This folder contains files to automate generation of shell-scripts for sbatch and submittion of these.

autogen.sh:

\*\*\*\*\*\*\*\*\*\*\*\*

The overall sbatch-file.

Part 1: Finds all subfolders with fastq.gz and put them in the mapper.txt file

Part 2: Runs the filer.py python file.

Part 3: Runs files created by filer.py

filer.py

\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*\*

The file runs through each of the folders contained in mapper.txt and creates a sbatch-file for each and inserts the information from template.txt

The files will be created with the following data:

Filename: name1-name2-auto.sh

J/O/E: J/O/E\_name1-name2

Variables you can change:

name1: The first part of your file name. The name will be defined as the the first character after name1 and have the length=lenname1. It only takes the first case of the substring.

name2: The second part of your filename. The name will be defined as name2 and to the end of the line.

name3: Alternative to name2, if name2 is not found, then use name3.

The script then takes the file template.txt an replaces so all cases of 'sample' -> name1+name2 and 'sti' -> 'folder-path' and writes this modified template to the file 'name1-name2-auto.sh'

Next the script makes a sbatch-file called ny.sh file, and adds 'sbatch filename.sh' if filename contains '-auto.sh'

The ny.sh file is run by autogen.sh

BE CAREFUL, this script will submit an sbatch for each folder contained in mapper.txt.

The overall goal is to run the K9-pipeline for each subfolder containing fastq.gz files in a folder.