supernemo collaboration

Hitchhiker’s guide to Cimrman module

A Mostly Harmless Guide to Track Reconstruction

Tomáš Křižák

Collaboration meeting | July 2026


"Space is big.
It's really, really big.
You just won't believe
how vastly, hugely,
mind-bogglingly big it is."
– The Guide
ββ candidate
SUPERnEMO
HITCHHIKER'S GUIDE TO CIMRMAN MODULE
A MOSTLY HARMLESS GUIDE TO TRACK RECONSTRUCTION
CIMRMAN
HOW TO RECONSTRUCT A TRACK (MOSTLY HARMLESS)
1. Collect hits
2. Build candidates
3. Fit in Legendre space
ρ
z
4. Select the best one
z
y
y
x
DON'T PANIC.
JUST RECONSTRUCT.
42
Vertex
Track candidate
Likelihood
ℒ(θ)
Time
t
Mostly Harmless
Drift hits
Reconstructed track
Calorimeter cluster
DON'T PANIC

Topics

1. Full algorithm overview + code implementation

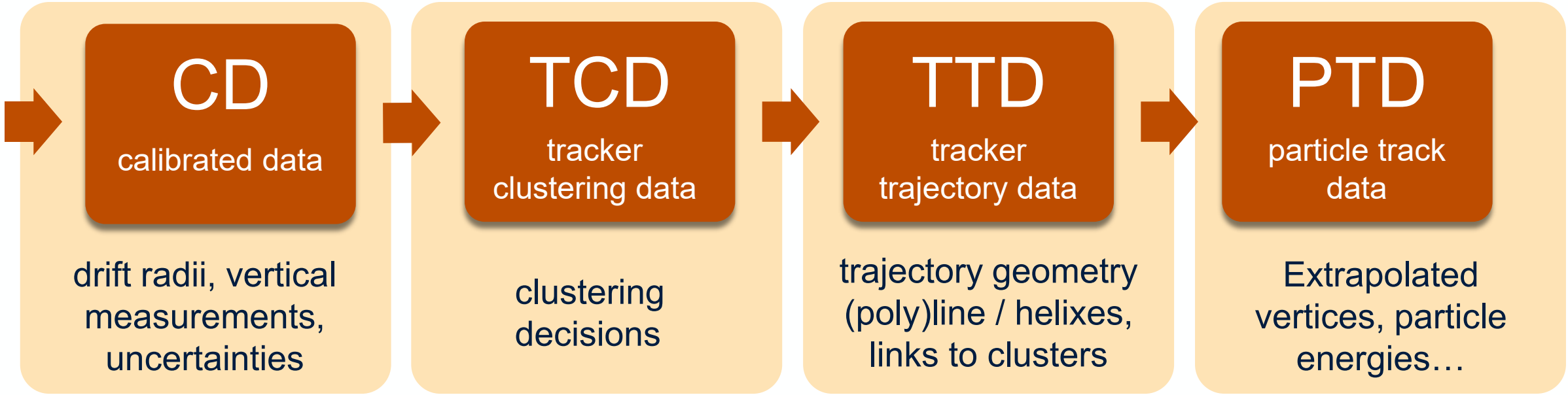
Topics

1. Full algorithm overview + code implementation
2. New polyline reconstruction framework

supernemo collaboration

1. Algorithm overview

Cimrman's place in the pipeline



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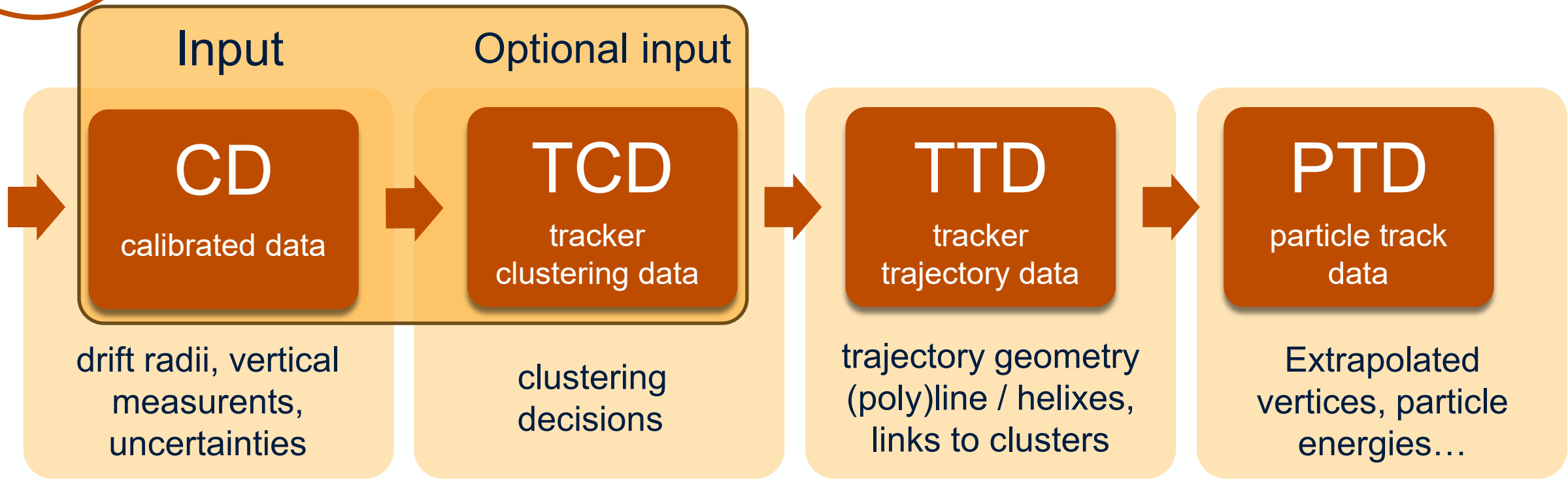

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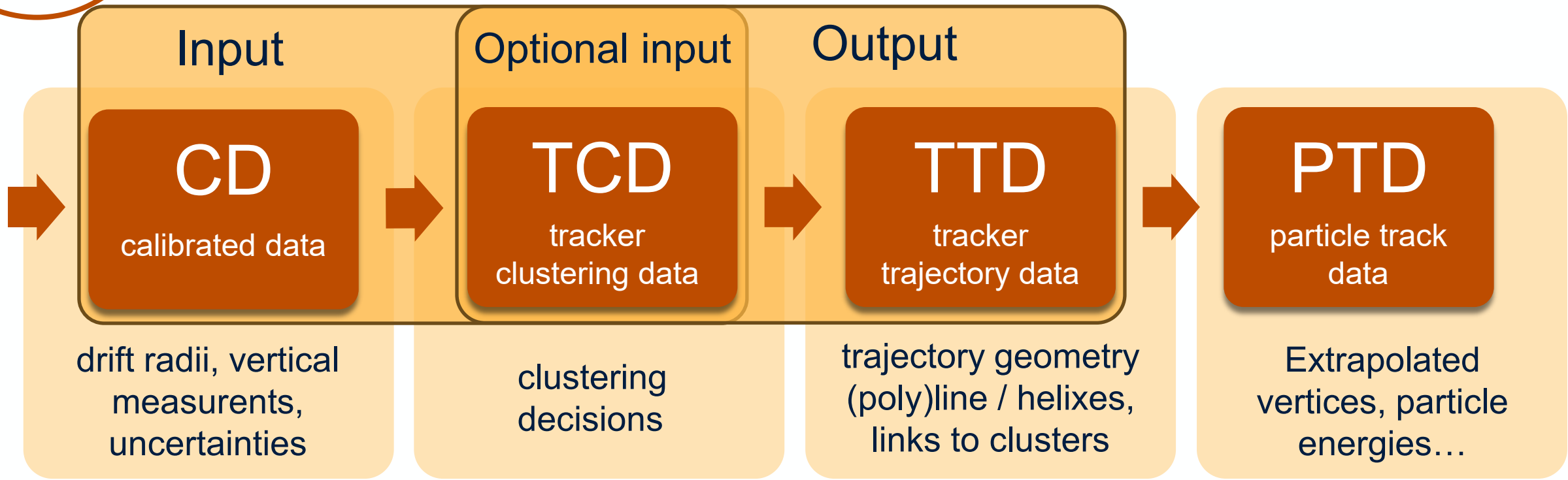
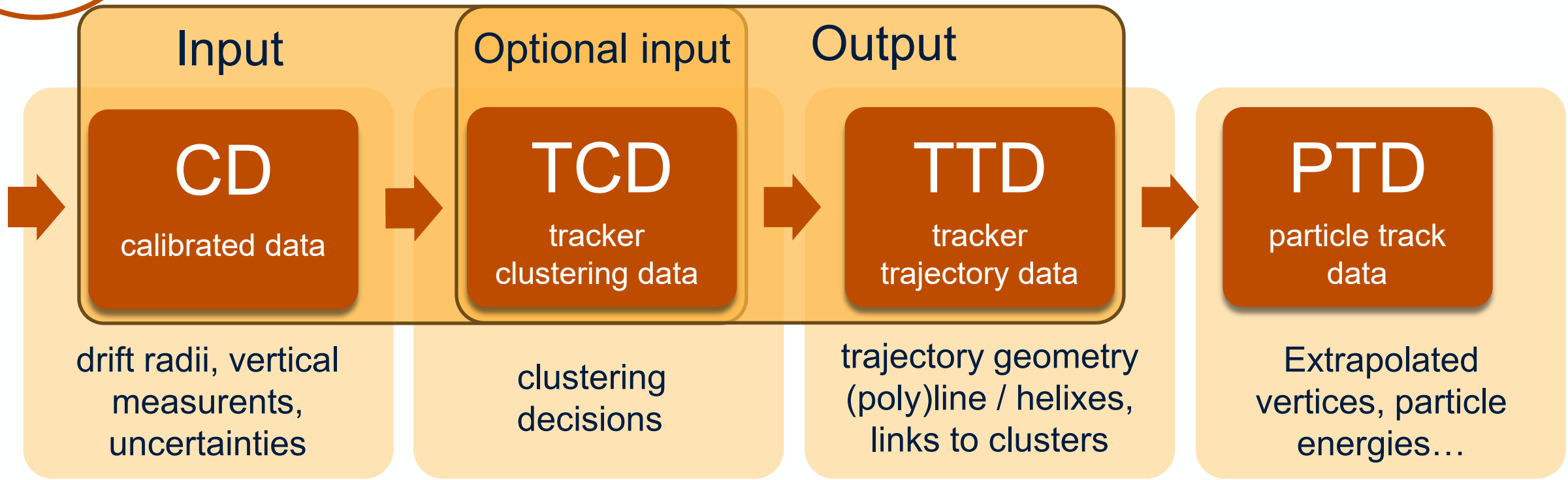


Cimrman's place in the pipeline



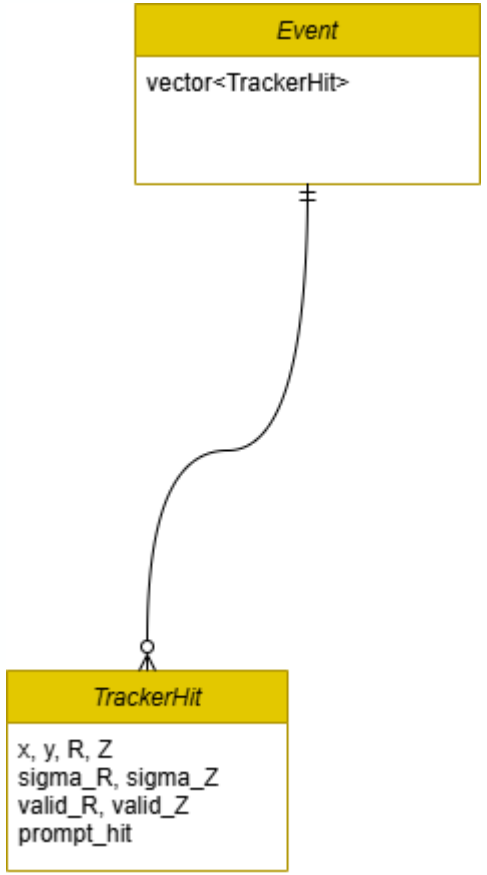
Warning: Cimrman currently changes existing TCD bank. Should create a new bank instead.

Cimrman.cpp

- What happens when you run flreconstruct with Cimrman?
- Once at the beginning:
  Cimrman::initialize(…)

Cimrman.cpp

- What happens when you run flreconstruct with Cimrman?
- Once at the beginning:
  Cimrman::initialize(…)
- Algos: Cimrman's internal worker class
- Per event:
  Cimrman::process(…) {
    CD, (TCD) → Cimrman data structure
    Algos::process(…)
    Cimrman data structure → TCD, TTD
  }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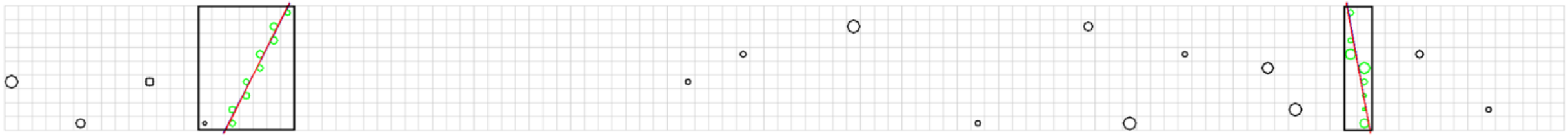
TrackerHit
x, y, R, Z
sigma_R, sigma_Z
valid_R, valid_Z
prompt_hit

Step 1: preclustering

- Division of event into subevents = ***preclusters***
- Based on:
  - (horizontal 2D) distance



Step 1: preclustering

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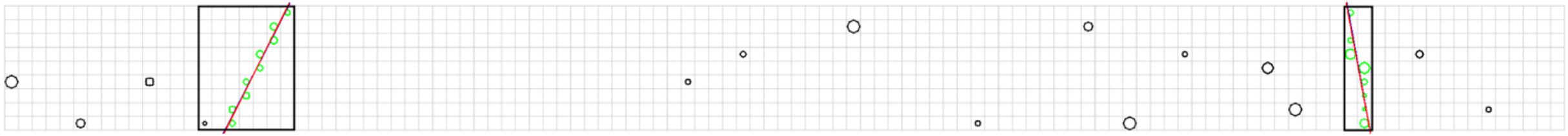

Step 1: preclustering

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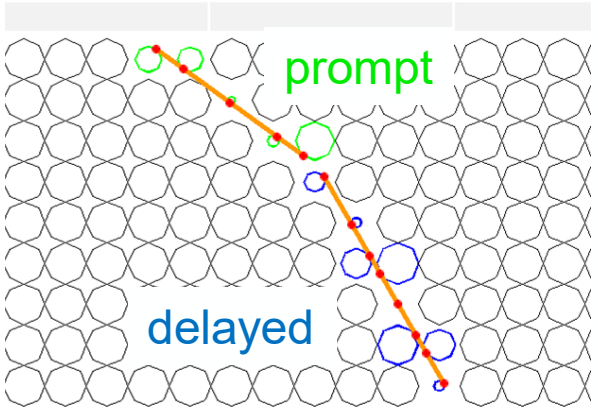
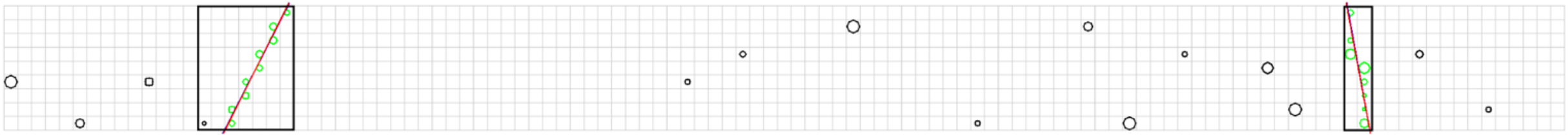
  - delayed/prompt





