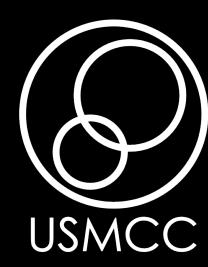


investigation of the BIB BUG

Tova Holmes University of Tennessee, Knoxville



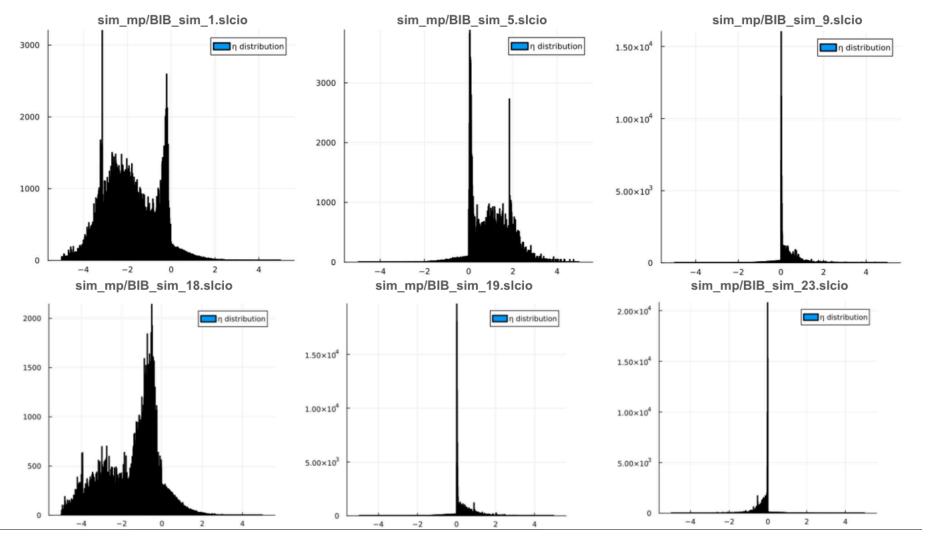
MAIA Meeting October 24, 2025

THE PROBLEM

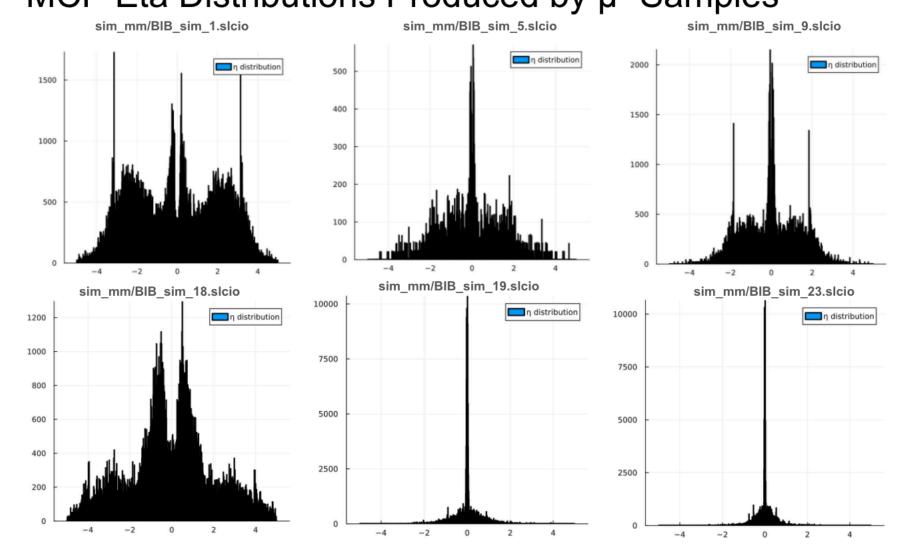
Identified by Hubert Pugzlys

- Troubling BIB distributions in slcio files
 - µ- beam appears symmetric
 - suspiciously peaked and totally different for each file (true for both beams)
- Overall resulting asymmetry <u>confirmed</u> by Rose

MCP Eta Distributions Produced by µ+ Samples



MCP Eta Distributions Produced by μ- Samples



WHERE DOES THIS COME FROM?

