

## ncct-mibi/nxf-bcl pipeline

For fastq files generation and demultiplexing, the [nxf-bcl pipeline](#) is used.

### Prerequisites:

- docker, nextflow
- in case docker is not available, the conda environment can be recreated using this env file:

<https://github.com/angelovangel/nxf-bcl/blob/master/environment.yml>

### Input:

- A sample sheet, which can be prepared with the [Illumina samplesheet generator](#) app (does not work in the Klinikum network, from within the Klinikum use [this link](#)). Download the sample sheet to the project folder
- Copy the whole Illumina run folder from the machine to a suitable location, e.g. to `~/Desktop/ncct-projects/20-bcls/`
- Locations of raw Illumina data - `/home/sysgen/novaseqdata` (IMGAG machines) and `/home/sysgen/illumina` (own machines)

### Output:

- results-bcl folder with fastq files
- multiqc report

For example, if the samplesheet is in the current project working directory, the nxf-bcl can be run like this:

```
nextflow run ncct-mibi/nxf-bcl --runfolder /path/to/runfolder --samplesheet  
20210118_samplesheet.csv
```