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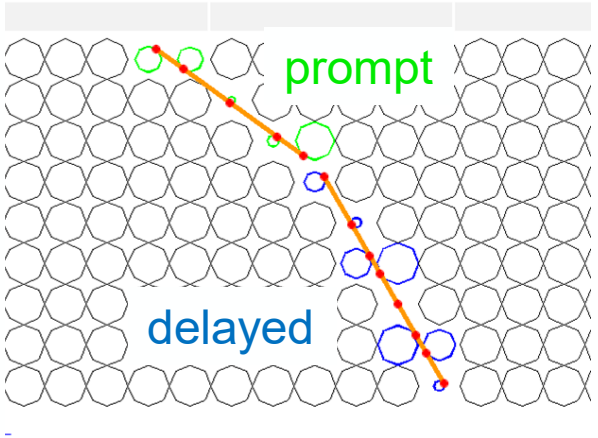
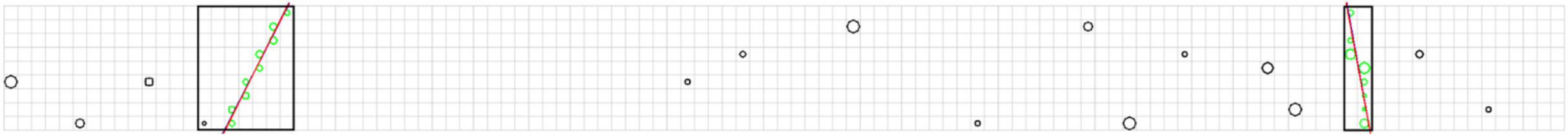
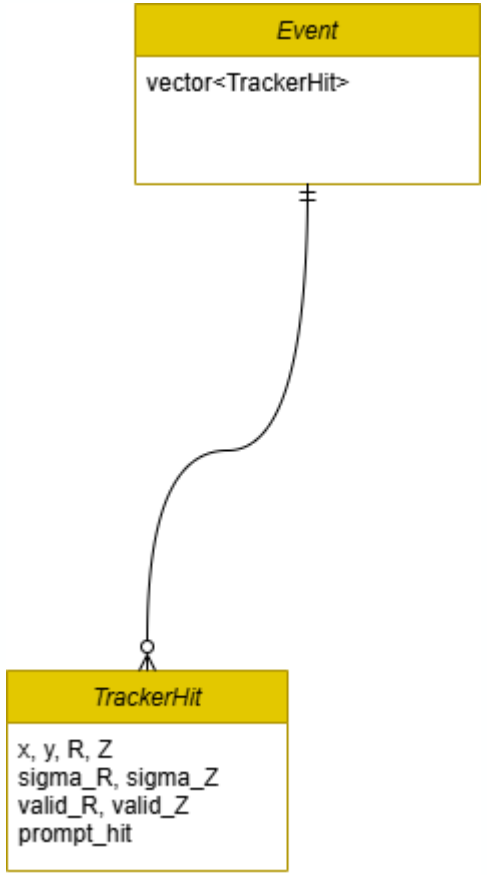




- **Rest of reconstruction done for each *precluster* separately**
  (saves time, avoids exponential blowup due to ambiguities)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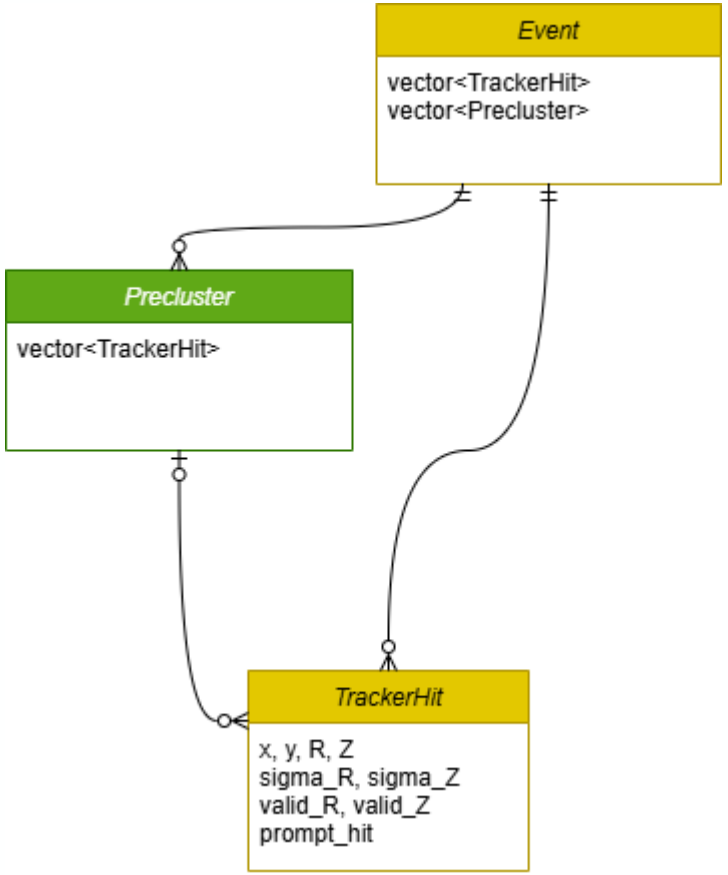
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Step 2: clustering and line estimation

- Legendre transform approach (detailed explanation in article 1)
  - Dedicated worker class for clustering (*Sinogram* class)

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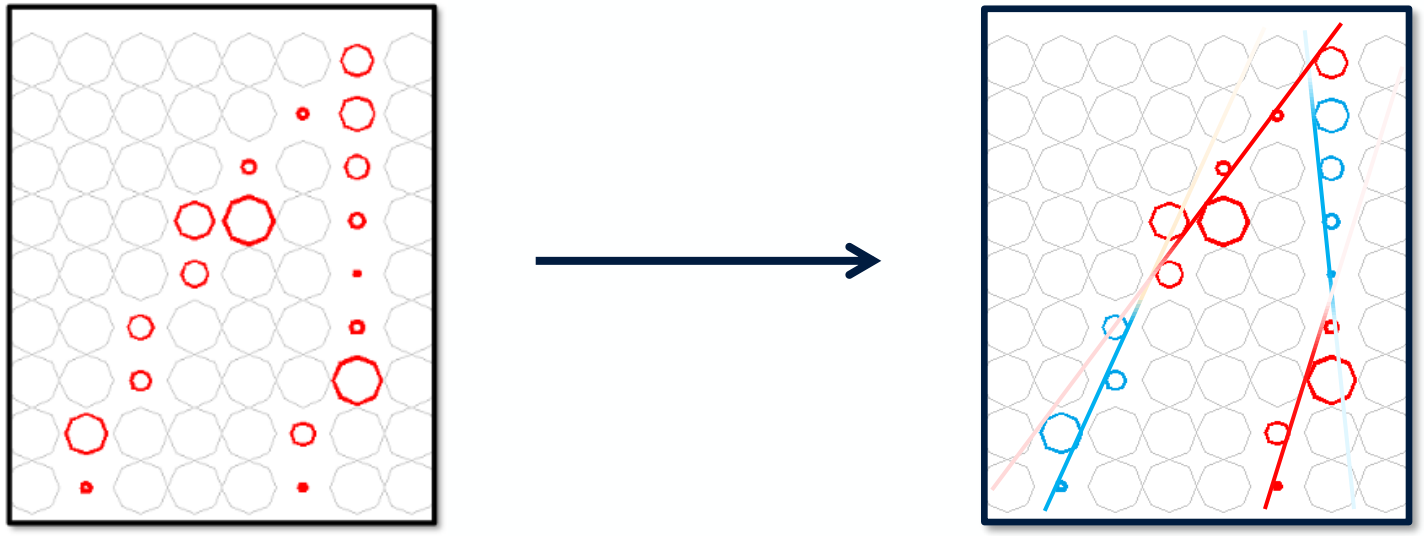
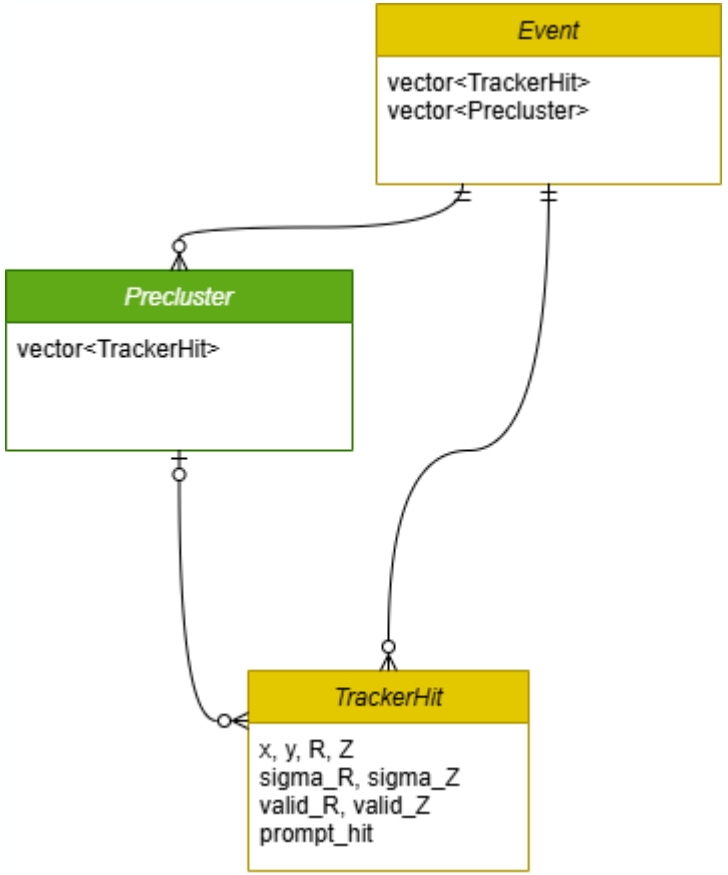
- Legendre transform approach (detailed explanation in article 1)
  - Dedicated worker class for clustering (*Sinogram* class)
- Two outputs:
  - **Line fit estimates** (only horizontal part of the fits)
  - their pairing to tracker hits (***clusters***)



(4 clusters, 4 lines estimated)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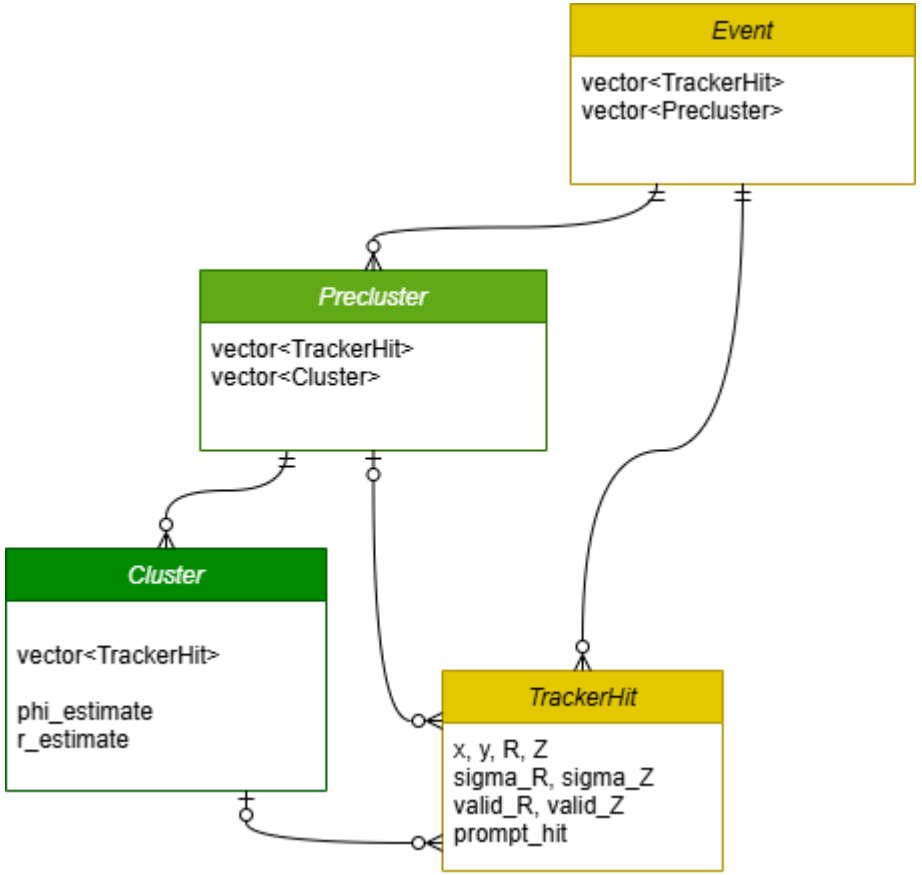
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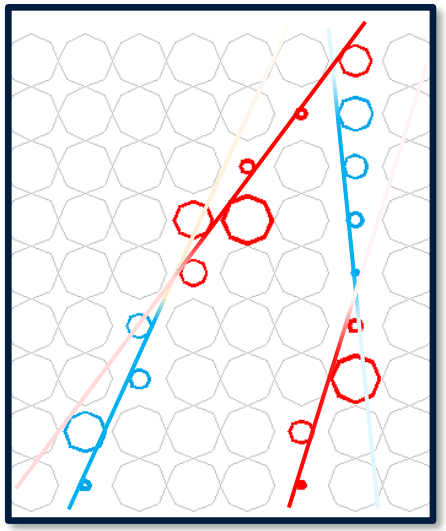
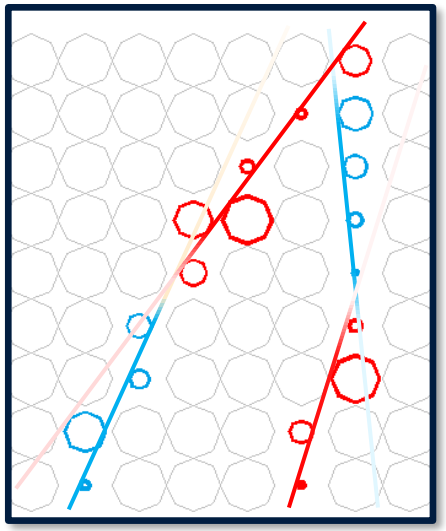
Step 3: ambiguity checking and fitting

- Checks each cluster for **symmetry** (ambiguities)



Step 3: ambiguity checking and fitting

- Checks each cluster for **symmetry** (ambiguities)
- **Maximum likelihood method** for fitting → ***LinearFit***
  - Refines existing horizontal estimates
  - Adds vertical components of the fits



