Here are the files for ARC1. I need to make beam files for other arcs but my script is not working so have to do it manually.

Once you run this with “bdsim --file=arc1.gmad” you should get a root file “output.root”.   
Run that output through rebdsimHistomerge using the command “rebdsimHistomerge output.root new\_file.root”.

If you use this script below, you can get a plot for the dose rate.  
  
**import pybdsim**  
**import matplotlib.pyplot as plt**  
  
**a = pybdsim.Data.Load("new\_file.root")**  
  
**# get the 3d scoring mesh histogram**  
**sc = a.histograms3dpy['Event/MergedHistograms/phantomMesh-doseInGy']**  
  
**# data, errors, and cell positions**  
**data = sc.contents[0,0,:]**  
**err = sc.errors[0,0,:]**  
**z = sc.zcentres # similar for x & y**  
  
**plt.errorbar(z, data, yerr=err)**  
**plt.xlabel('Local Z position (m)')**  
**plt.ylabel('Dose per event (Gy)')**  
  
**plt.show()**

You can also take a look at the new root file by using root in command line. In linux you can do this by typing

“root new\_file.root” and then when you get to root command line you can say “TBrowser b” which will give you an interactive browser to look at the root file in depth.