_to_cdm (p1000)
[-          ] process > CALL_STAPHYLOCOCCUS_AUREUS:copy_to_cron
WARN: Access to undefined parameter `symlinkDir` -- Initialise it to a default value eg. `pa
Completed at: 15-Aug-2024 22:35:43
Duration      : 5m 29s
CPU hours     : 2.4
Succeeded     : 26

```