- Distribution in simulated in FLUKA for one beam (μ +)
 - Files available on osg: /data/fmeloni/FLUKA/summary*_DET_IP.dat
- Python scripts for turning these FLUKA files into slcio files <u>here</u>
 - Since v4, have been using fluka_remix.py
 - Before that (not sure exactly when) <u>fluka_to_slcio_new.py</u>
- Notes from 10TeV doc on how to run:
 - > python3 detector-simulation/utils/fluka_to_slcio_new.py -n NUMBER path/to/FLUKA/summary1_DET_IP.dat
 BIBinput.slcio
 - run with -i 1 to mirror the beam, to get full BIB every input file needs to be run twice, with and without this option.
 - -n NUMBER defines how many times each particle should be cloned to a random phi. The NUMBER depends on the fraction of total bunch crossing that we simulate in FLUKA.

note: using mapping /ospool/uc-shared/project/futurecolliders/data:/data

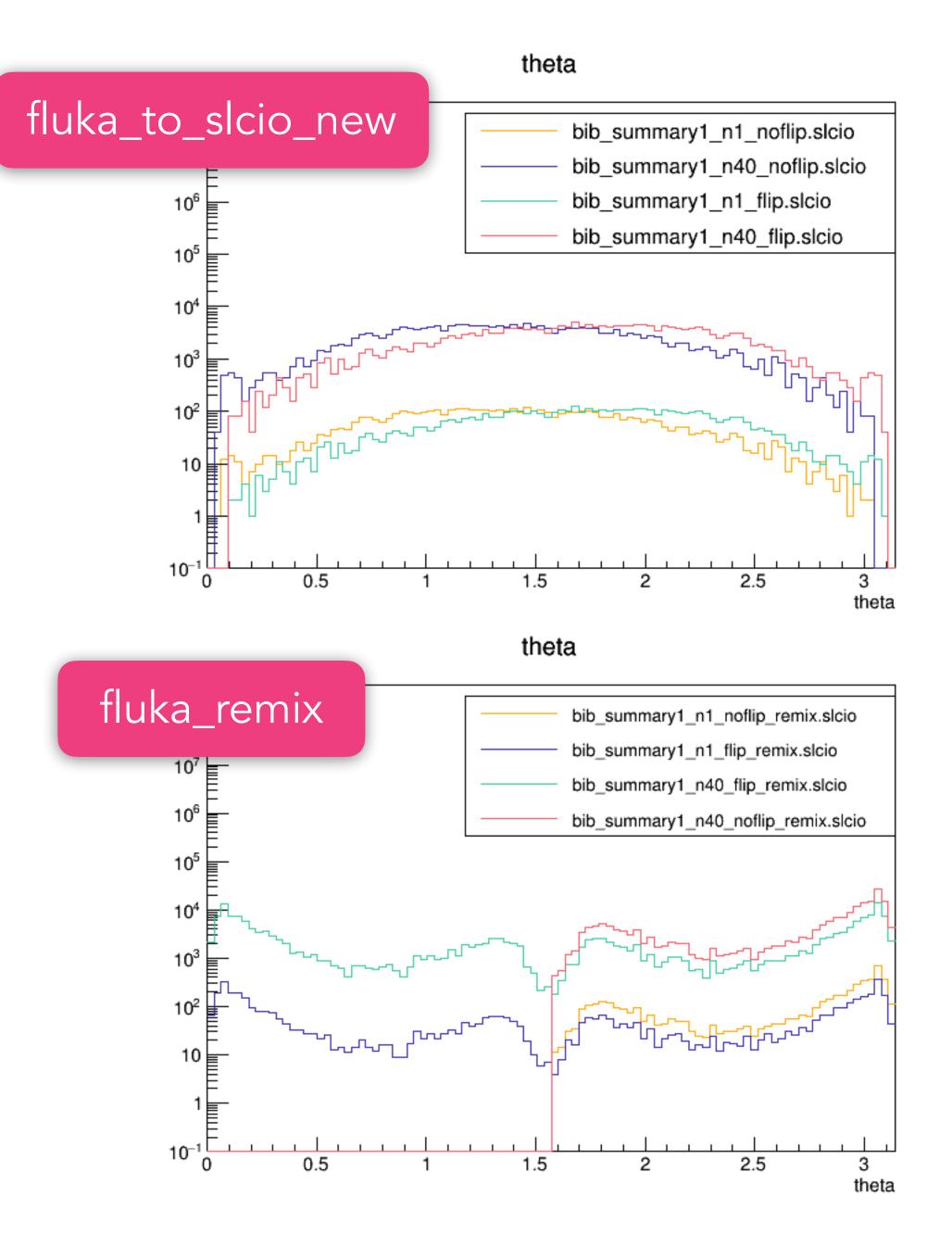
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- Distribution in simulated in FLUKA for one beam (μ +)
 - Files available on osg: /data/fmeloni/FLUKA/summary1_DET_IP.dat
- Python scripts for turning these FLUKA fill
 - Since v4, have been using <u>fluka_remix</u>.
 - Before that (not sure exactly when) fluk
- Notes from <u>10TeV doc</u> on how to run:
- major change with fluka_remix.py was to rotate all particles with the same parent muon together to preserve correlation
- resulted in some restructuring of the code
- > python3 detector-simulation/utils/fluka_to_slcio_new.py -n NUMBER path/to/FLUKA/summary1_DET_IP.dat
 BIBinput.slcio
 - run with -i 1 to mirror the beam, to get full BIB every input file needs to be run twice, with and without this option.
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RUNNING THESE FILES

