

# Software instructions

## The cytokine model

In this section, we give the instructions on how to operate the software to

1. draw posterior samples of the mean log value of a certain cytokine in a certain group of patients
2. compare two groups' values of a certain cytokine

### Sampling posterier mean

To draw samples of the mean log value of a certain cytokine, for example TNF, in a group  $\mathcal{A}$ , execute

```
[cytk_mean, cytk_mean_smpls] = cytk_model(<log_cytk>, <y_bar>, <sigma>)
```

where input

- log\_cytk is a row vector of log(TNF) values of the patients in group  $\mathcal{A}$
- y\_bar is the mean of log(TNF) across **all** patients in the dataset
- sigma is the standard deviation of log(TNF) across **all** patients in the dataset

and output

- cytk\_mean\_smpls is a column vector of 3400 posterior samples of the mean log(TNF) in group  $\mathcal{A}$
- cytk\_mean is the mean of the above samples, and is viewed as the posterior mean of log(TNF) in group  $\mathcal{A}$

### Comparing two groups' cytokine values

To determine which one of group  $\mathcal{A}$  and  $\mathcal{B}$  has, on average, higher value of a certain cytokine, *e.g.* TNF, first execute the command in section 2.3.1 for group  $\mathcal{A}$  and  $\mathcal{B}$  respectively, then execute

```
p = comp_prob(<cytk_mean_smpls_A>, <cytk_mean_smpls_B>)
```

where

- cytk\_mean\_smpls\_A is the posterior samples of the mean log(TNF) in group  $\mathcal{A}$  drawn in the first step
- cytk\_mean\_smpls\_B similar for group  $\mathcal{B}$

and the output  $p$  is the mean posterior probability of group  $\mathcal{A}$  having, on average, lower TNF measurements than group  $\mathcal{B}$ .