**Folder and File Dictionary**

## Model Core Files

This folder contains all the folders and files needed for the model

### Documentation

This folder contains various word documents explaining aspects of the model. This includes a suer guide about how to run the model, details about the model parameters, and diagrams explaining the models. Some of these are a little out of date and need updating before version 1.3 is released but should give you a general idea about how the model works hopefully.

### Mancriskscreen

This folder contains all the stuff needed to run the model and analyse the results.

#### MANC\_RISK\_SCREEN\_main\_script.R

This is the main R script for running the model to generate data for different screening strategies which you can then analyse separately. You can change the controls at the start of the script to run different screening strategies. The model outputs a large number of tables with outcome data from individuals as RData files.

#### MANC\_RISK\_SCREEN\_functions

This script contains most of the core functions required to run the model. These are imported in by the main script at the start of running the model so you don’t need to do anything with these.

#### Negsample function

This is an additional function which runs the simulation for people who don’t get cancer in the model. It works by working out who does and doesn’t attend different screening appointments in a big table using vectorised functions which dramatically increases the speed of the model. QALYs and costs are calculated for each individual and they are saved in an output RData file.

#### Risksample function

This is an additional function which is called at the start of the model when gensample is set to TRUE. This function creates a new sample of women to simulate through the model. It can also draw PSA values or PSA values with wider distributions for PSA analysis or GAM fitting depending on the control settings in the main script.

#### Params, PSA\_params, intervals\_params

These R scripts contain the core parameters used as inputs to run the model in the base case, for PSA, or for wide distribution PSA (for GAM fitting). These can be edited by the user if they wish to use different input data.

#### Analysis folder

This folder contains scripts which are used to analyse the data generated by the model. The main ones are the base case analysis and PSA analysis (which we are still working on). The misclassification\_analysis and preventative\_drug\_analysis scripts are left overs from some development work and will be deleted (after I check with my colleague that’s ok!).

The base case analysis script combines the saved output data from the model into a single data.table then can be used to create cost-effectiveness planes and a table with incremental cost-effectiveness ratios/net benefit/ranking of interventions at different thresholds. It is currently hard coded to the 6 interventions in the paper we are writing but I am going to work on generalising it depending on which strategies were chosen.

There is also a Validation script in this folder. This is a work in progress to allow us to quickly check the clinical outputs against observed data.

#### Data

This folder contains data in csv files which is read into the model for certain input parameters

#### Deterministic results/Deterministic results with misclass

This is where the outputs of the model are stored (tables with observed outcomes for each women) prior to combining for analysis.

#### GAM models

This is where the code for estimating GAM models for PSA is stored and the models themselves are stored (needs updating).

#### Profiling

Some development code, please ignore

#### PSA results

As deterministic results above but for PSA results

#### Risksample/risksamplewithmisclass

This is where the tables of women to simulate are stored after being generated by the risksample function. When gensample is turned off in the model the tables in this folder are re-used rather than re-generated. NB: when changing the sample size in the model or generally if errors occur in running the model try deleting the contents of this folder and re-running gensample.