

## Adding an intervention using ASPASIA

1. Solve `Polarisation_Model.xml` for 144 minutes with 1600 steps (1/10 of a day)
2. Add 1000 units of  $C_{17}$  to the model  
Add the following line to the settings file downloaded from the ASPASIA website (<https://www.york.ac.uk/computational-immunology/software/aspasia/>)

```
<!-- Path to SBML Model File-->
<pathToSimulationParameterFile>FILE PATH TO Polarisation_Model.xml INCLUDING
FILE NAME AND EXTENTION</pathToSimulationParameterFile>
<!-- Event -->
<parameter method="add" value="1000">C17</parameter>
<!-- Give new param file name -->
<newParamFileName> C17.xml</newParamFileName>
<!-- Path to your SBML solver results -->
<sbmlRunResultsFile>FILE PATH TO RESULTS FROM SOLVING MODEL INCLUDING FILE
NAME AND EXTENSION</sbmlRunResultsFile>
```
3. Using the `-s` option use ASPASIA to create the new file  
`./ASPASIA.bash -s FILEPATH TO SETTINGS FILE INCLUDING NAME AND EXTENSION`
4. Solve new model (`C17.xml`) for 144 minutes with 1600 steps (1/10 of a day)

## Generating files for Sensitivity Analysis Using ASPASIA

1. Update or add the following sections to the settings file.  
Add one `<parameter>` tag for each parameter that you want to vary. The ranges used in the model are contained in Supplementary File 3.

```
<!-- Parameters for Sampling -->
<algorithm>normal</algorithm>
<parameter min="0.002"max="2">a6</parameter>
<numberparameterSamples>200</numberparameterSamples>
```
2. Using the `-l` option use ASPASIA to create the new folder "LHC" in the file path containing 200 model files called `ParamFile1.xml` etc  
`./ASPASIA.bash -l FILEPATH TO SETTINGS FILE INCLUDING NAME AND EXTENSION`
3. Solve all 200 models in the absence of cytokine and following an intervention with  $C_{17}$  using the methods described in the previous section to add an intervention
4. Add the following tag to the settings file (and LHC if you are performing an LHC sensitivity analysis)

```
<experimentType>LHC</experimentType>
```
5. Using the `-h` option use ASPASIA to perform the analysis and produce graphs in the same folder as the supplied output files.  
`./ASPASIA.bash -h FILEPATH TO SETTINGS FILE INCLUDING NAME AND EXTENSION`

This process can be repeated any number of times using the output files generated following each intervention as new input files, allowing for the creation of multiple interventions. For example, the output files from solving the models after adding  $C_{17}$  can be used as an input before adding  $C_1$  or  $C_X$  to investigate stability or phenotype switching.