Method for parametrisation of nuclear interaction

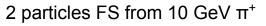
Parametrised nuclear interaction

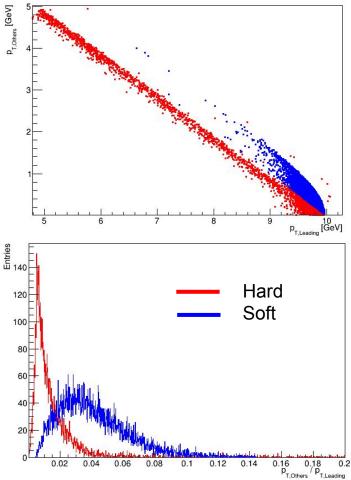
- Dataset production
 - Geant4 used as reference truth data
 - Particle gun used for <u>different, fixed</u> initial momenta
 - Record of final state (FS) particles + properties
- Filter events
 - Only interested in common hadrons
 - Remove leptons, photons, nuclei etc. from FS
 - These are usually small / rare contributions
 - Remove events with decays
 - Significant different kinematics
 - Handled by different module
 - Remove FS particles below 50 MeV
 - i.e. particles captured in detector material
- Event labeling / categorisation
 - Events from different categories have different FSs
 - Labels:

Labeled soft

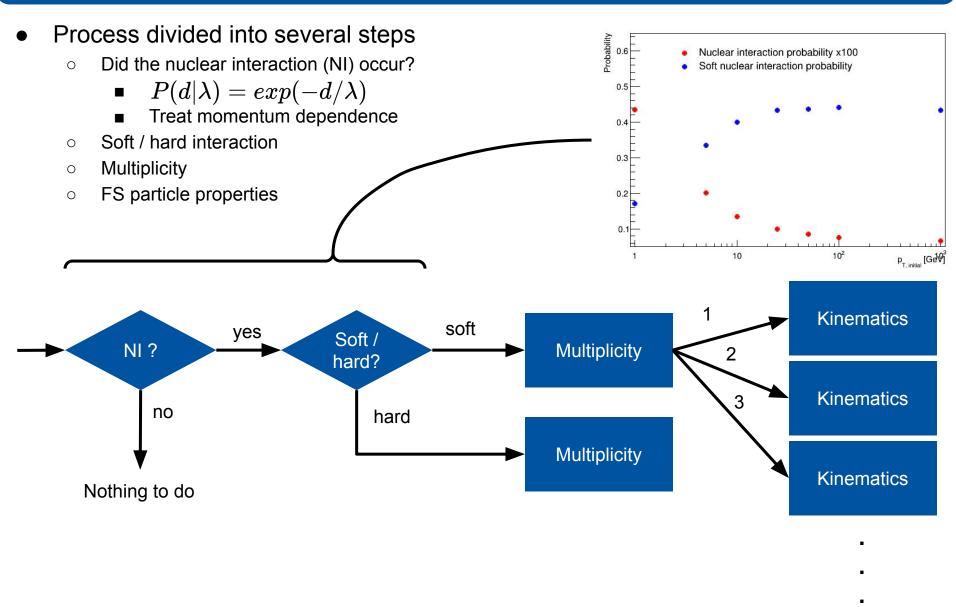
if all fulfilled

- Nuclear interaction in event?
- FS Multiplicity
- Soft / hard nuclear interaction
 - Did the initial particle survive? (same PDG ID & most of the initial momentum)
 - Kinematic separation by $\Sigma_i p_{T,i} \geq p_{T,initial}$
 - Is there a FS that looks like that?



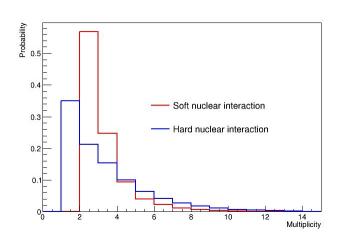


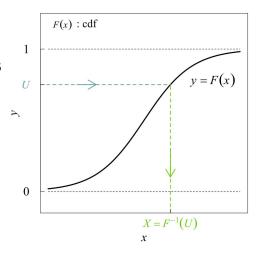
Workflow



<u>Multiplicity</u>

- Multiplicity distribution derived from data
- Sampling according to distribution required
- Inverse transform method
 - Consider the CDF
 - $\circ \quad y = F(x) \propto U(0,1) \Leftrightarrow x \propto F^{-1}(U)$
 - \circ Sample from uniform distribution rather than from F(x)
 - $\circ \quad \textbf{Bin lookup} \text{ instead of searching for F} \rightarrow \textbf{No fit functions!}$
- At that point the interaction type and the multiplicity is known
- Particle kinematics need to be calculated next
- Starting with the momentum:
 - Each generated particle is constrained by the momentum of others
 - Ordering required for structuring
 - FS particles are ordered by momentum (= generations)
 - Individual FS momentum distribution derived for each generation
 - Inverse transform method applicable (theoretically...)