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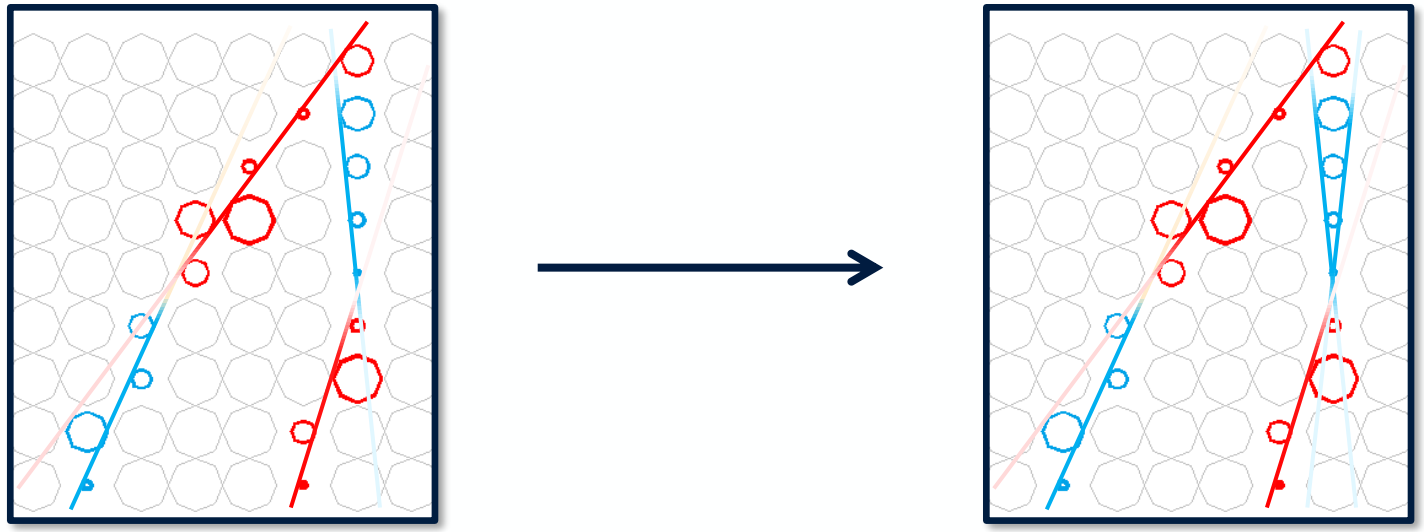
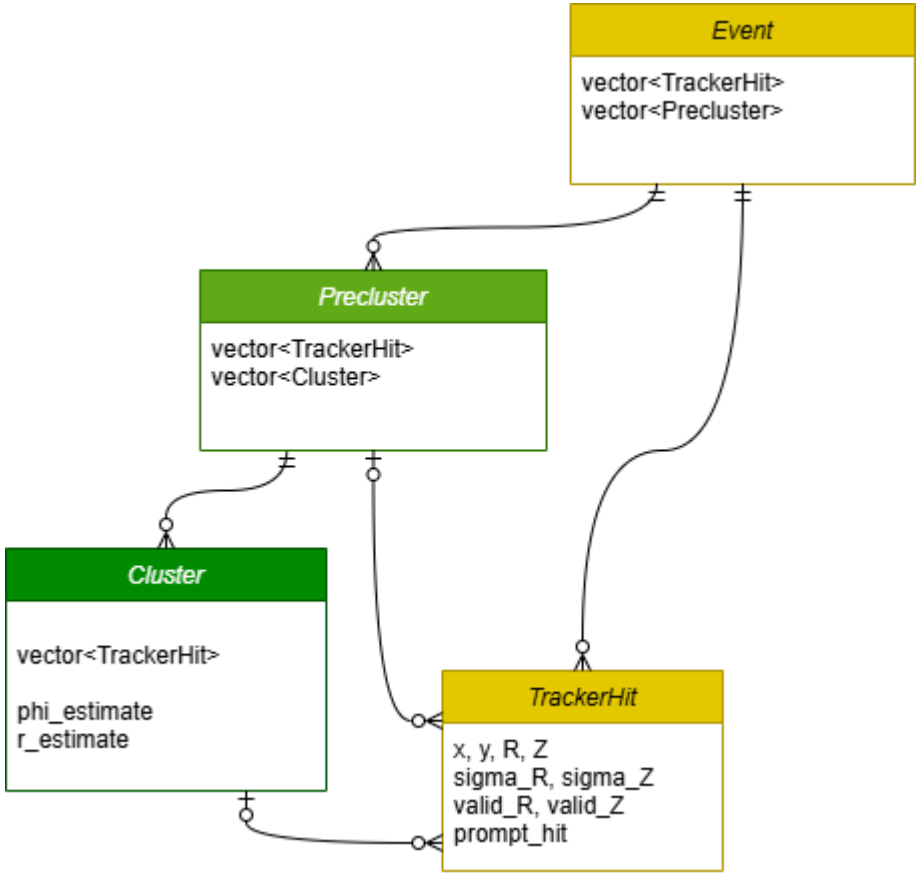


4 lines estimated

5 lines fitted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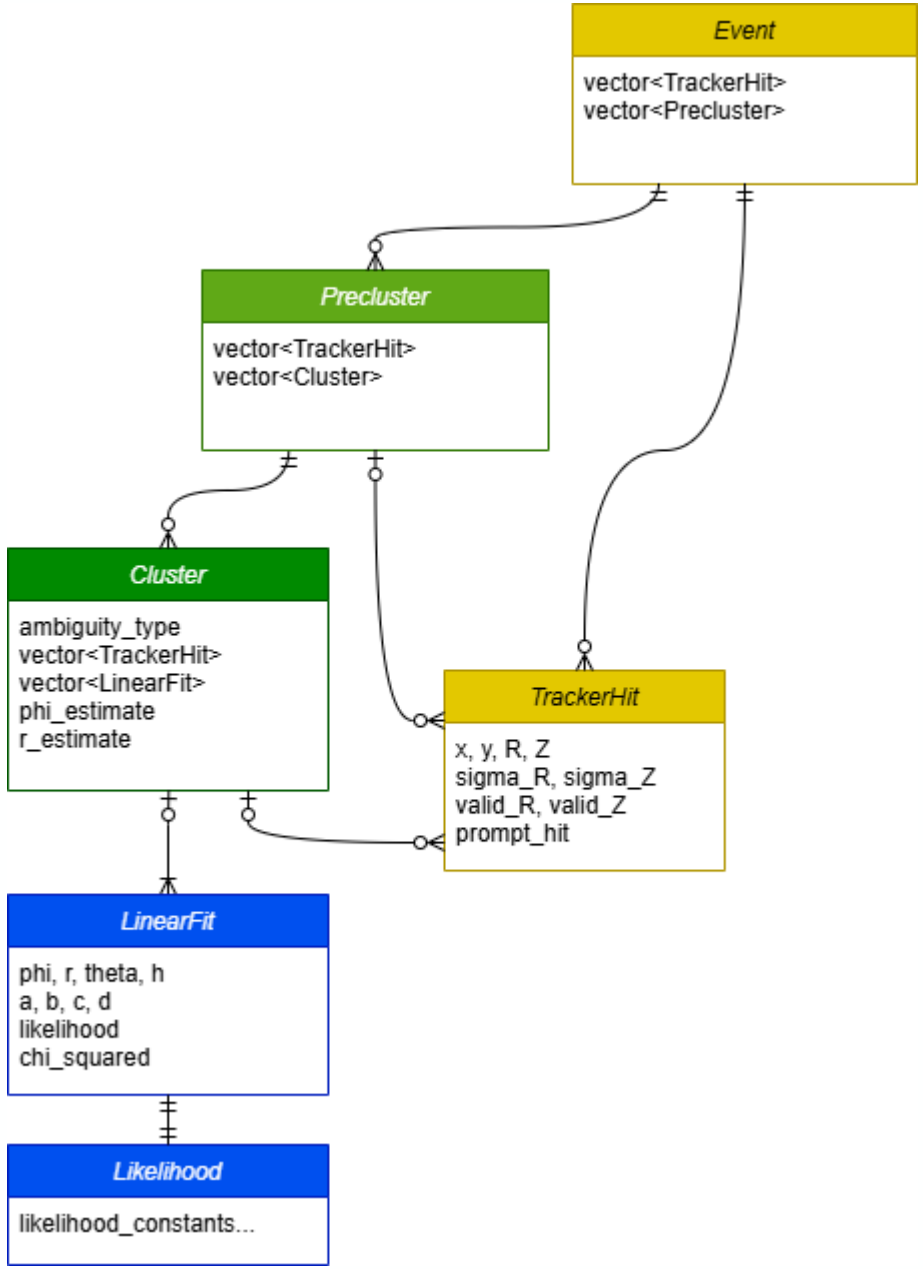
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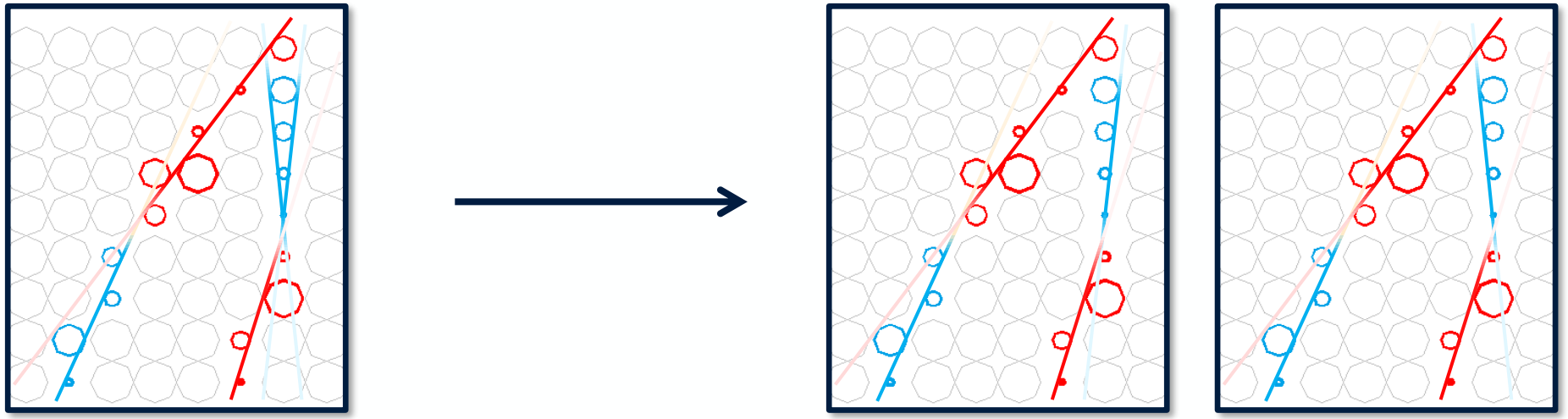
Step 4: Precluster solutions

- Creates "***precluster solutions"*** = unique collection of fits explaining the precluster
- Rest of the process done separately for each *precluster solution*



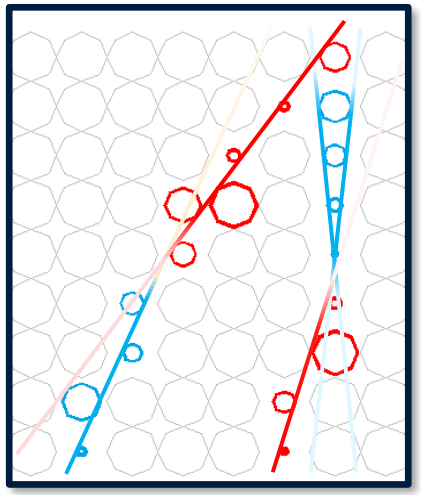
4 clusters, 5 fits

Precluster solution 1

Precluster solution 2

Step 4: Precluster solutions

- Creates "***precluster solutions"*** = unique collection of fits explaining the precluster
- Rest of the process done separately for each *precluster solution*
- ***LinearFits*** → ***Tracks*** (*LinearFit* + tracker hit association points)



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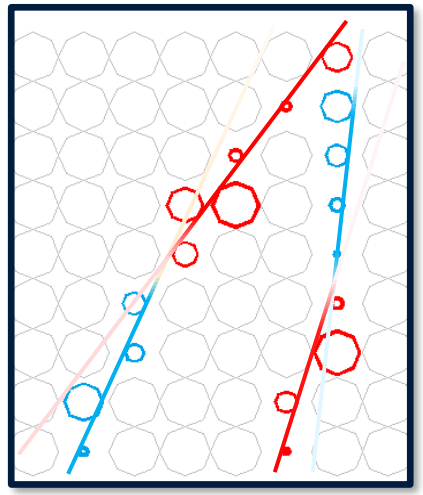
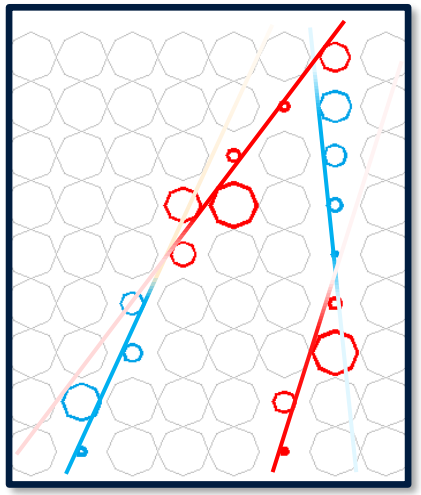
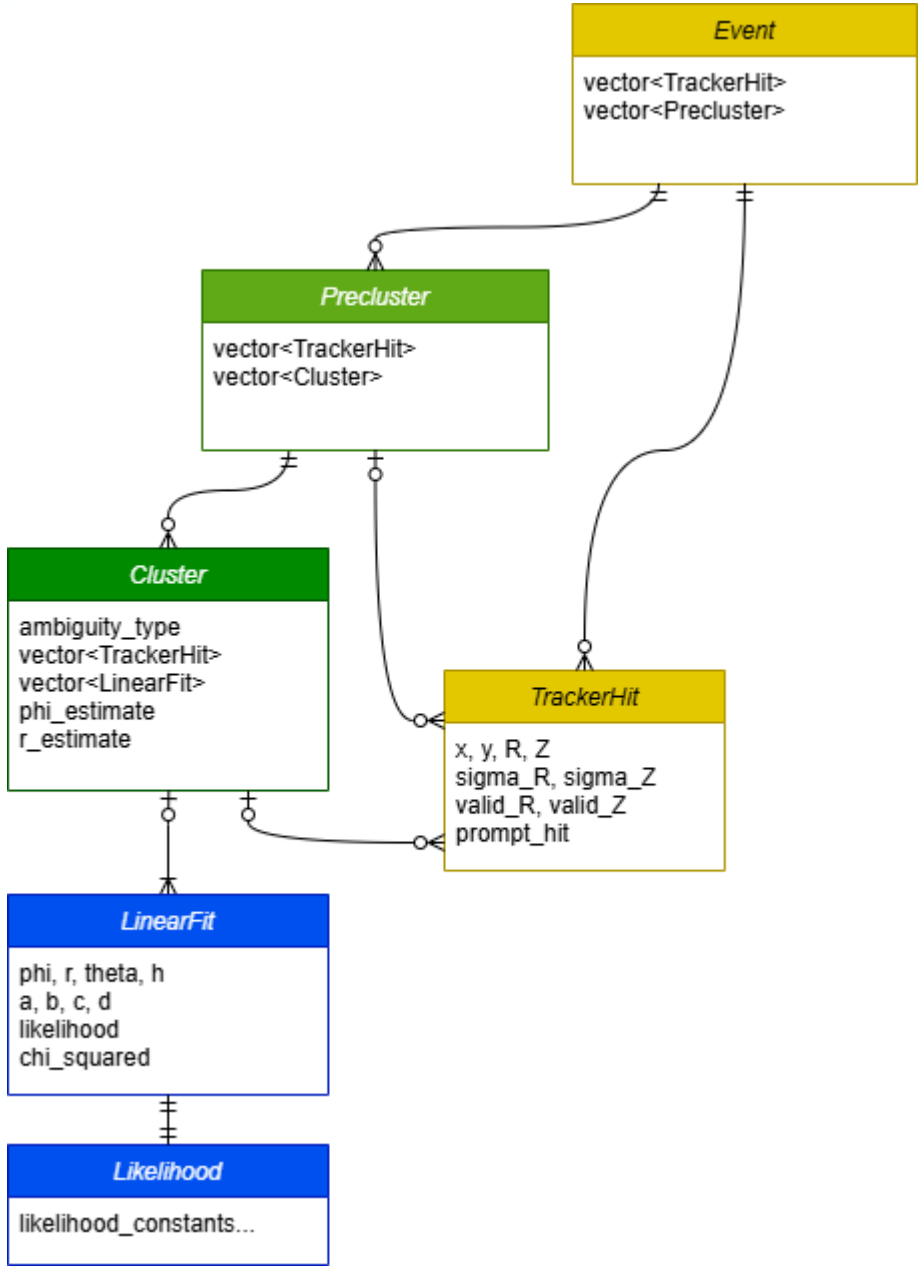


