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### 1. Introduction

This manual provides an outline of the processing pipeline for NGS data based on the sUMI protocols developed in the lab. This pipeline performs the following steps, split into stages:

#### Stage 1:

- a) Join forward and reverse reads (merging)
- b) Split sequences according to sample barcode

#### Stage 2:

- c) Identify RNA barcode and collapse/error correct based on groups of sequences sharing same barcode

**If you find the methods in sUMI\_PROCESSING\_PIPELINE, please cite the following reference:**  
**Ahmed et al. Ultrasensitive amplicon barcoding for next-generation sequencing facilitating sequence error and amplification-bias correction. 2020**

## 2. User's guide

### a) Installation

Install CD-HIT(3):

- Download current CD-HIT at <http://bioinformatics.org/cd-hit>
- Unpack the file with “tar xvf cd-hit-XXX.tar.gz --gunzip”
- Compile the programs by “make”

Ensure that the following python module dependencies are installed:

- re, math, sys, collections, os, operator, commands

### b) Usage

```
python SUMI_PROCESSING_PIPELINE.py <input directory> <sample ID> <sample ID of pooled library> <SUMI primer file> <SUMI sample barcode id> <sample barcode file> <cd-hit location>
```

Where:

<b><i>Input command</i></b>	<b>Description</b>
<b><i>input directory</i></b>	Directory where source and output files will be located. Note that a TMP directory will be created here.
<b><i>sample ID</i></b>	ID of the sample to be analysed.
<b><i>sample ID of pooled library</i></b>	ID of the sequence library from which the sample sequences will be filtered. These must be in the following format for forward and reverse paired end reads respectively: /input directory/Sequences_ID_1.fasta /input directory/Sequences_ID_2.fasta
<b><i>sUMI primer file</i></b>	File containing information about the sUMI primers.
<b><i>sUMI sample barcode id</i></b>	ID of the sUMI primer used in for this sample
<b><i>cd-hit location</i></b>	Directory where CD-hit is installed.

For example:

```
python SUMI_PROCESSING_PIPELINE.py EXAMPLE_DIRECTORY/  
GR3_CLL_37_MB_CLL_1_Primers_MALBAC_barcode_FR2_table.txt  
MALBAC_UNI_Ind8_Barcode_groups_FR2_MALBAC.txt /local/cd-hit-  
v4.5.7-2011-12-16/
```