Correlated sampling

- Goal: Find $ec{p} = \{p_1, p_2, \dots, p_n\}$ for multiplicity n and absolute values p
- Momenta constrained by correlation
 - Distributions transformed to $erf^{-1}(2F(x)-1) \propto G(0,1)$ with the gaussian distribution G 0
 - This is equivalent to a mapping from Uniform to Gauss distribution Ο
 - Considering $F(x) \Rightarrow \vec{F}(\vec{p})$ which leads to 0

Explicit correlation!

$$G(\vec{p}'|\vec{0},\vec{1}) \propto exp(-rac{1}{2}\vec{p}'^T \Sigma^{-1} \vec{p}')$$

Correlated sampling

Ο

De-correlate the distribution = diagonalise Σ Transformation of G into eigenspace of Σ with $\Sigma_{i,j} = \begin{cases} e_i & i = j \\ 0 & i \neq j \end{cases}$ with the eigenvalues $\{e_i\}$ Ο

$$\rightarrow$$
 Sample distribution becomes:

$$G(ec{p}''|ec{0}, \sqrt[]{e}) \propto exp(-rac{1}{2}\Sigma_i rac{p_i''^2}{e_i}) = \Pi_i G(p_i''|0, \sqrt{e_i})$$

Produced samples ${\,\vec{p}}^{\prime\prime}$ are transformed back to recieve ${\,\vec{p}}$

Independent distributions!

- Momentum samples are related relatively to each other
 - No constrained for their combination, yet 0
 - Combined constraint given by adding the distribution of the **sum of momenta** \rightarrow n+1 distributions Ο
 - Allows re-scaling afterwards Ο
- Convenience scaling: Parametrisation of $\vec{p} = \left\{ \frac{p_1}{p_{initial}}, \frac{p_2}{p_{initial}}, \dots, \frac{p_n}{p_{initial}}, \frac{\Sigma_i p_i}{p_{initial}} \right\}$

Angular distributions

 Sampled momenta allow calculation of polar opening angles θ_{ij} via invariant mass between particle i and j

$$M_{ij} = \sqrt{2p_i p_j (1 - cos(heta_{ij}))} \Leftrightarrow heta_{ij} = cos^{-1} \left(1 - rac{M_{ij}^2}{2p_i p_j}
ight)$$

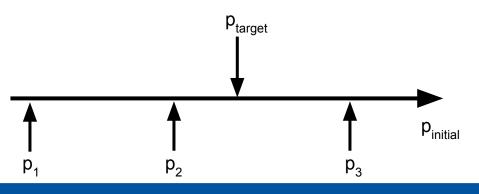
- First approach used j = i + 1
 - Dangerous since each value would affect the next one
 - An unfortunate sampling would produce strange results
 - More stable choice: Consider angle wrt initial particle (i = 0)
- Same sampling idea used as for the momenta
 - \circ But without re-scaling \rightarrow n distributions
 - Produces set of invariant masses
- Matching
 - Domain of cos^{-1} is [-1,1] but p_i and M_{0i} are sampled independently

$$\circ$$
 A match is achieved iff $orall j:rac{M_{0,j}^2}{2p_0p_j}\in[0,2]$

- If this is not the case:
 - As these are 2 correlated samples, no value could be modified independently
 - $\blacksquare \quad \text{Need to re-sample a set} \rightarrow \text{It was chosen to be the momenta}$
 - This scenario occurs in low density regions in the M-p-phase space
- Calculated polar opening & (assumed) azimuthal angle $\propto U(0, 2\pi)$ can be translated to particle angles

PDG ID and interpolation idea

- FS particles are recorded and re-ordered
- PDG ID association by creation a dedicated table
- Model:
 - i-th particle only creates the (i+1)th particle
 - Initial particle produces the 1st particle
- Look-up table derived from data for which PDG ID produces which PDG IDs with which probability
- Until now: Parametrisation using a sample with fixed initial momentum
- Next step: Interpolation using the parametrisations
- Strategy:
 - Repeat the parametrisation for initial momenta $p_{initial} \rightarrow Parametrisations$ for $p_1,...,p_n$ obtained
 - \circ Construct FS for ${\rm p_{target}}$ by using only the two neighbours ${\rm p_2}$ and ${\rm p_3}$



Interpolation

• Spacing between the samples

- If the distributions of p_2 look similar to the ones from p_3 then the ones from p_{target} should be similar, too
 - Refers to the general shape (except a scaling factor)
- If p_{initial} becomes bigger the shapes of the distributions change slower
 - Spacing increases as p_{initial} is increased
- How to obtain the target distribution from p_2 and p_3 ?
- Two ideas were tested:
 - (Considering only the kinematics)
 - Distributions are assumed to be similar \rightarrow Spectra of eigenvalues are also similar (for M&p)
 - Define a weighted set of eigenvalues from p₂ and p₃ that looks like a set from p_{target}
 - Sample from this distribution (in eigenspace)
 - Perform the back-transformations for p₂ and p₃ independently
 - Receive a weighted combination from both sets
 - It was observed that the matching rate dropped significantly
 - Use the weights as probabilities to choose between p_2 and p_3
 - Perform all samples & back-transformations using the chosen one
 - Scale results to p_{target}
 - Provided a high matching rate but allows only one weighting scheme
- Latter more promising
- Quality of interpolation depends (only) on the weighting scheme

<u>Summary</u>

- Parametrisation for nuclear interaction derived
- Process is separable into individual sub-steps
- Allows sampling from histograms without requiring fit functions
- Out-of-the-box applicable for arbitrary initial momentum
- Parametrisation can be extended for interpolation
 - Only requires weighting of neighbouring distributions
- Spacing between parametrisation adaptable
 - New samples extend the set of parametrisations
 - No re-parametrisation of prior samples required!
 - Interpolation quality can be improved by additional samples
 - Similarity can be improved
 - Importance of weighting scheme can be suppressed