# **Data preparation:**

Utilizing Ubuntu windows (bash), to clean and prepare the data.

## 1. Folder Original\_data

Save all the original datasets which offer by clients.

### 2. Folder Clean\_data

#### Data:

Each patient has 8 datasets, which are activated or resting TCR record in 4 time points, a day before vaccinating and a week after vaccinating in 2016 and 2017.

After cleaning the data, each cdr3 correspond to its V-gene name, counts, and frequency. (cleaned data in sub-folder '2-digits' and '4 digits', as the client's request, the data cleaned into two versions, 2 and 4 digits which represent the digits number of V-Gene name.)

## If test needed:

```
2244 Oct 4 20:45 data_clean_2d
2243 Sep 3 20:15 data_clean_4d
141 Sep 3 20:10 run_2d
141 Sep 3 20:10 run_4d
```

There are 4 bash script in folder Clean\_data.

```
2. Clean data$ ./run_2d 2_digits
```

Just type (./run\_2d new\_folder), notice the

first parameter is new folder name, don't use the already existing one.

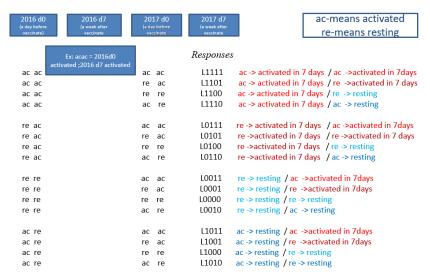
The script will create a new folder, all cleaned data would save in that folder.

```
2. Clean data$ ./run_4d 4_digits Same as 4 digits.
```

2. Clean data\$ chmod +rwx \*

PS: if meet the permission limited.

### 3. Folder data\_preparation



**FigureA:** Label activated TCR as'1', and resting as'0'.

#### Data:

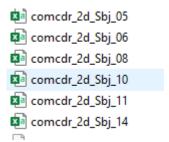
Then Intersect data sets (common cdr3 as the main key), we get 16 kinds of responses (FigureA). In joined dataset (common cdr3), except cdr3 and V-gene names, we have 8 attributes columns which are 4 time points' TCR count and frequency, and a target column which is the response.

#### If test needed:

In folder common cdr3, for example in the sub-folder 'VGene-2digits', which include cleaned data and several bash script.

```
VGene-2digits$ ./cmcdr 06 2016 2017 2d
VGene-2digits$ ./cmcdr 08 2016 2017 2d
VGene-2digits$ ./cmcdr 10 2016 2017 2d
```

While we just need to run script 'cmcdr', the **first parameter** is the patient number, **second** is the year 2016, **third** is the year 2017, **fourth** is 2d which represents handle 2 digits V-Gene datasets.



The common cdr3 dataset would appear in the same folder, Which would be used in machine learning and analysis.

VGene-4digits\$ ./cmcdr 06 2016 2017 4d VGene-4digits\$ ./cmcdr 08 2016 2017 4d VGene-4digits\$ ./cmcdr 10 2016 2017 4d Generate 4 digits datasets is the same.