**AR sequencing analysis pipeline – command line download**

**Purpose:** This document describes the bioinformatics analysis of antigen receptor sequencing data starting from the fastq file download from Basespace and including the Interrogate analysis.

The analysis can be done on a **local computer** or on a **Compute Canada cluster**. Transfer of fastq files from Basespace to a local computer using the ‘Download’ option on Basespace will create a different folder structure than the download using command line (as is the case when using ComputeCanada for the analysis). The following refers to the download via command line and analysis on a Compute Canada cluster.

Log into compute Canada account

cd /work/def-smkeller/Shared/SequencingData/

#create project folder (see name in Basepace)

$ mkdir Run<no>\_<RunName>

#Clone folder with analysis scripts

$ cd Run<no>\_<RunName>

$ git clone https://github.com/theKellerLab/IntrgAnalysis

#create folder for Basespace data

$ mkdir –p Data/Basespace

#========= Transfer fastq files from Basespace to Compute Canada ==============

$ cd Data/Basespace

See separate document:

0\_preClntab/0\_FastqBasespace2ComputeCanada.docx

$rm download.txt

The resulting folder structure looks like this:

ds.0baa9e37cb924a74aa950860a791ea2f/

18-069171-2D1P3C1L1P1\_L001\_ds.0baa9e37cb924a74aa950860a791ea2f.json

Parry-Lola\_S23\_L001\_R1\_001.fastq.gz

Parry-Lola\_S23\_L001\_R2\_001.fastq.gz

...

#========= Change file structure ==============

$ bash 0b\_moveFastq\_AfterCommandLineDownload\_separateFolders.sh

#====== Combine fastq in one folder =============

bash 0\_Move&QcFastqFiles/0b\_moveOriginal\_commandLineDownload.sh

#====== Option 1: using fastqc & multiqc & trimmomatic (see fastp approach below) ===========

Advantage:

* fastqc output is amenable to multiQC analysis

Disadvantage:

* QC & trimming are two separate steps
* trimmomatic is apparently slow compared to other programs (<https://academic.oup.com/bioinformatics/article/34/17/i884/5093234>)

#====== run QC & multiQC =============

bash 1\_qcOriginal.sh

#====== trim reads =====

bash 2\_trim30.sh

#====== run QC & multiQC on trimmed reads =============

bash 3\_qcTrimmed30

#====== Option 2: using fastp ===========

Advantage:

* QC and trimming are done in one step
* fastp is faster than trimmomatic

Disadvantages:

* fastp output seems not amenable to multiQC analysis

1\_qcAndTrim\_fastp.sh

#========= upload to Interrogate ============

Upload