

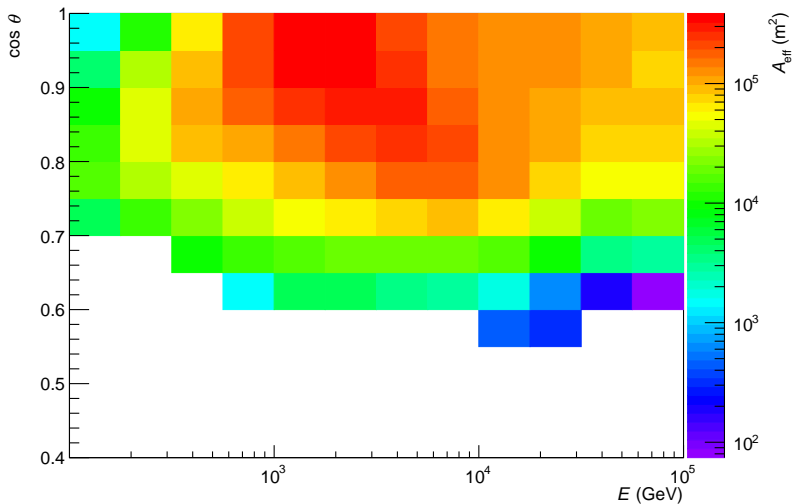
Understanding feed-down in Crab analysis

- How much does mixing matrix distort observed bin contents?
- Can answer by comparing reconstructed-energy distribution with expected true-energy distribution under best-fit spectral hypothesis.
- The latter is calculated as flux times effective area times live time.

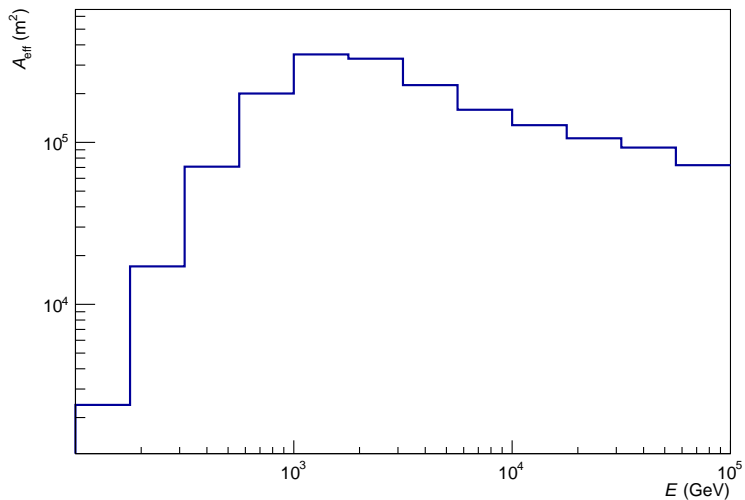
Computing effective area

- AERIE has a Python script that computes effective area but does not allow arbitrary cuts or event weighting.
- XCDF's Python bindings don't allow use of arbitrary cut strings, so I wrote an AERIE C++ application with the desired functionality, `sweets-eff-area`.

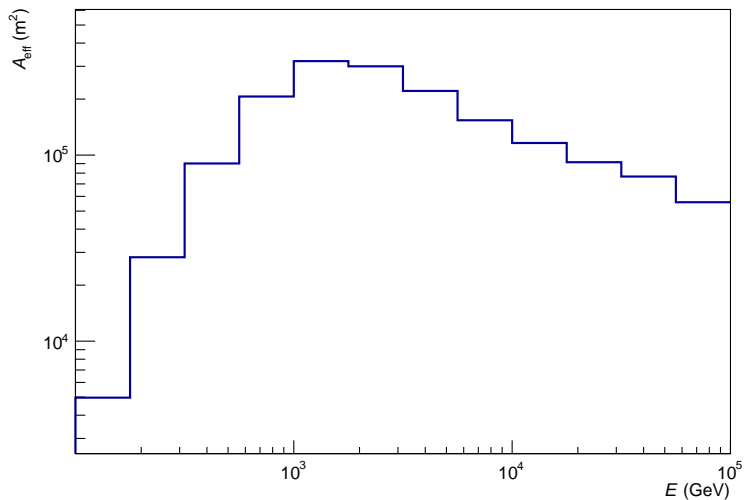
Effective area vs. energy and zenith (sweets.TWgt)



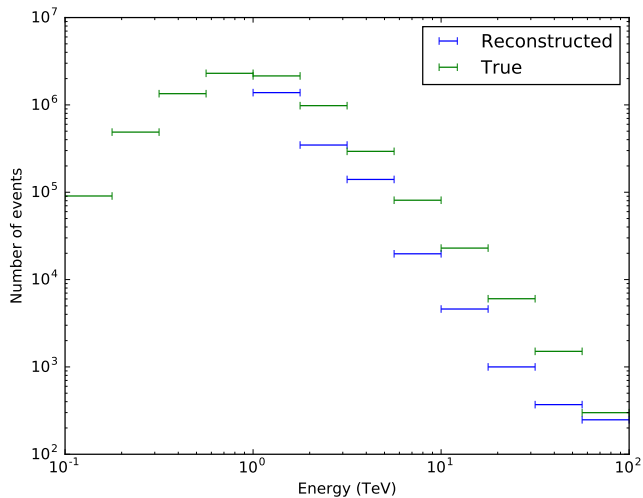
Effective area vs. energy (sweets.TWgt)



Effective area vs. energy (sweets.oneWgt)



Effect of convolution



- Reconstructed distribution only seems noticeably flatter near the end.
- Feed-down may be mostly mitigated by the fact that the bin width is larger than the resolution of the energy estimator.
- Not clear why the True curve lies above the Reconstructed one.