Precluster solution 1



Precluster solution 2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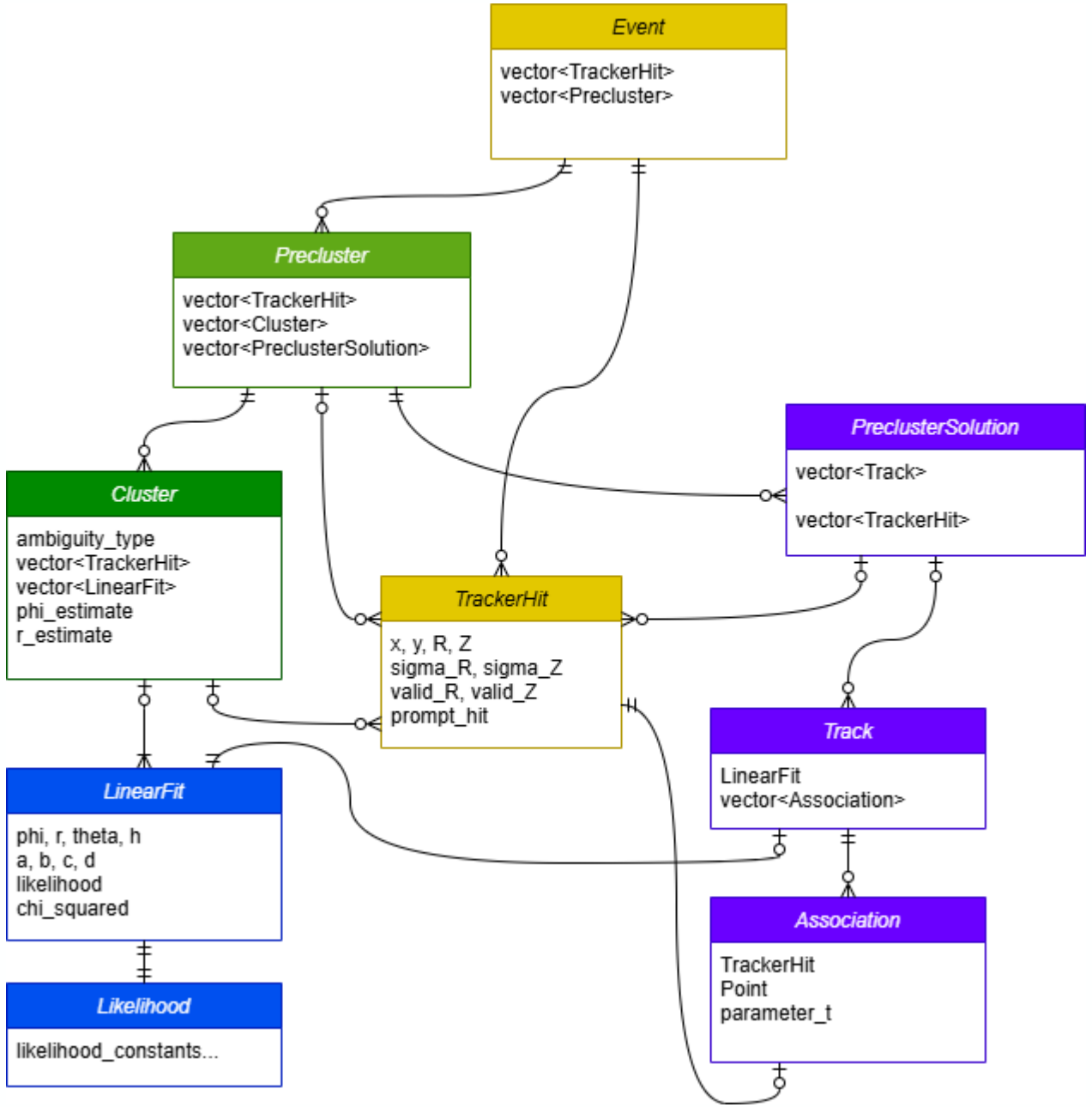
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phi, r, theta, h
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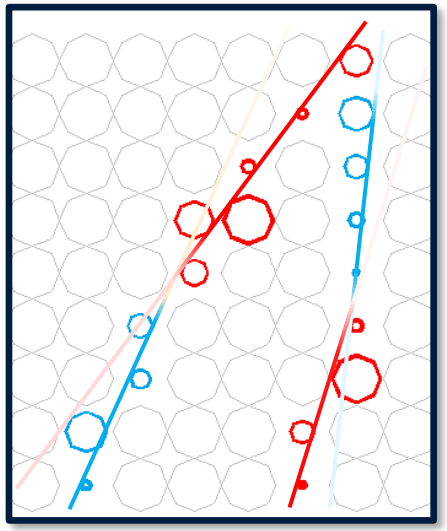
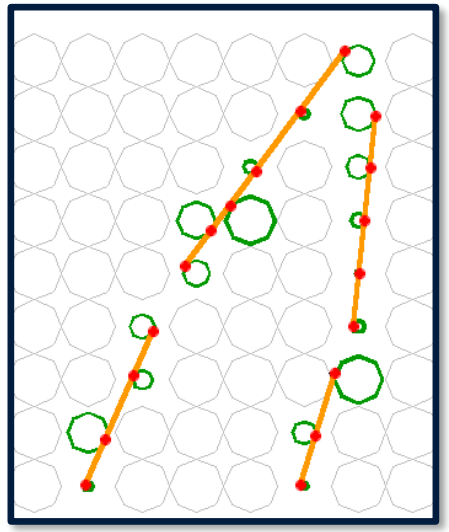
Step 5: Line trajectories

- ***Track*** → ***Trajectory*** (*Tracks* + endpoints)
- **Endpoints** = furthest association points



Precluster solution 1



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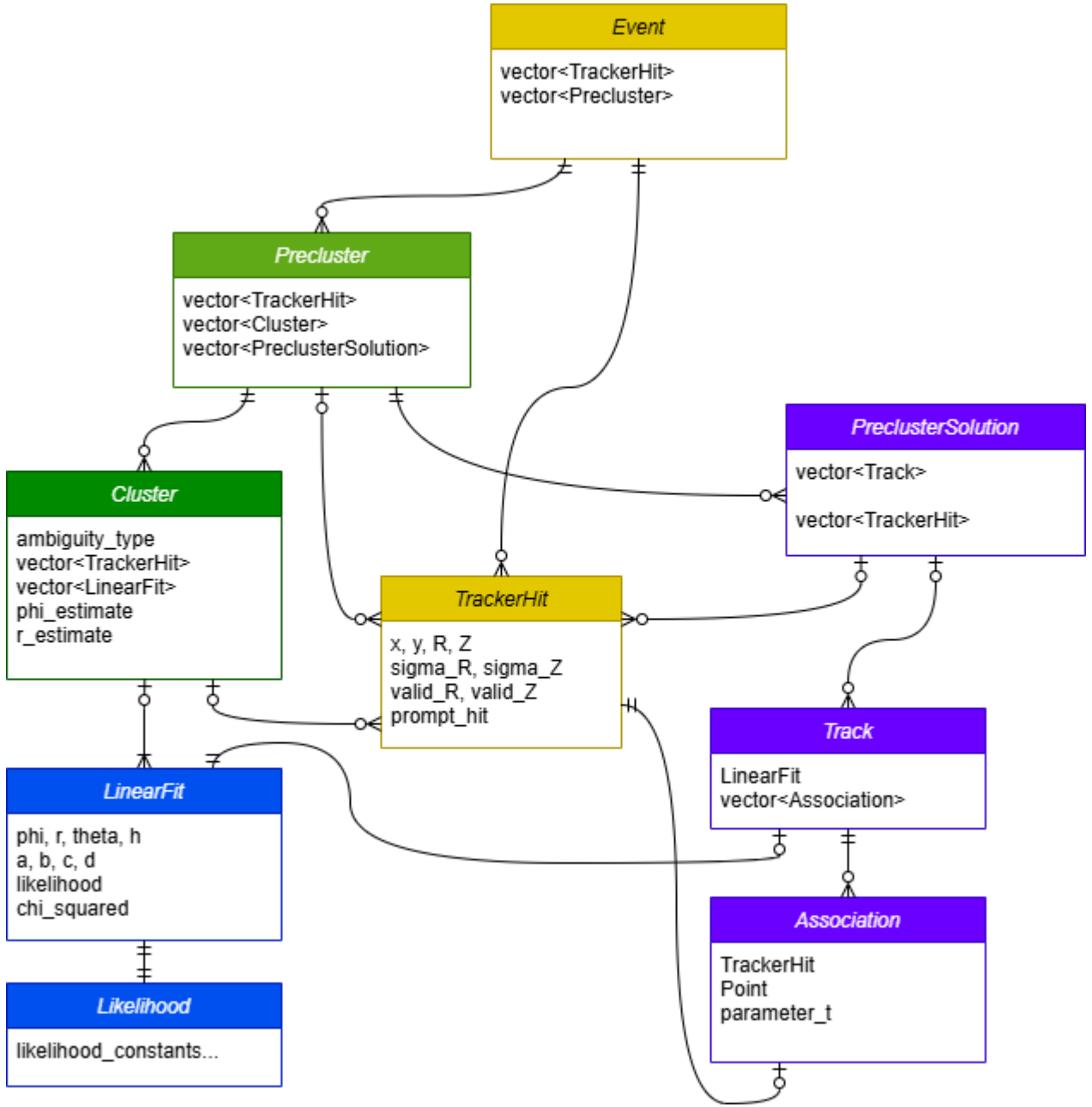
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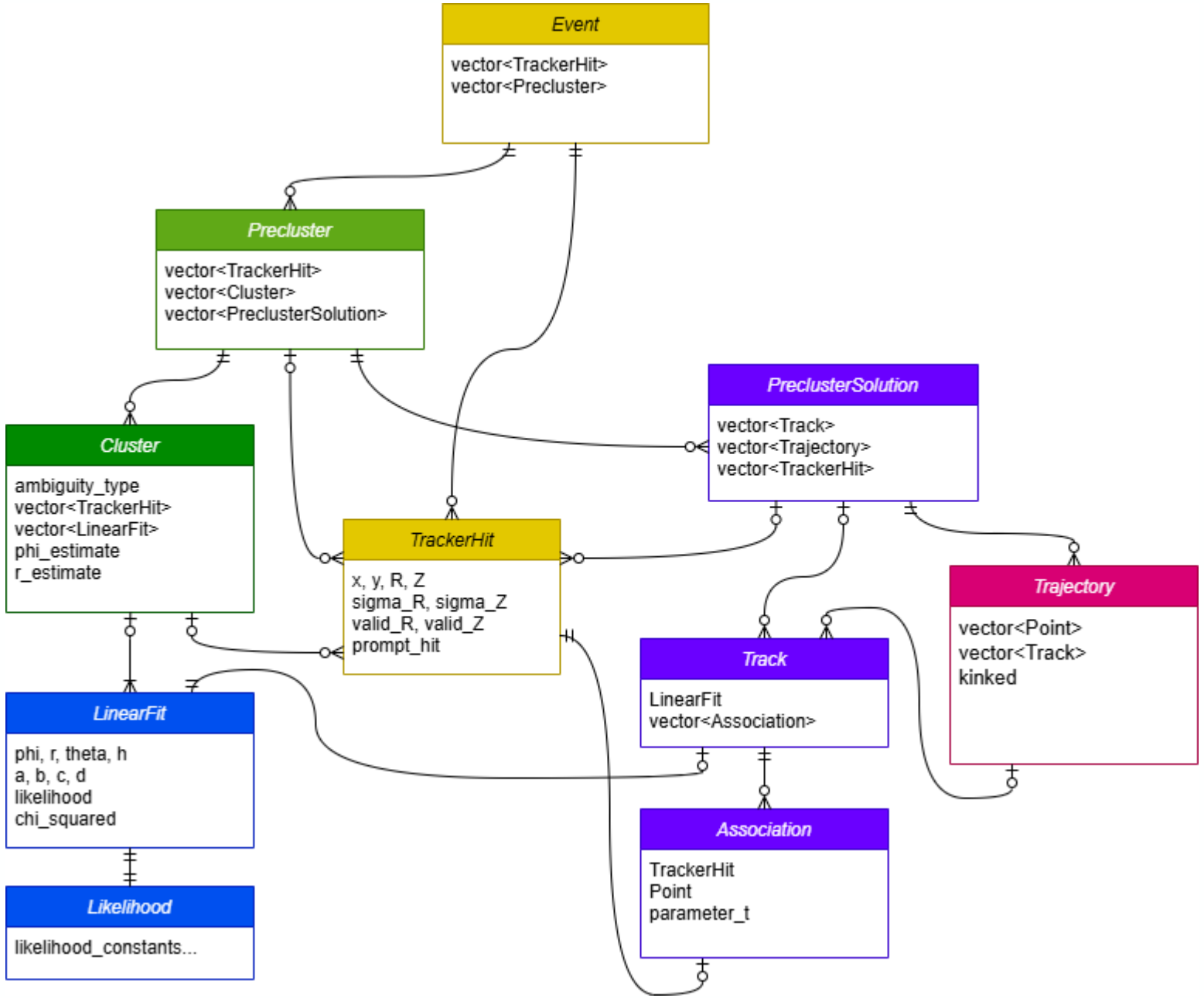
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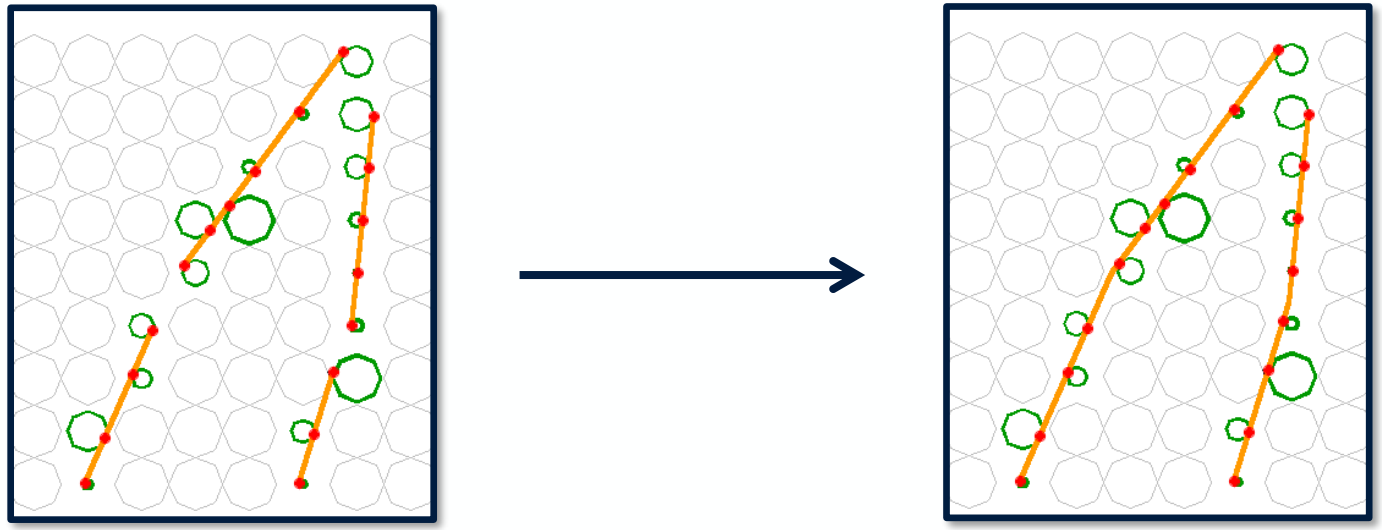
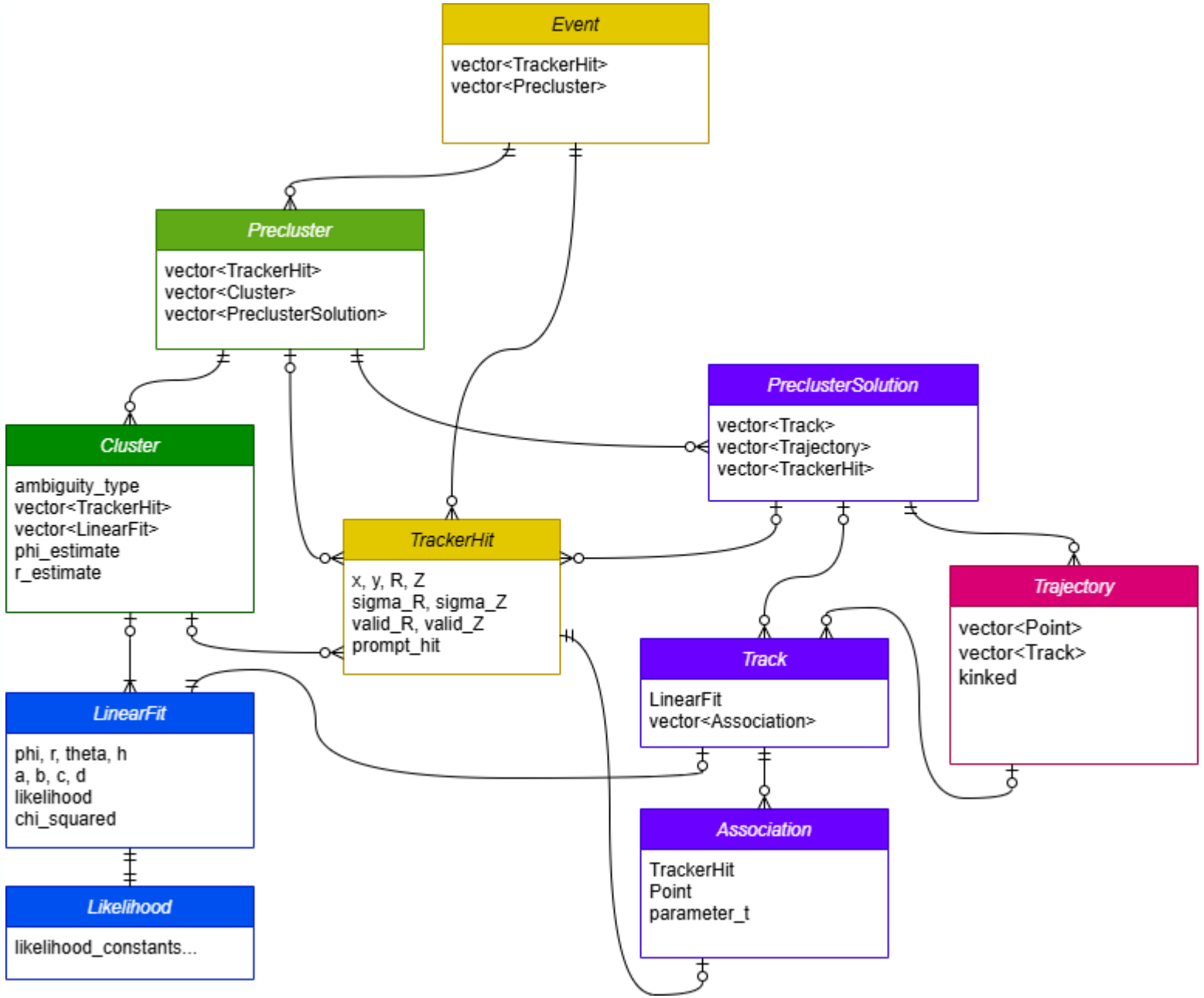
Step 6: Building polylines