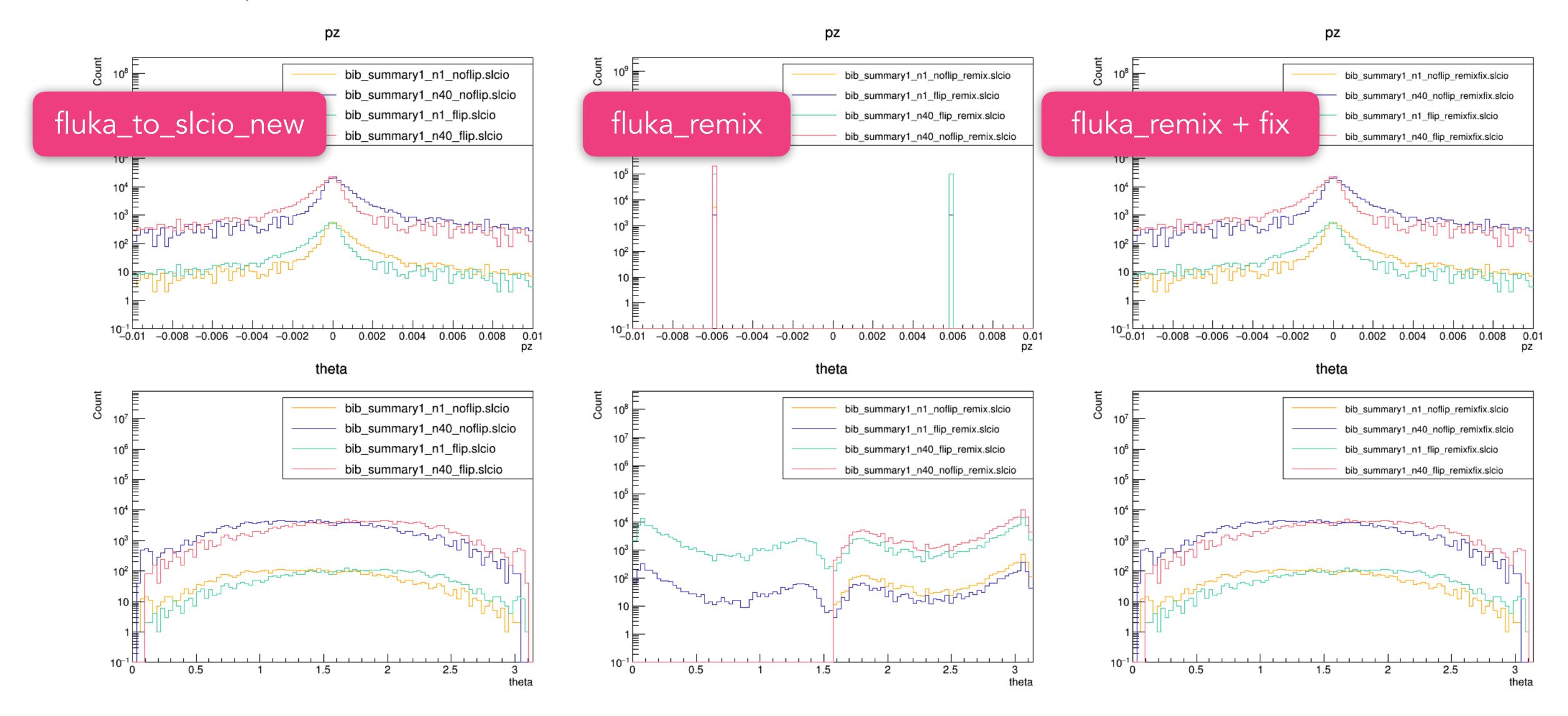
- In all cases, running on the same input file:
 - /data/fmeloni/FLUKA/ summary1_DET_IP.dat
- Ran version flipped/not flipped, and with just one phi value/40 iterations
- Clearly introduced this bug with the switch to fluka_remix.py
- With fluka_remix, see both flipped and non-flipped change, but see the symmetry introduced in the flipped version



