

SURPI

How to run SURPI

June, 2014

The test dataset used here (SRR1106548) is derived from plasma samples spiked with known titers of HIV (10^4 , 10^3 , 10^2 copies/ml) as described in Supplemental Methods [Naccache et al 2014](#) and is found [here](#).

The test dataset SRR1106548.sra includes paired-end data as well as orphan single-end read 1 (R1) and read 2 (R2) data from 3 separately barcoded samples corresponding to spiked HIV titers of 10^4 , 10^3 , 10^2 copies/ml. To restore the original FASTQ files (with the human reads removed), execute the following steps:

- 1) Install the SRA Toolkit (required for fastq-extractBarcodedSRA.sh). Installation instructions can be found [here](#).

- 2) Extract barcoded reads from SRR1106548.sra.

```
$ fastq-extractBarcodedSRA.sh SRR1106548.sra
```

- 3) Combine extracted FASTQ files into one input file SRR1106548.fastq.

```
$ cat bc*.fastq > SRR1106548.fastq
```

- 4) Create a config file

```
$ SURPI.sh -z SRR1106548.fastq
```

- 5) Start SURPI

```
$ ./go_SRR1106548 &
```

We've found it useful to monitor a SURPI run by using htop, and monitoring the logfile (SURPI.SRR1106548.log for the above example)

When complete, SURPI (when running in comprehensive mode) generates the following folders within the original run folder:

```
DATASETS_SRR1106548
deNovoASSEMBLY_SRR1106548
LOG_SRR1106548
OUTPUT_SRR1106548
TRASH_SRR1106548
```

The most useful data can be found in the OUTPUT_SRR1106548 folder. For more information on this data, look at the *Output_Interpretation.pdf* document.