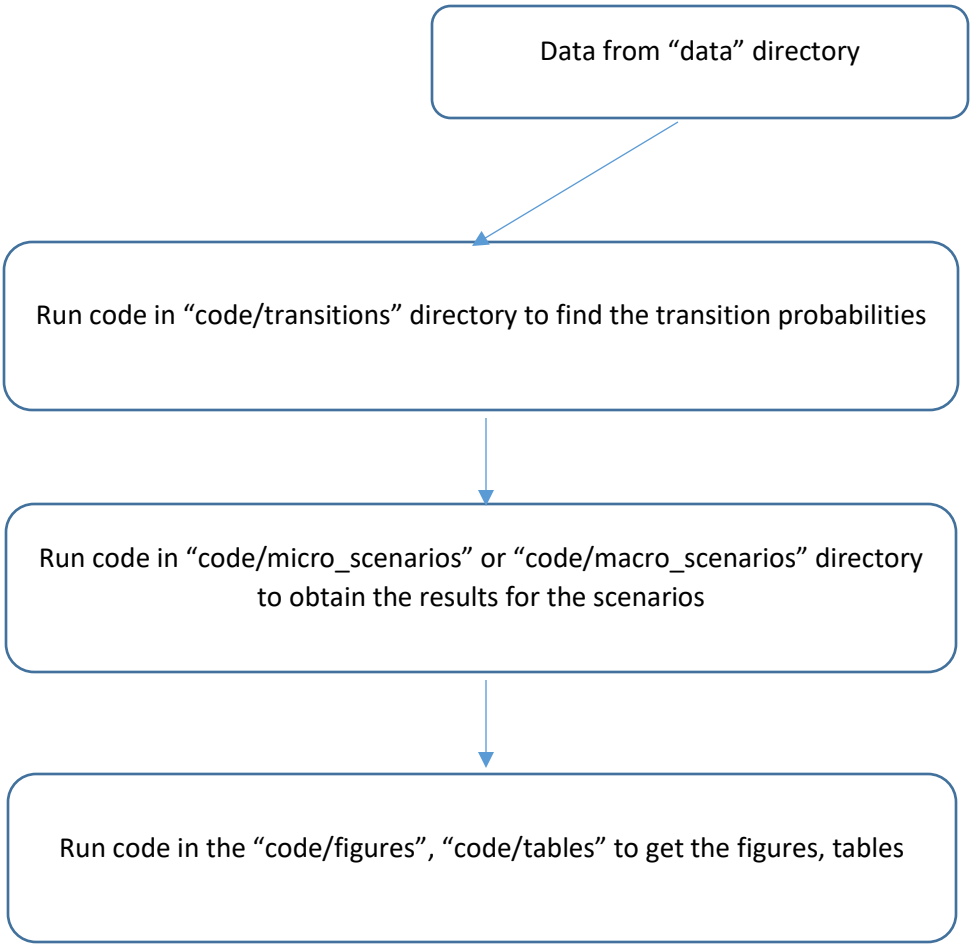
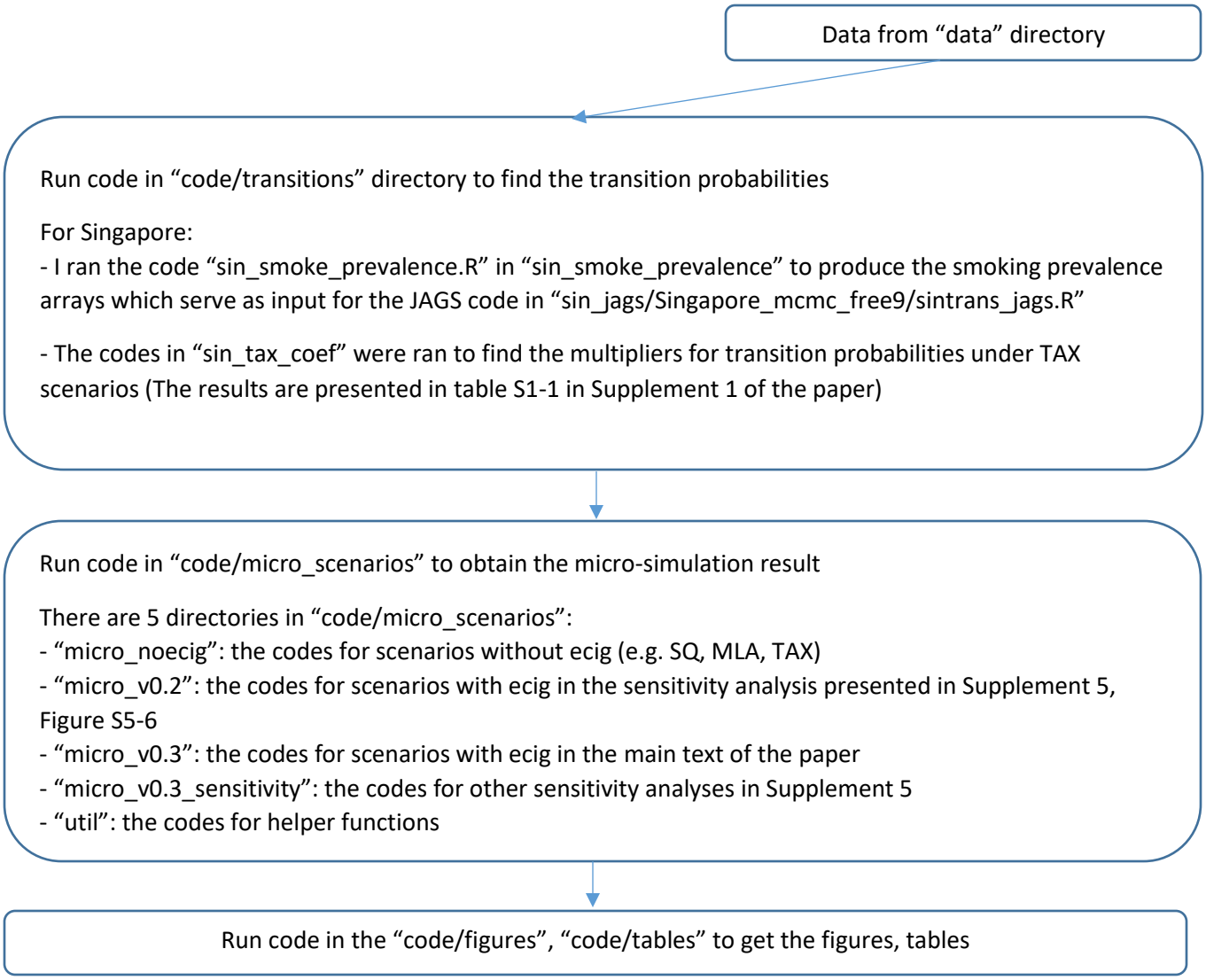
Outline


Data from “data” directory
Run code in “code/transitions” directory to find the transition probabilities
Run code in “code/micro_scenarios” or “code/macro_scenarios” directory to obtain the results for the scenarios
Run code in the “code/figures”, “code/tables” to get the figures, tables

More details

Please set the working directory in R to the "ecig_code" directory (i.e. the directory containing sub-folders: code, data, references) before running the codes



A direction to expand the codes to find transition probabilities to account for gender and race

If you follow the approach that I used, a simplistic way to expand the codes to find transition probabilities for different genders and races is:
- Write a code which is similar to “code/transitions/sin_smoke_prevalence/sin_smoke_prevalence.R” but filter for the specific gender and race. Then use the output smoking prevalence arrays as input to a JAGS code similar to “sin_jags/Singapore_mcmc_free9/sintrans_jags.R”

If you are comfortable with hierarchical modeling, perhaps you could also explore that option.

Please feel free to come up with more reasonable/efficient approaches.

A note about the micro-simulation approach that I used:

I wrote the micro-simulation in R utilizing vectorization. The code is easy to write and able to produce results quite fast. However, it takes up quite sizable memory.

You can reduce the memory used by writing code in Rcpp.