

N of simulated tracks vs pT



N of associated tracks (simToReco) vs pT

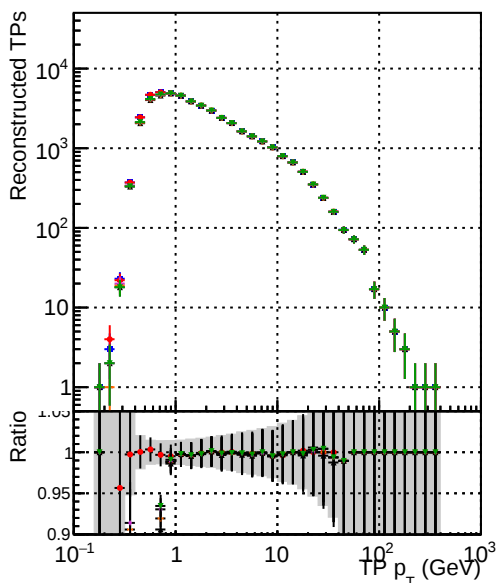
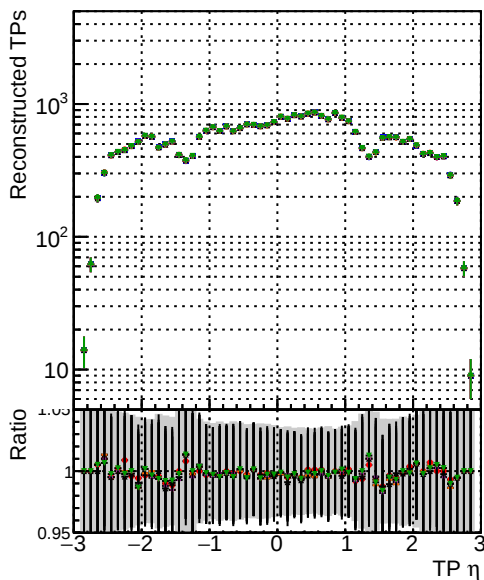
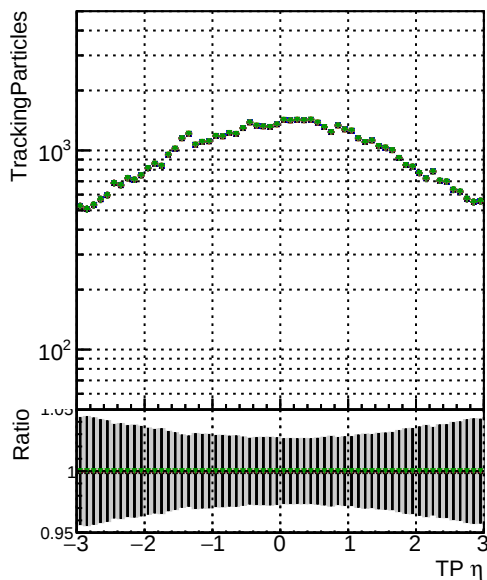
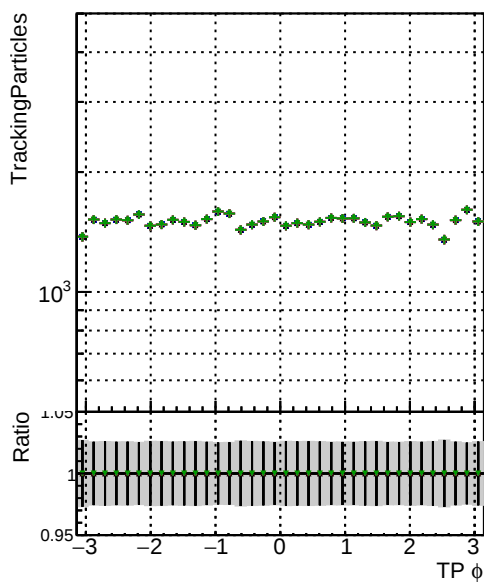


Figure 1 displays a grid of 180 small plots showing the number of significant genes (N of significant genes) for various combinations of methods and parameters. The methods are DCM, DCM+step2, tibar-phase1, and tibar-phase1-newgeom. The parameters are original, step2, tibar-phase1, and tibar-phase1-newgeom. The plots are arranged in a 6x5 grid (with the last row having 4 plots). The y-axis for each plot is 'N of significant genes' ranging from 0 to 100. The x-axis for each plot is the parameter name. The plots show that the number of significant genes generally increases as the parameter value increases, with the tibar-phase1-newgeom method showing the highest number of significant genes.



N of simulated tracks vs phi



N of associated tracks (simToReco) vs phi