- Line ***Trajectories*** → (poly)line ***Trajectories***
- **Merging trajectories together**
- More details in the second part of the presentation



Precluster solution 1

Precluster solution 1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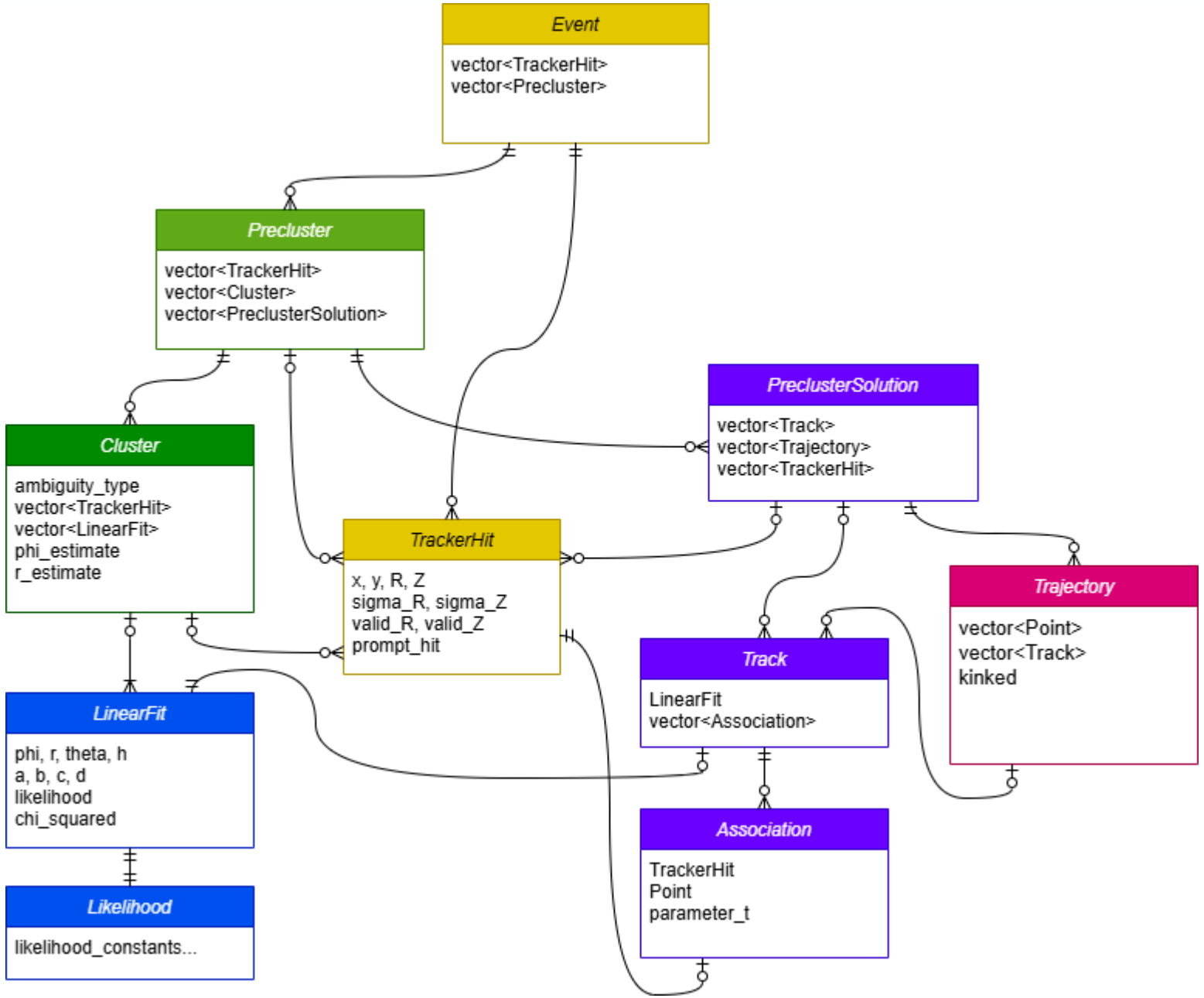
Step 7: Trajectory evaluation

- Total χ^2 of trajectories
  - requires tracker hit uncertainties
- RMSE of trajectories (root mean square error)
  - no uncertainties required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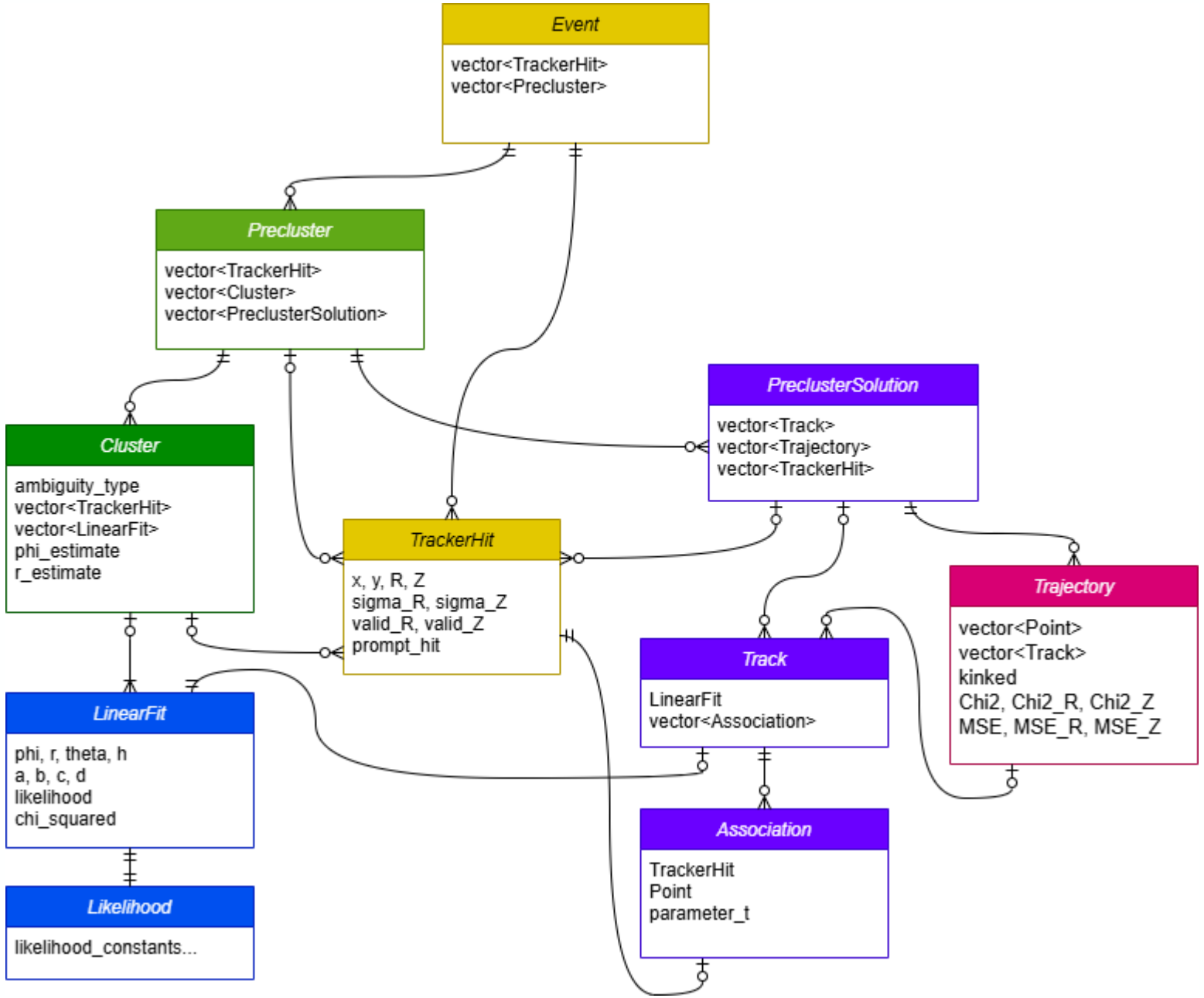
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Step 8: Merging into solutions

- Combining *precluster solutions* into full event ***Solutions***

Precluster A:

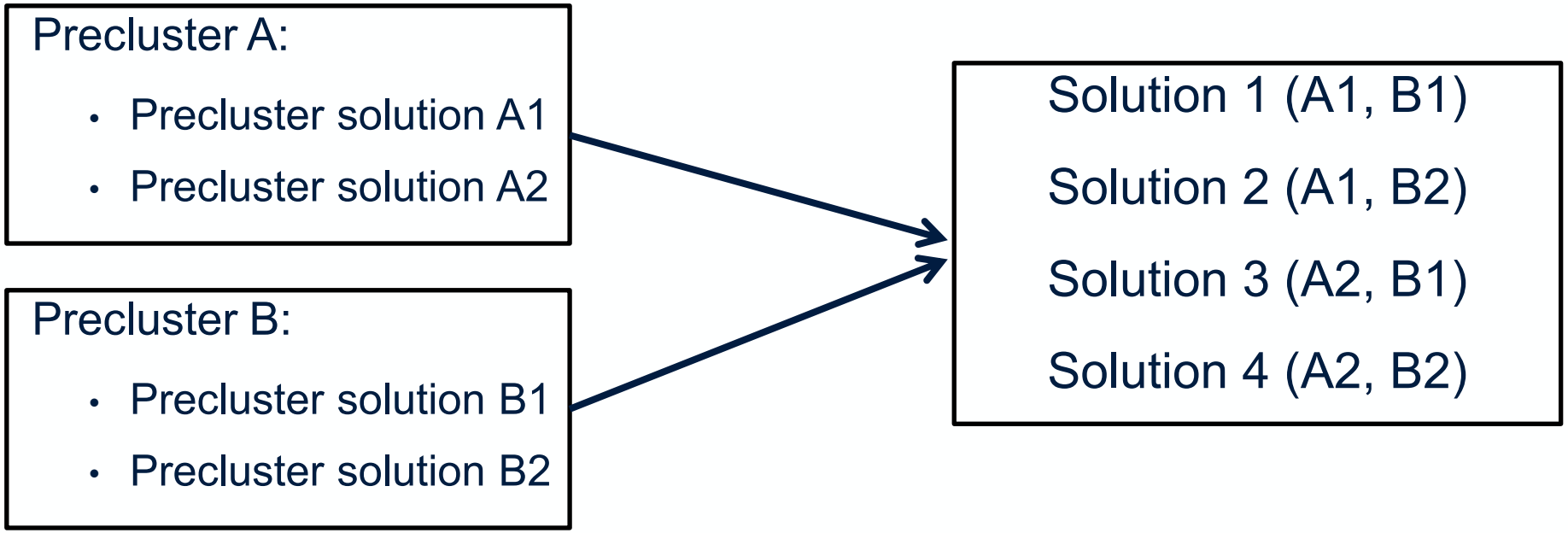
- Precluster solution A1
- Precluster solution A2

Precluster B:

