Feedback for Group 5 (Koeken et al.) by Alex and Rusheel

BSC Model

1. Please don't use setwd() to set the working directory manually. It will only work on your PC and no one else's. Use relative paths inside the root directory.
2. Files missing/Not all files provided: The supplementary files required to run the program such as getSingleAttribute.R, getMultipleAttributes.R and trial_dataset.Rdata was not present in the zip. This made it impossible to run the program unless the user had the files already and placed their copies in the folder. Always helps to provide files even if not strictly necessary rather than leaving out files and potentially handicapping your program from the beginning. **Alex:** Totally agree with Rusheel on this. As scientists, we should make it as easy as possible for others to replicate our results. It's good programming practice too.
3. Use of descdist positive but I don't understand the graph. An explanation via a comment of the graph or how it helped you decide which distributions to check would be better.
4. Line 67 has an error/typo(s) where the distributions are labelled incorrectly. For example, Weibull is labelled exponential in the test and thus gives the wrong conclusion. Lognormal is the best fit not gamma.
5. Similar error on line 88 again.
6. Positive: use of filters instead of for loops to stratify data.
7. Positive: calculating response based on tx1.ci.event: compact one line code instad of using for loops.
8. Line 355. You use the wrong data (with instead of without response) which gives you the wrong probability on line 399.
9. Rest of the code seems fine.

EXP Model

1. Most if not all of the data analysis/distribution fitting is the same as the previous model. Feels unnecessary to erase everything and begin again. Would save time to do this part just once. Combining the two files will help with this. Or you could use the

source() function to load the variables into the global environment from one file dedicated to distribution fitting.

2 Line 253. You use the wrong data (with instead of without response) which gives you the wrong probability later.

3 Aside from these minor issues, rest of the code seemed fine.

PSA

1 Please name your files descriptively. You have a file named Part2 group5.R (which is the PSA simulation) and then a file named group5_11932_2305696_step2.9+PSAresult-group5-1.r which is actually the data analysis.

2 We see that the analysis has been repeated. If you make one single mistake (like we found above) you have to change the code in, what, 3 different files? This is very error-prone.

3 Variable naming: I am a fan of expressive variable names rather than terse ones, but Percentage_Minor_Event_Poor_condition_withresponse is too long even for me. Think creatively about how you can shorten the names.

4 It's good that you defined all the parameters in named subsections.

5 For function Tx2.Response.Exp, you made an else if case for every possible combination, which is very hard to read. You could have first split the function with if (Tx1.Response==1) / else, then used nested if statements.

6 Good that you put comments to describe what each event means.

7 Could you explain how you implemented Tx1.Event? We are not entirely sure if the way you have done it would produce correct results. You are basically checking if the random number falls between a certain range like death % + some other %.

8 The Tx1.Event function is a mess of else if statements. It is good programming practice to use helper functions.

9 Line 764: good that you are testing death first. The events are mutually exclusive and you test the most important event first.

10 Tx1.Event.exp could have been cut down on length. You only need to assign a value to rand once.

11 In function FollowUp1.event.Exp one line 904, you are returning time (?!) when you should only return the event and use the FollowUp1.time to determine the time from the event.

12 Why did you code this function: Followup2.event? It is pointless as it always returns 0, and there is no followup 2 in the model anyway; the patients go into palliative care and survive for 100 days.

13 Line 1194 does not look correct to us. You are adding a value to the QALY attribute (that's what `mod="+"` does). You should only need the following code:

`set_attribute(key="QALY", mod="+", value=function() ((get_attribute(bsc.sim, "QALY"))*Followuputility)` The extra addition is practically doubling the QALY value.

14 Actually, shouldn't you be taking into account how long the patients spend in the follow up period? It looks like they get the same amount of utility regardless of whether they live or die.

15 Line 1299 and 1300: The names seem a bit strange: `"Exp.Tx2.Response.Exp"`

Data Analysis

1. You are meant to analyse the data we were provided with (1000 runs) not your own PSA simulation data.
2. It's nice that you used the literature to inform your discussion. We are more skeptical than you regarding the simulation results—a WTP of €27,000 is already one of the highest in the world, and if only 50% of the simulation results fall under that, well, let's just say it's not a very promising intervention strategy. That means there is a 50% chance the strategy is not cost-effective. Would you introduce a new best standard of care procedure based on a cost-effectiveness probability of 50%? We wouldn't.