BUGHUNT

- Compared the two files to hunt down the bug
- Eventually identified the source:
 - due to the code restructure, a momentum vector was not being reinitialized with each new particle
 - px, py were being recalculated due to the phi rotations, overwriting the uninitialized value, but pz was either left alone or flipped in sign (depending on flip or no flip)
 - symmetry in flipped file was due to flipping the same pz over and over
- Committed a fix here

FIX IMPACT



NEXT STEPS

- day to have some CI/CD capable of running these spot checks!

 Fix is in, now need to
 - re-run on all FLUKA files (and ideally run a validation script on those)
 - propagate to all our samples
 - re-make all our plots
- Impact?
 - the asymmetry should go away
 - the amount of BIB won't change
 - ullet only p_z was affected, and each file would have had a different value not clear if this would have created many systematic effects besides asymmetry? we shall see!

Tova Holmes, University of Tennessee

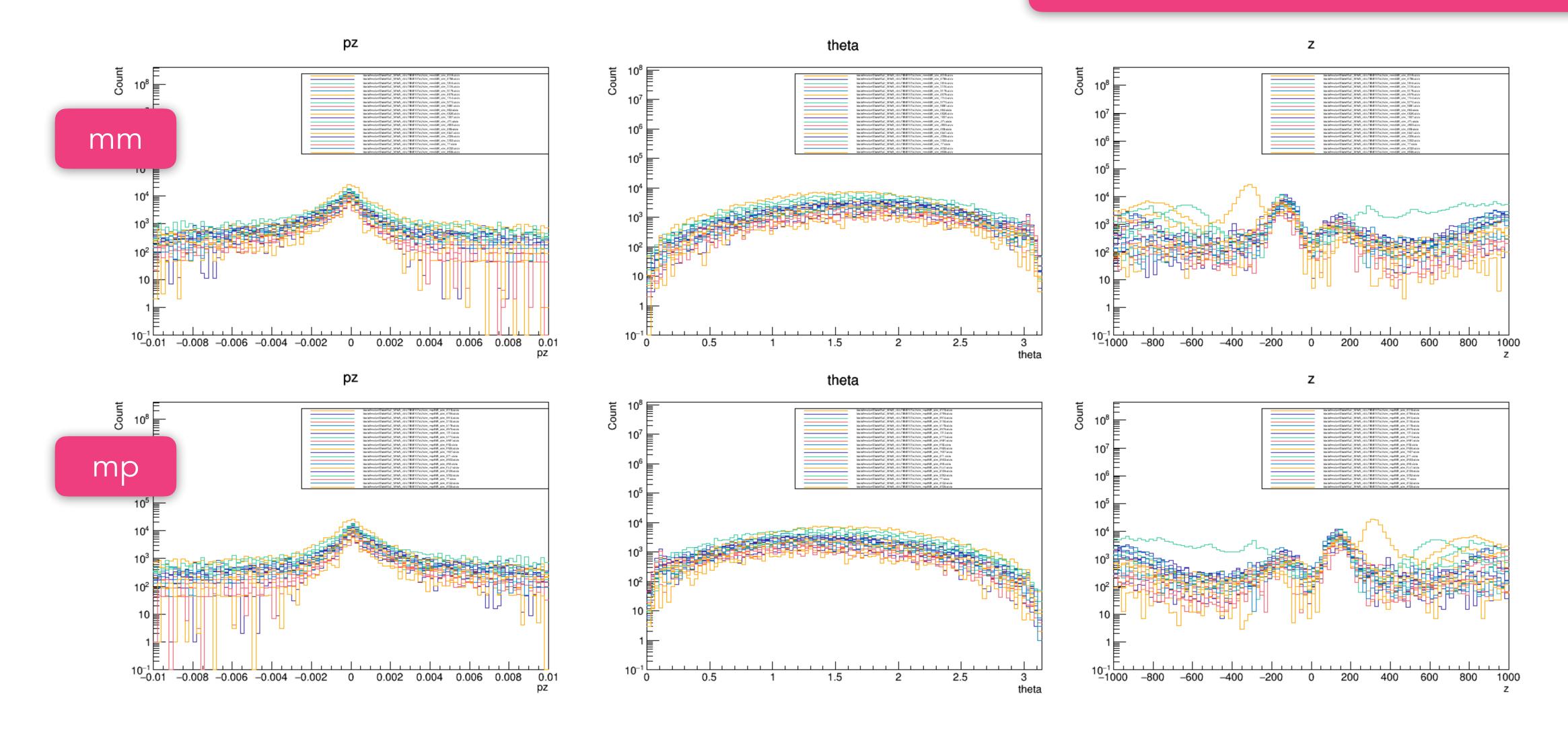
note: would be great one

FOLLOW UP

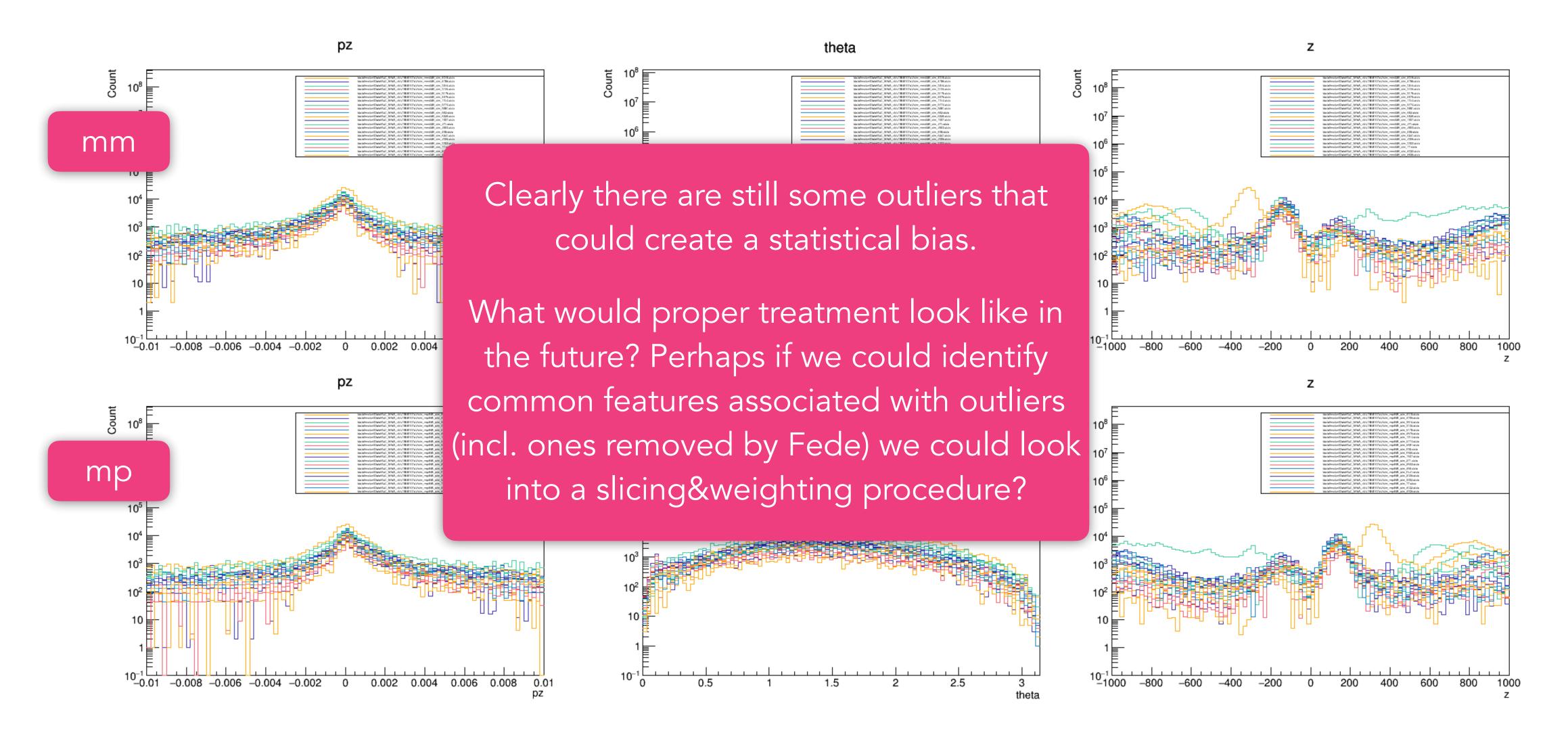
- Federico turned around new input files very quickly!
 - /ospool/uc-shared/project/futurecolliders/data/fmeloni/ DataMuC_MAIA_v0/v7/BIB10TeV
 - Note from Fede: "there were 3 files where the 42x particle cloning resulted in files that were huge outliers in particle multiplicity/file size (>>1 GB per file instead of the typical <20 MB). I have arbitrarily removed these as they could easily bias our overlays"
- Made some quick plots from them to see if things look OK