- Precluster solution B1
- Precluster solution B2

Step 8: Merging into solutions

- Combining *precluster solutions* into full event ***Solutions***



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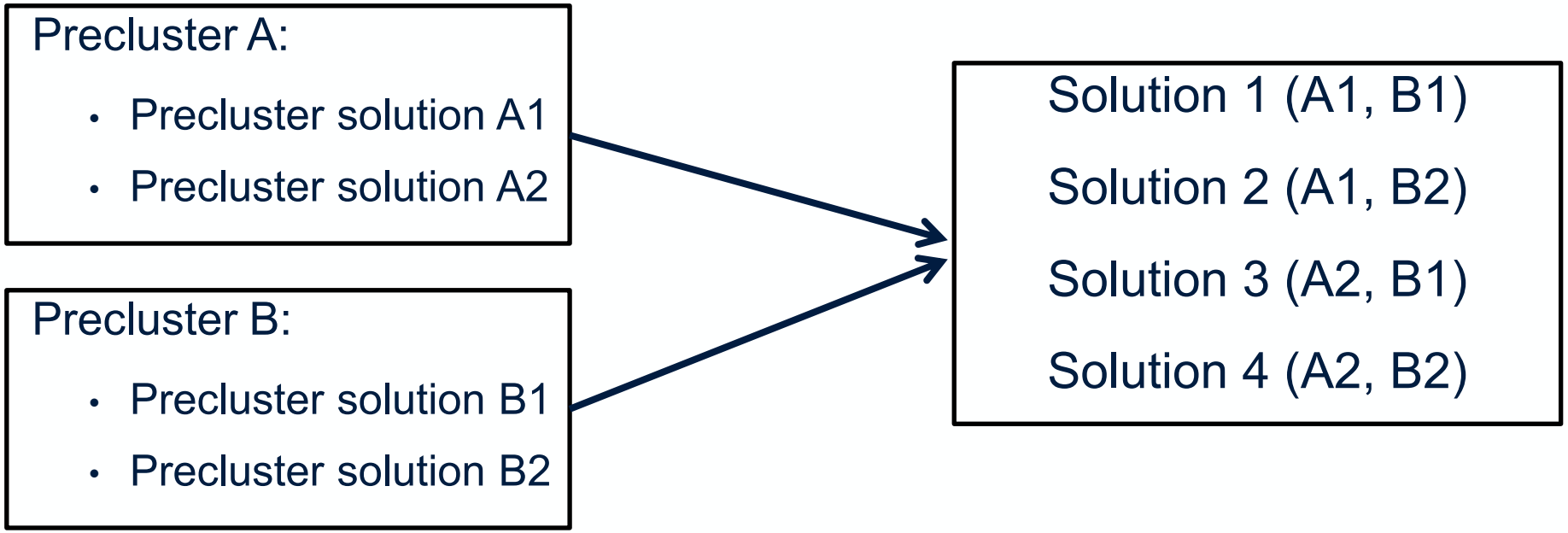
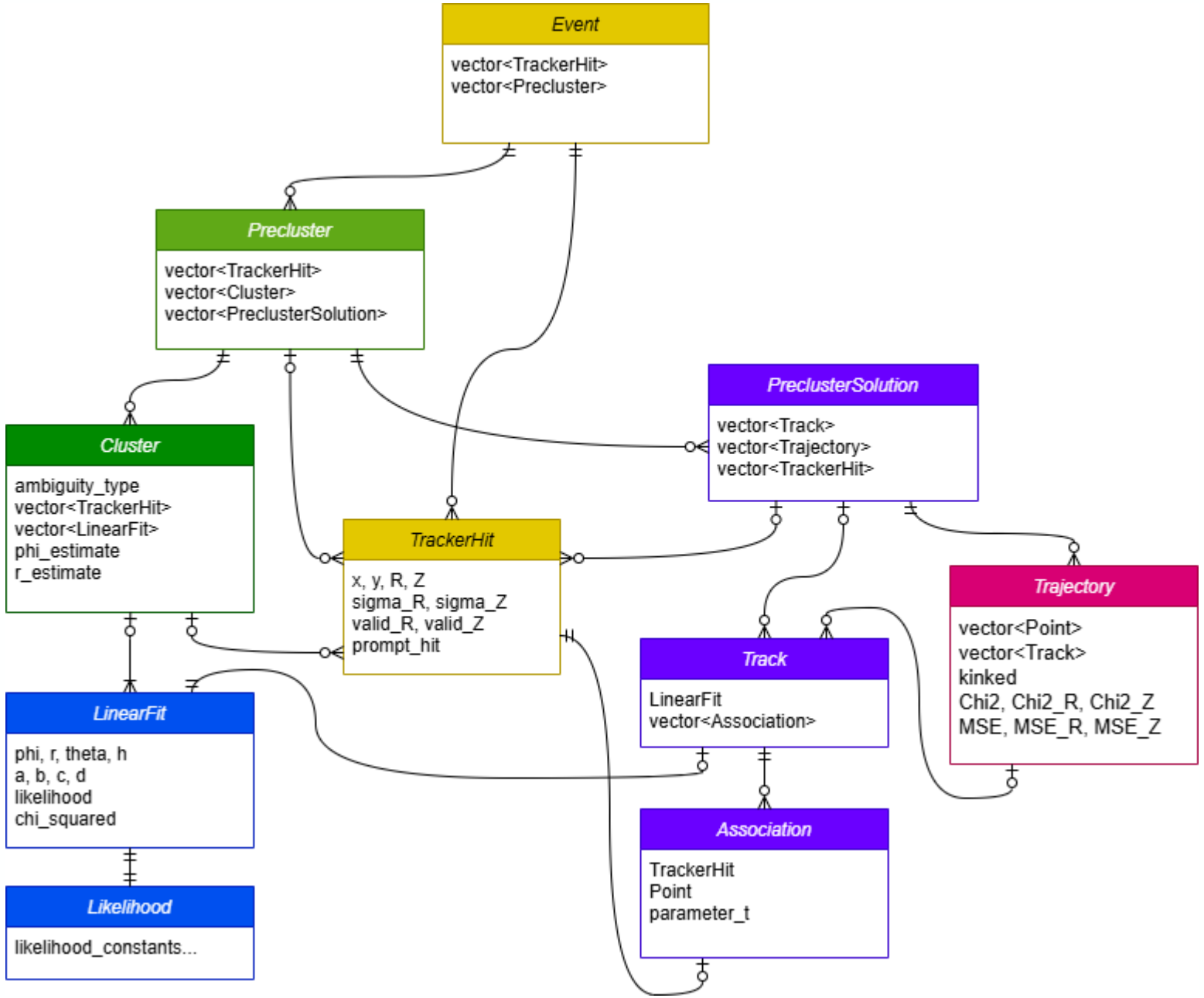
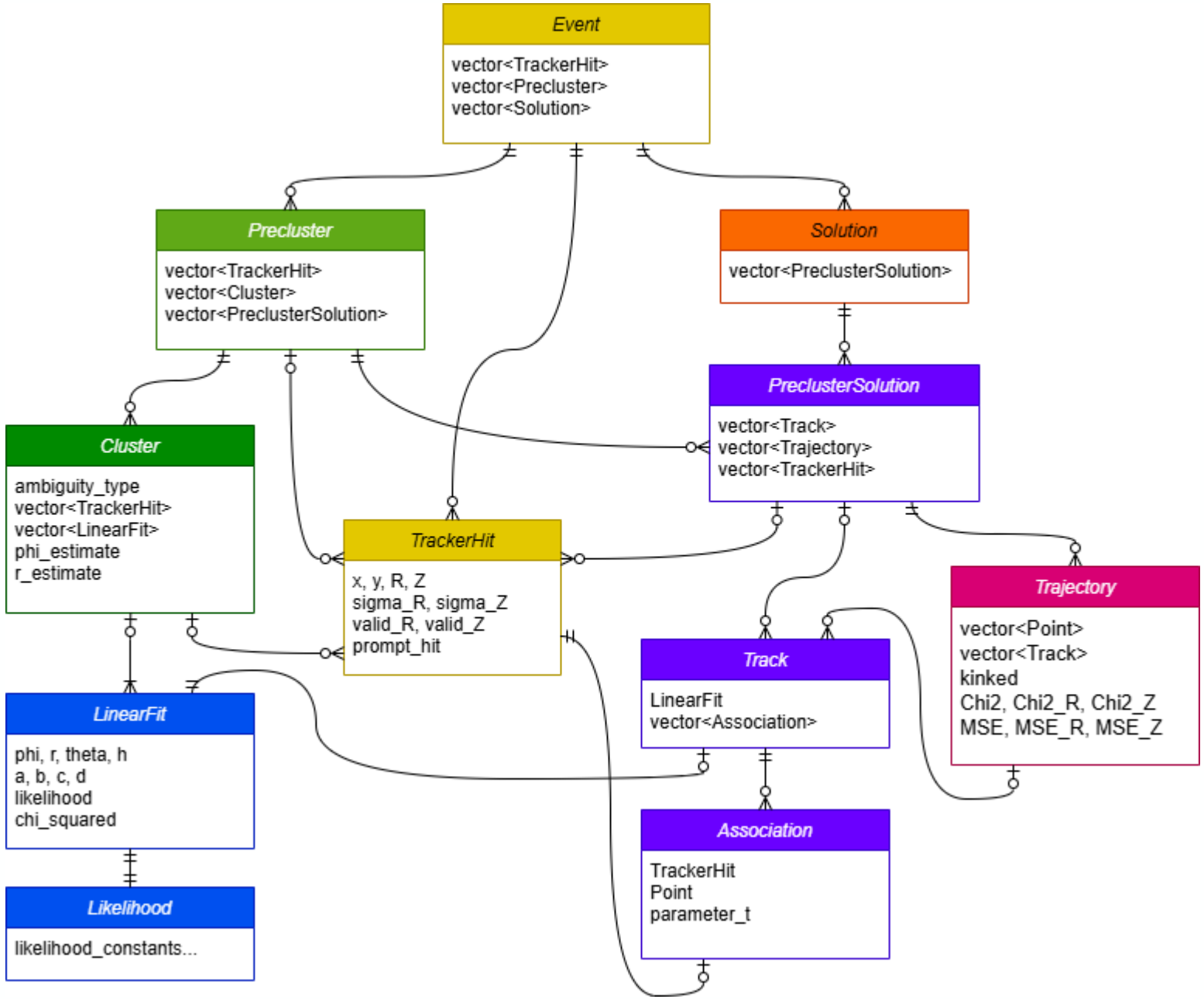


- Ordering solutions (# linear fits, # trajectories, # total χ^2)
- Optionally removing the worst solutions


Event
vector<TrackerHit>
vector<Precluster>
Precluster
vector<TrackerHit>
vector<Cluster>
vector<PreclusterSolution>
PreclusterSolution
vector<Track>
vector<Trajectory>
vector<TrackerHit>
Cluster
ambiguity_type
vector<TrackerHit>
vector<LinearFit>
phi_estimate
r_estimate
TrackerHit
x, y, R, Z
sigma_R, sigma_Z
valid_R, valid_Z
prompt_hit
Trajectory
vector<Point>
vector<Track>
kinked
Chi2, Chi2_R, Chi2_Z
MSE, MSE_R, MSE_Z
Track
LinearFit
vector<Association>
LinearFit
phi, r, theta, h
a, b, c, d
likelihood
chi_squared
Association
TrackerHit
Point
parameter_t
Likelihood
likelihood_constants...


Event
vector<TrackerHit>
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vector<Solution>
Precluster
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Solution
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PreclusterSolution
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x, y, R, Z
sigma_R, sigma_Z
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vector<Point>
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kinked
Chi2, Chi2_R, Chi2_Z
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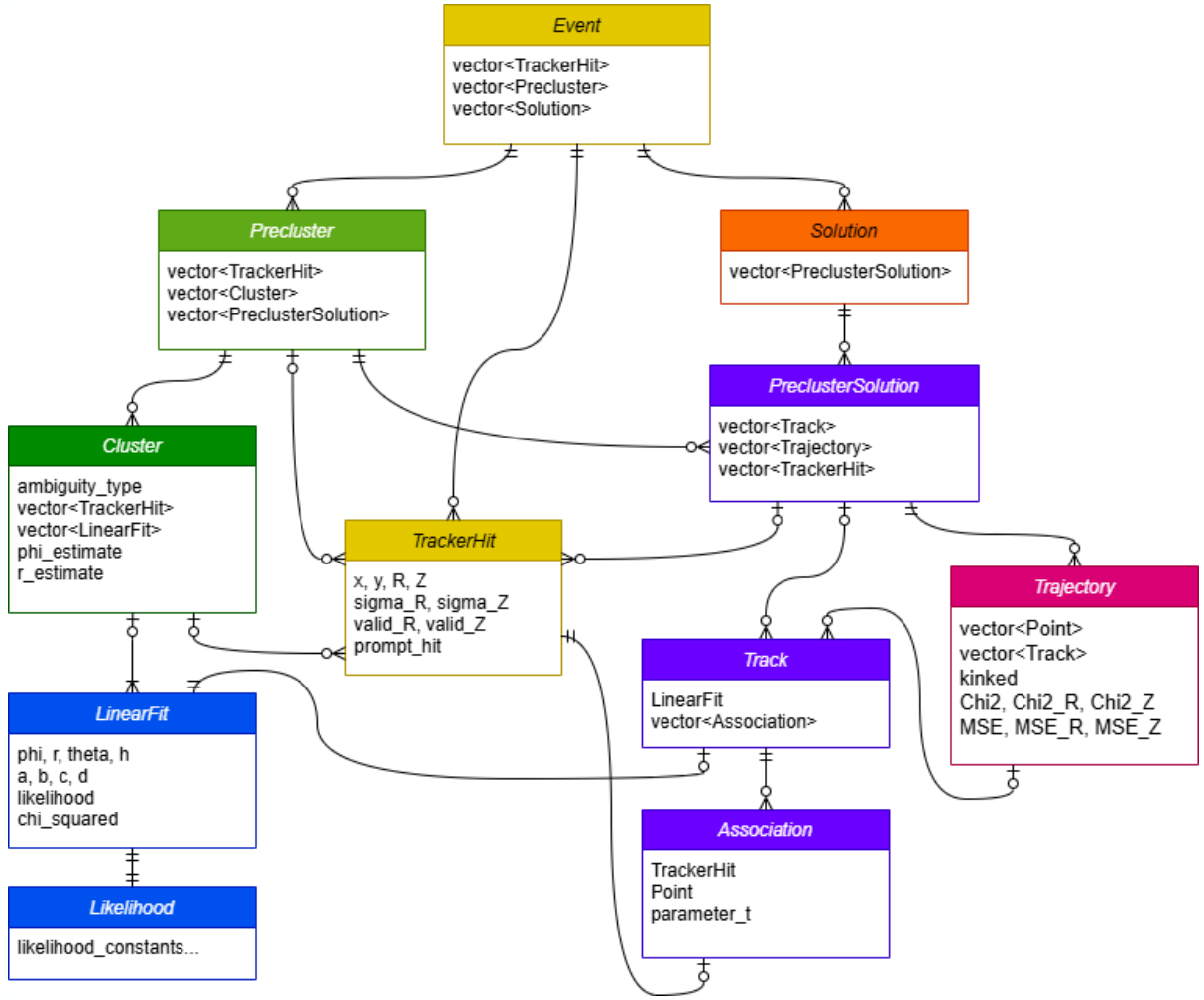
Track
LinearFit
vector<Association>
LinearFit
phi, r, theta, h
a, b, c, d
likelihood
chi_squared
Association
TrackerHit
Point
parameter_t
Likelihood
likelihood_constants...

Algorithm summary

```
Algos::process(Event&) {
    precluster();

    for(precluster) {
        clustering();
        make_MLM_fits();
        combine_into_precluster_solutions();

        for(precluster_solution) {
            create_line_trajectories();
            build_polylines();
            evaluate_trajectories();
        }
    }
    create_solutions();
}
```



supernemo collaboration

2. Polyline reconstruction framework

Polyline reconstruction framework

Cimrman 1.1.0 (current official version):

- Chaotic unmanageable implementation

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Cimrman 1.2.0? (development version):

- Functionally (almost) the same
- Clean structured implementation

Polyline reconstruction framework

Cimrman 1.1.0 (current official version):

- Chaotic unmanageable implementation

Cimrman 1.2.0? (development version):

- Functionally (almost) the same
- Clean structured implementation
- Dedicated worker class ***TrajectoryBuilder***
- Could be reused for connecting tracks outside tracker volume (crossing tracks, BiPo events, double beta events…)

TrajectoryBuilder

- Dedicated class for connecting trajectories
- Modifies one *precluster solution* at a time (no ambiguities involved)

TrajectoryBuilder

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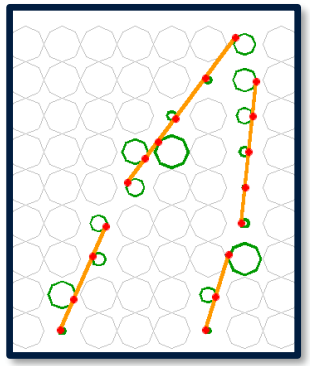
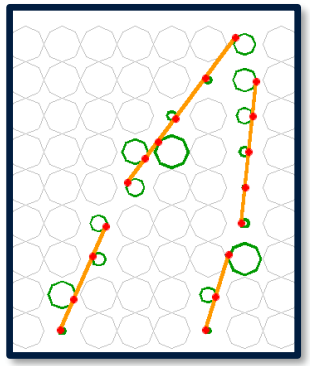
- Input: collection of (line) trajectories (with associated hits)



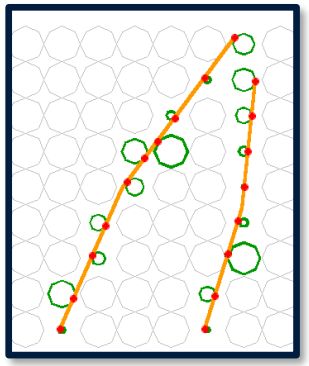
(T_1, T_2, T_3, T_4)

TrajectoryBuilder

- Dedicated class for connecting trajectories
- Modifies one *precluster solution* at a time (no ambiguities involved)
- Input: collection of (line) trajectories (with associated hits)
- Output: collection of (polyline) trajectories



$$(T_1, T_2, T_3, T_4) \rightarrow (T_1, T_2, T_3) \rightarrow (T_1, T_2)$$



TrajectoryBuilder

Process():

- For each pair of trajectories (T_i, T_j):

TrajectoryBuilder

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  - For each pair of their endpoints (E_k, E_l):

TrajectoryBuilder

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- For each pair of trajectories (T_i, T_j):
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    - Can T_i and T_j be connected? (*KinkFinder*)
    - If yes, merge T_j into T_i

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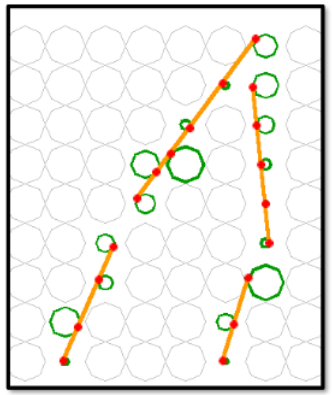
4 line trajectories = 6 pairs

$\rightarrow$ 6 x 4 = 24 endpoint pairs



Solution 1

KinkFinder

- Dedicated class for connection decisions
- **Can two trajectories be connected? If yes, how?**

KinkFinder

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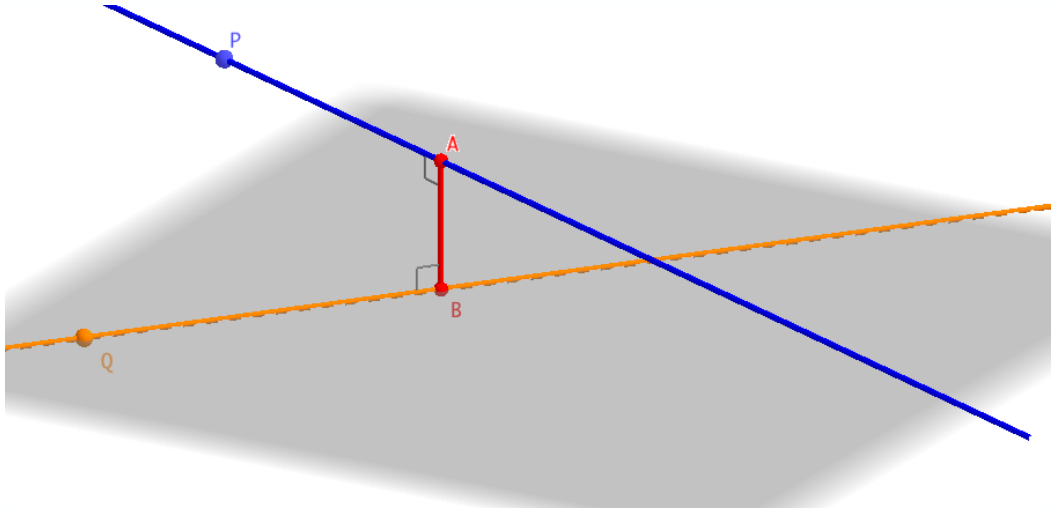
- **Can two trajectories be connected? If yes, how?**
- Two lines in 3D have (almost certainly) no intersection!

  → Fits must be changed to enforce continuity



KinkFinder

- Dedicated class for connection decisions
- **Can two trajectories be connected? If yes, how?**
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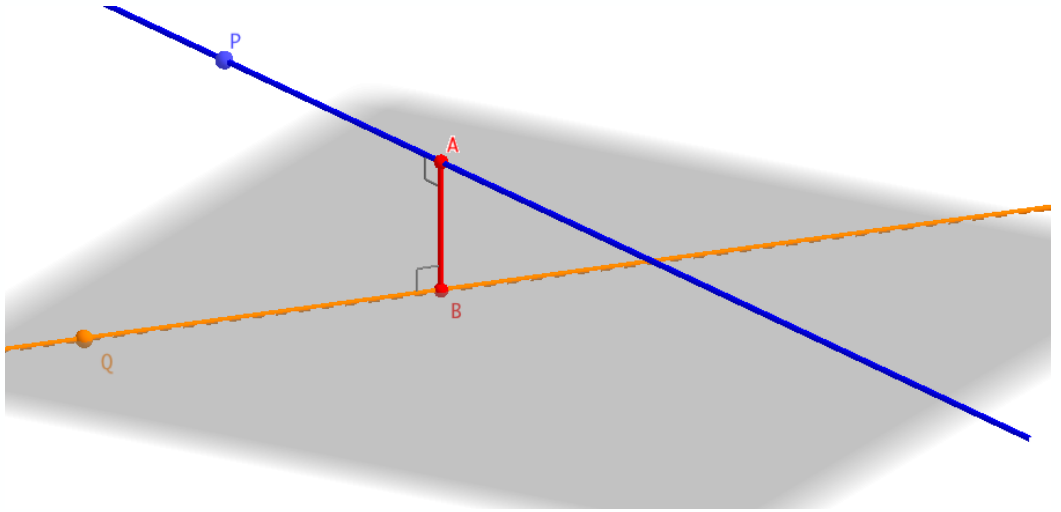
- Two ingredients:

  1. Kink point construction strategy

  - How do you construct the point?



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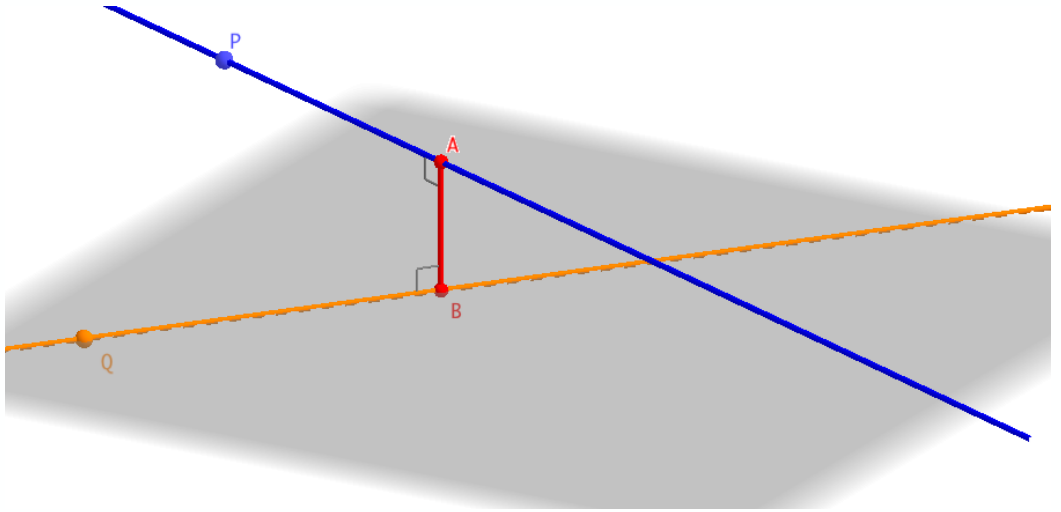
- Two ingredients:

  1. Kink point construction strategy

  - How do you construct the point?

  2. List of validation criteria

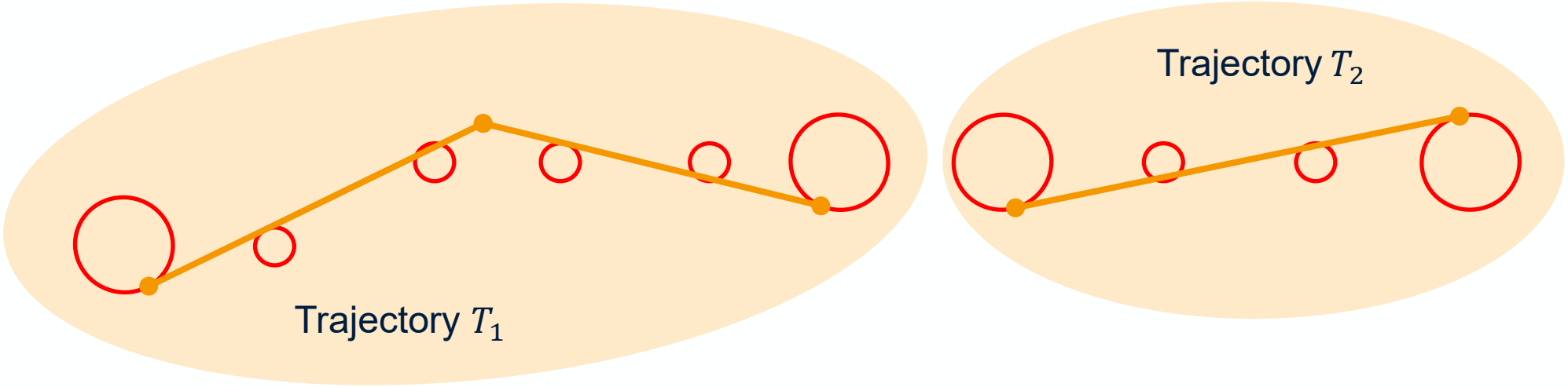
  - How do I check that it is valid?



KinkFinder

Inputs:

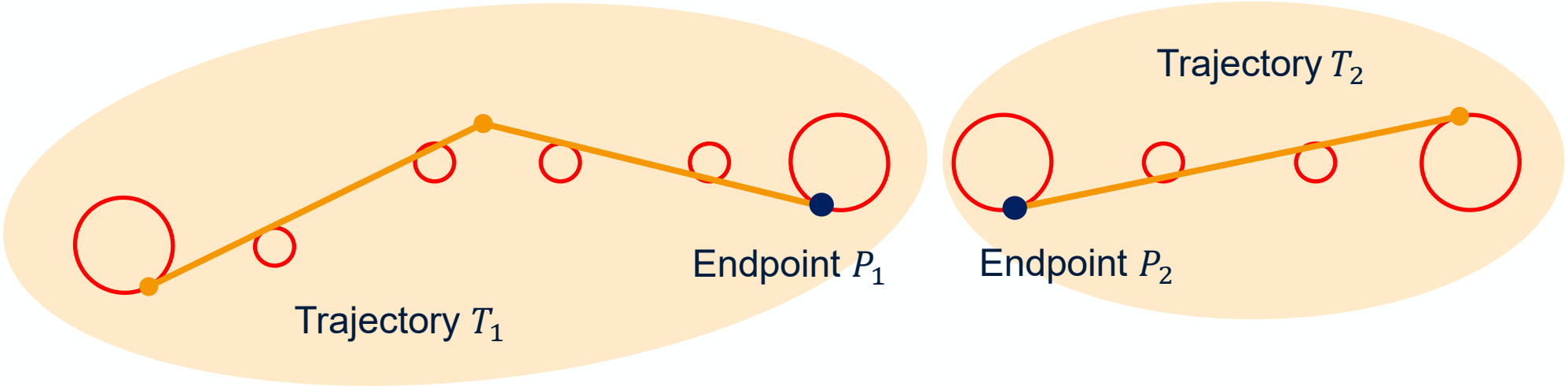
- Trajectories T_1, T_2



KinkFinder

Inputs:

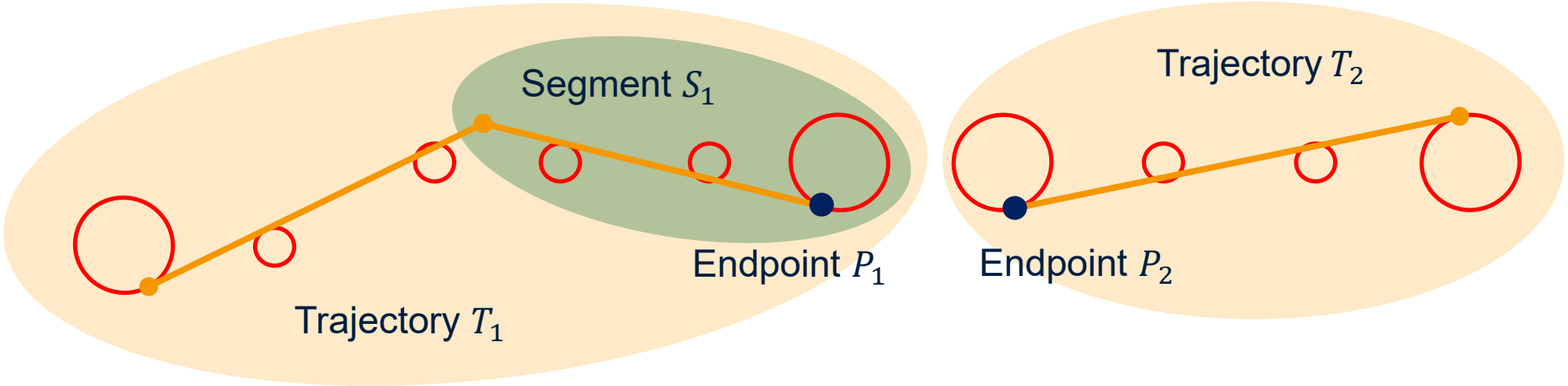
- Trajectories T_1, T_2
- Selected endpoints P_1, P_2



KinkFinder

Inputs:

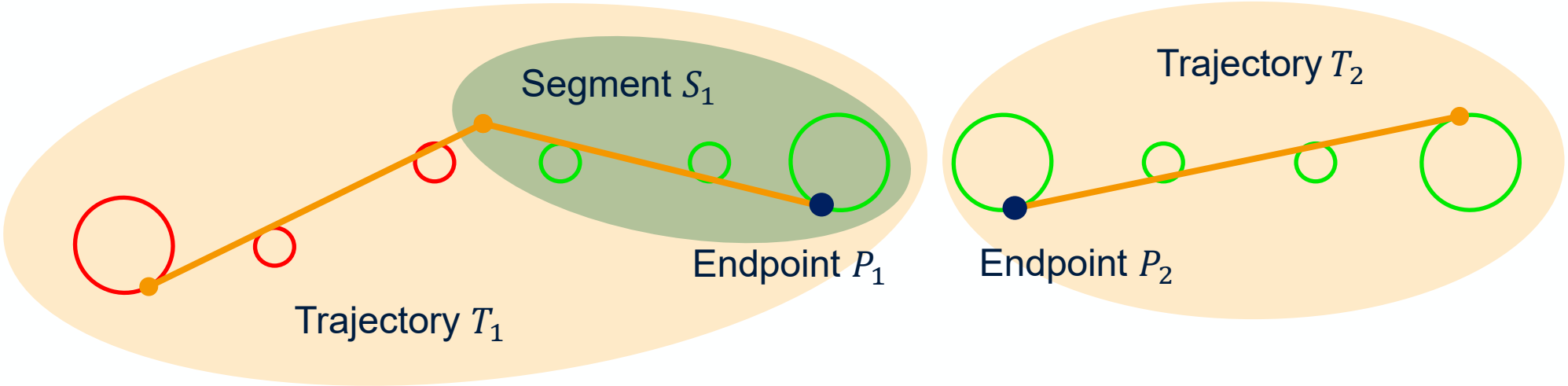
- Trajectories T_1, T_2
- Selected endpoints P_1, P_2
- Selected segments of the (poly)lines



KinkFinder

Inputs:

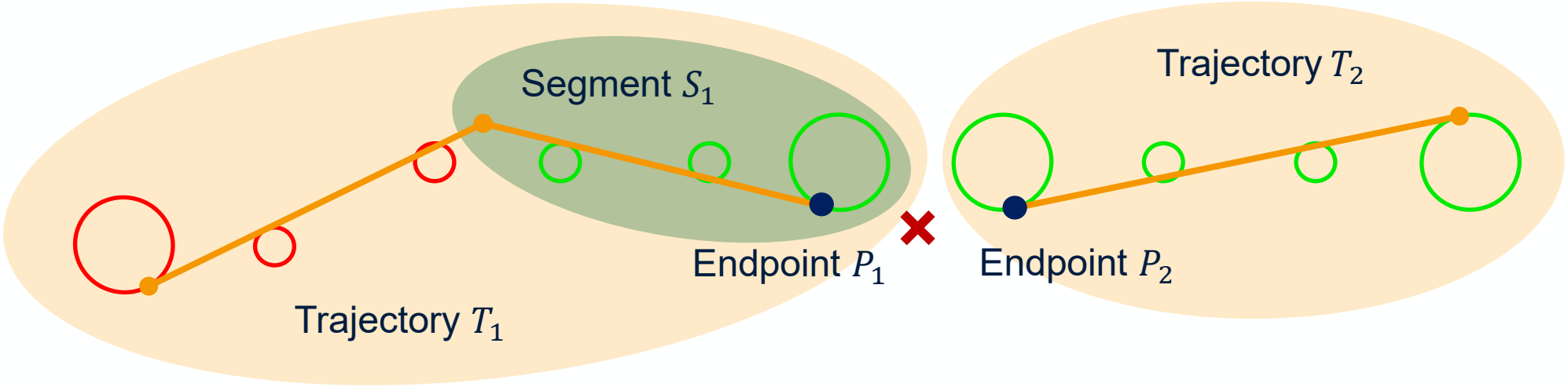
- Trajectories T_1, T_2
- Selected endpoints P_1, P_2
- Selected segments of the (poly)lines
- Associated hits