SPOT CHECKING

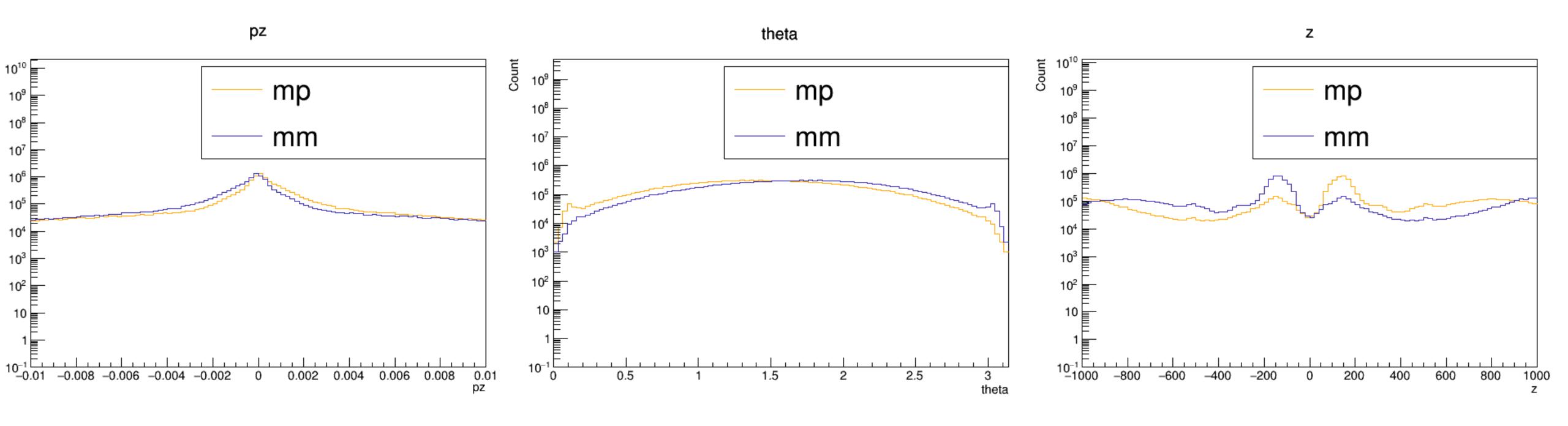
20 random files from mm and mp each (same file numbers for each sign)



SPOT CHECKING



OYERALL DISTRIBUTIONS



WHAT STATISTICS DO WE EXPECT?

- In an example input file I looked at, there were 62 unique mother muons resulting in around 5000 particles
 - We replicate each of these 62 by a factor of 42 with random phi rotations
- We have 6663 input files for mm, 6661 for mp (after removal of a few outlier files), so around 400,000 unique mothers, each replicated 42 times
 - Difference potentially due to difference in sim random seed?
- Our total sample with all the rotations produces 4 events worth of data
 - We randomly select ¼ of them for each event to overlay
 - i.e. each mother particle shows up ~10x in a given event

HOW COULD WE SLICE?

- Seems likely that the outlier events are due to showers with very little pathlength through the nozzle
 - Could be possible to correlate that with parent muon properties (or parent electron?)
 - Unfortunately only have this information in the FLUKA/ files, so would need to run on those to figure out potential solutions