KinkFinder

Outputs:

- Yes/No connection decision
- kink point position



Connection strategies

1. How to construct kink points?

Strategy 1: “Vertical alignment”

- **We enforce continuity by changing only the vertical parts**
- $\boldsymbol{\sigma_R \ll \sigma_Z}$ → horizontal parts of the fits are more trustworthy

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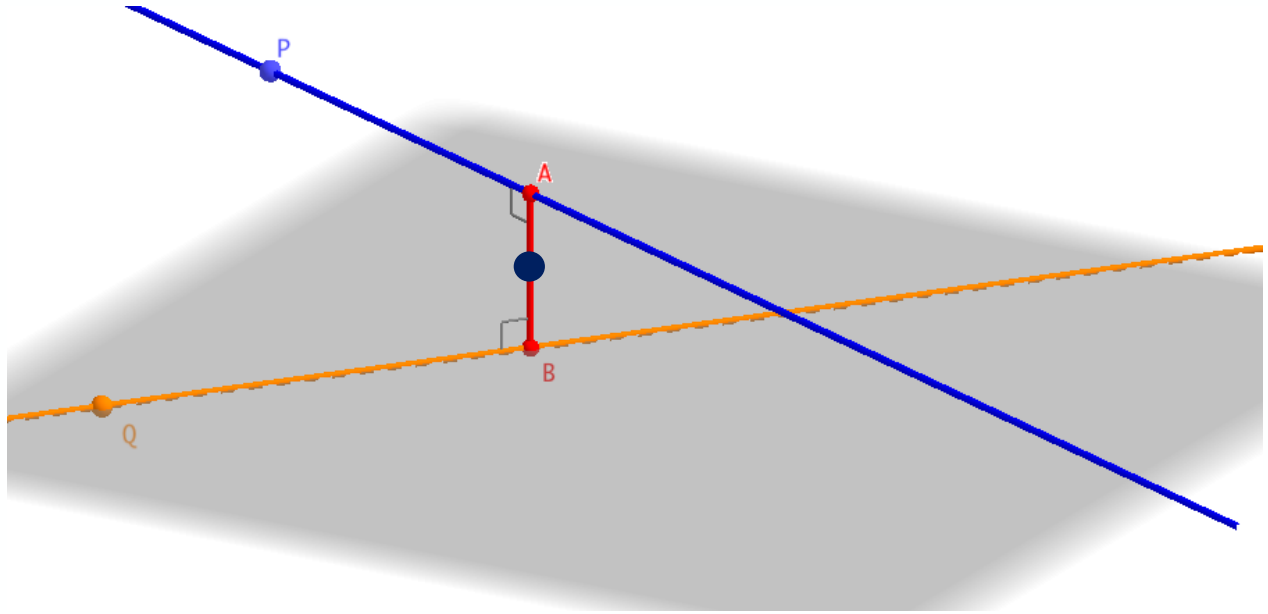
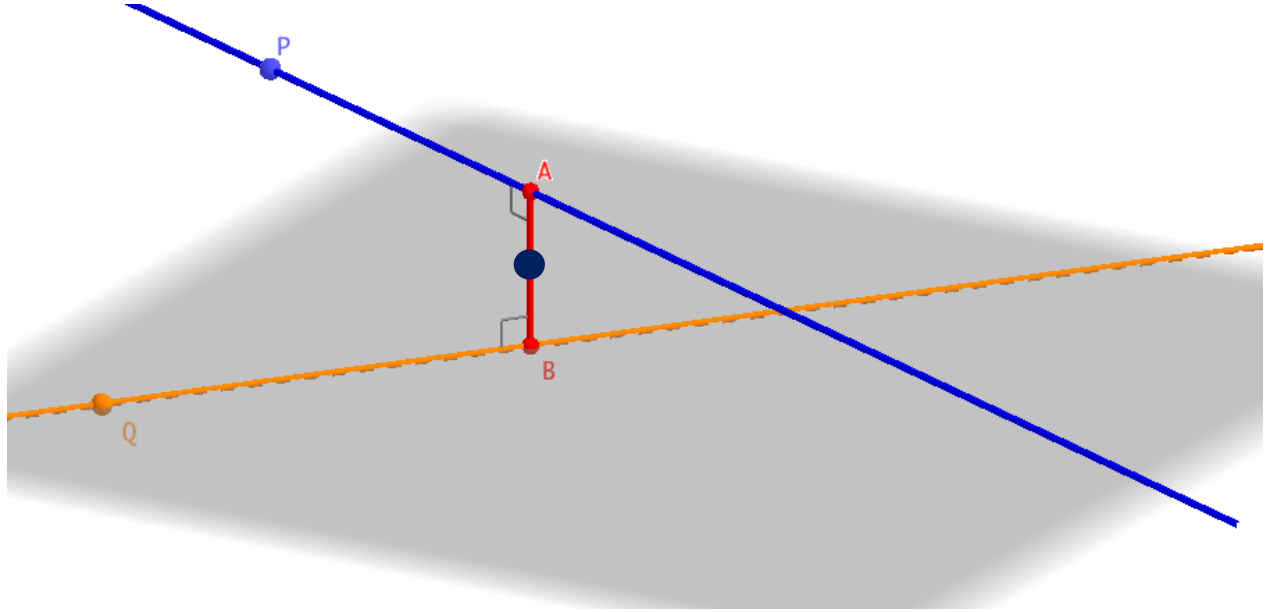


Strategy 1: “Vertical alignment”

- **We enforce continuity by changing only the vertical parts**
- $\boldsymbol{\sigma_R \ll \sigma_Z}$ → horizontal parts of the fits are more trustworthy
- Line trajectories T_1, T_2 have intersection (x_0, y_0) in 2D
- Z coordinates of T_1 and T_2 in (x_0, y_0) are z_1 and z_2
- Kink point = $(x_0, y_0, (z_1 + z_2)/2)$



Strategy 1: “Vertical alignment”

Pros: easy to calculate, works most of the time

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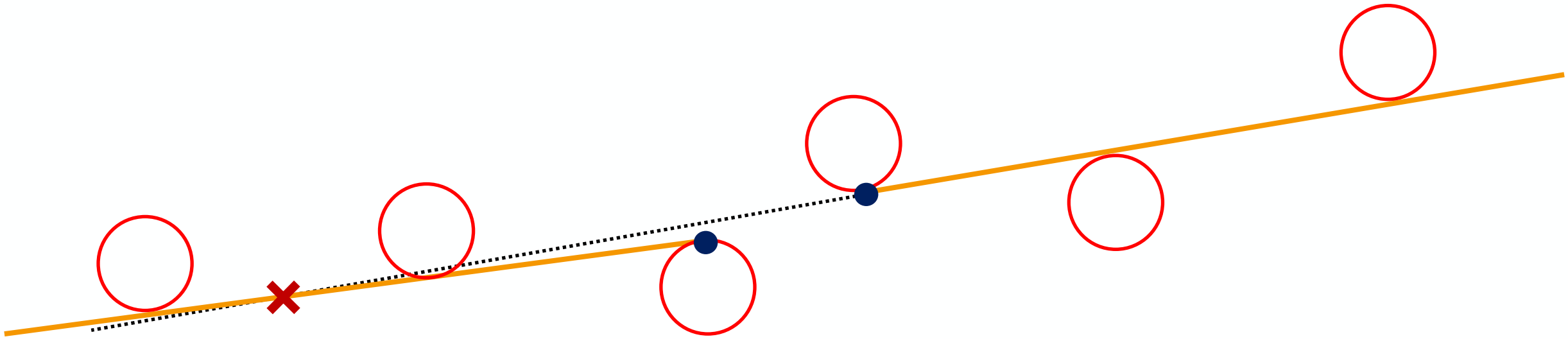
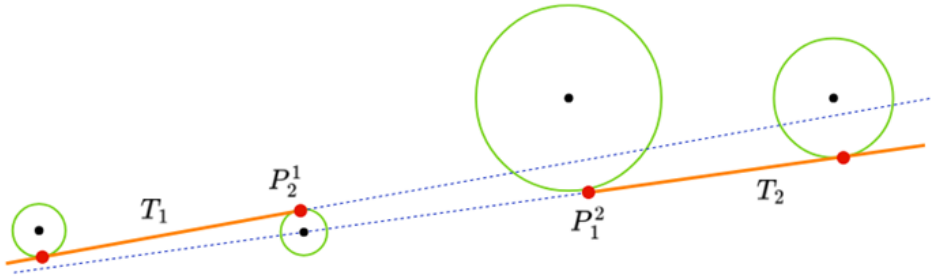
Pros: easy to calculate, works most of the time

Cons: unstable for smaller angles!

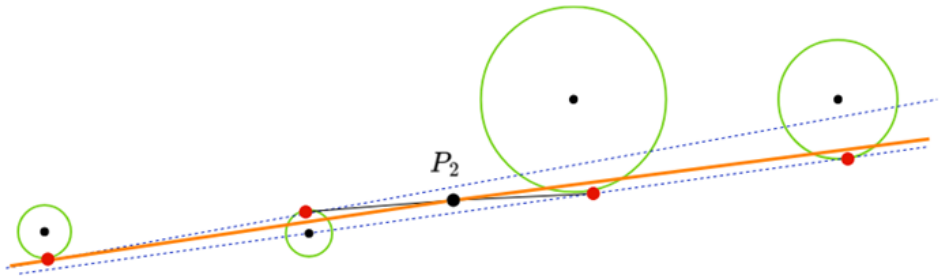


Strategy 2: “Endpoints middle”

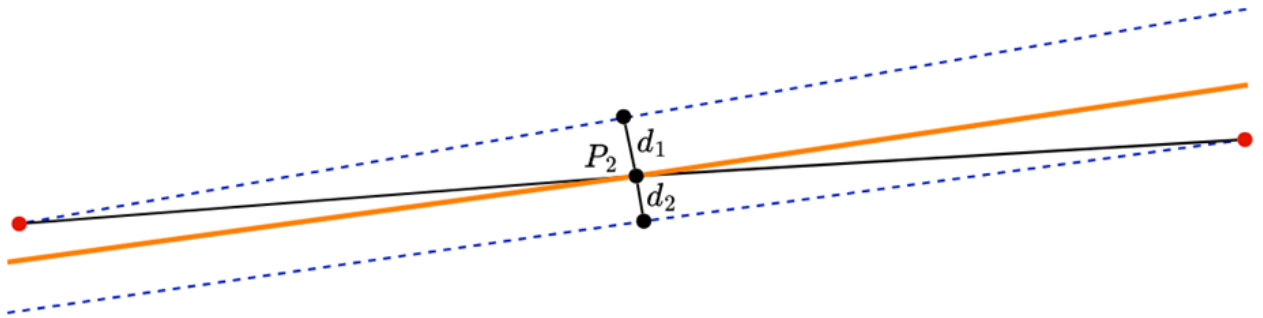
- Made as a correction for small angles
- Kink Point = middle point between the two ends



(a) Disconnected trajectories



(b) Connected trajectories



(c) Distances of new trajectory point to the original tracks

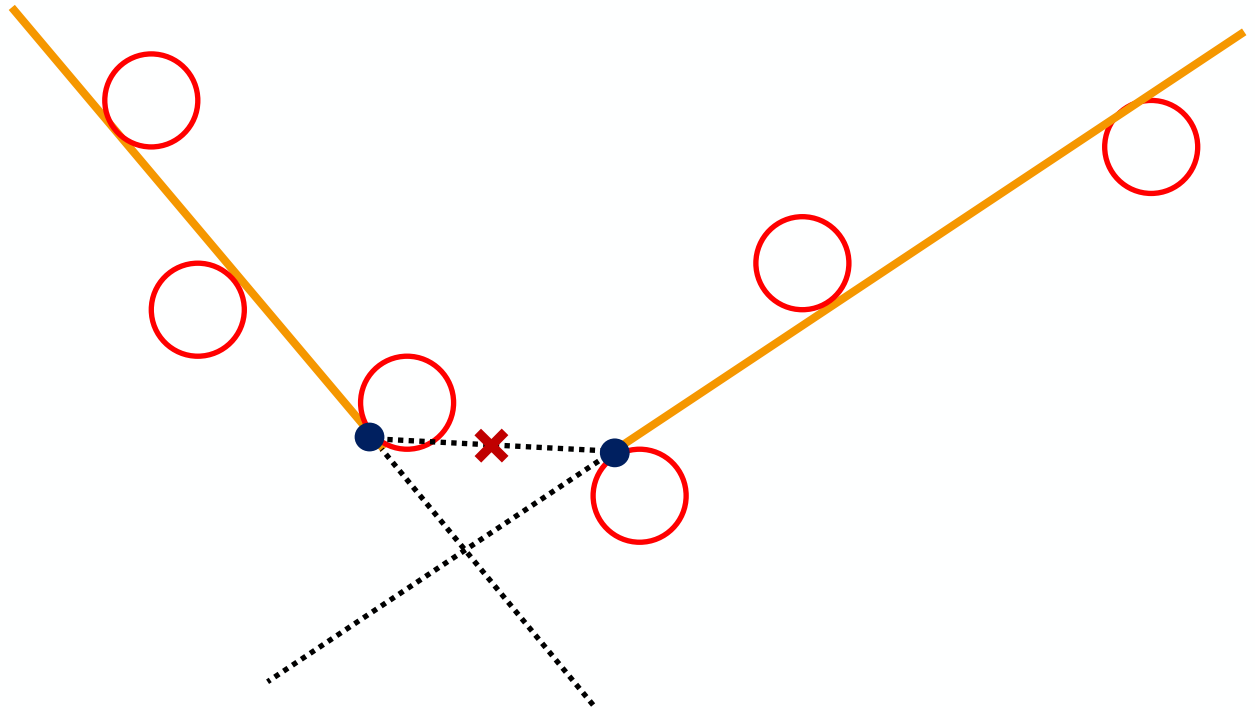
Strategy 2: “Endpoints middle”

Pros: great for small angles

Strategy 2: “Endpoints middle”

Pros: great for small angles

Cons: terrible for larger angles



Strategy 3: “closest approach”

- Point of closest approach between the two lines
- No obvious benefits
- Might be superior to “vertical alignment” strategy (needs testing)

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- Point of closest approach between the two lines
- No obvious benefits
- Might be superior to “vertical alignment” strategy (needs testing)

Pros: similar as “vertical alignment”

Cons: unstable for small angles

More possible strategies

- "*Point on wire*" strategy for Bi-Po events?
- "*Point on foil*" strategy for $\beta\beta$ events?

Validation criteria

2. How do we check validity?

Validation criteria

- Each strategy has its own set
- Modular reusable implementation

```
// angular criteria
bool check_angle_2D_after( const double min_angle, const double max_angle ) const;
bool check_angle_3D_after( const double min_angle, const double max_angle ) const;
bool check_angle_2D_before( const double min_angle, const double max_angle ) const;
bool check_angle_3D_before( const double min_angle, const double max_angle ) const;

// position criteria
bool check_is_inside_tracker() const;
bool check_distance_to_MW( const double min_distance ) const;
bool check_distance_to_XW( const double min_distance ) const;
bool check_distance_to_SF( const double min_distance ) const;

// associated tracker hit criteria
bool check_close_hits_2D( const double max_angle ) const;

// endpoints criteria
bool check_are_ends_close_2D( const double max_distance ) const;
bool check_are_ends_close_3D( const double max_distance ) const;

// distance criteria specific to the connection strategies
bool check_vertical_distance( const double max_distance) const;
bool check_middle_point_distance( const double max_distance) const;
```

Validation criteria

1. “Vertical alignment” criteria set:

```
// constructing a list of criteria
std::initializer_list<Criterion> criteria = {
  [&]{ return check_are_ends_close_2D( config.max_trajectory_endpoints_distance ); },
  [&]{ return check_close_hits_2D( config.max_tracker_hits_distance ); },
  [&]{ return check_angle_3D_after( config.min_kink_angle, config.max_kink_angle ); },
  [&]{ return check_angle_3D_before( config.min_kink_angle, config.max_kink_angle ); },
  [&]{ return check_kink_point_distance( config.max_vertical_distance / 2.0 ); },
  [&]{ return check_is_inside_tracker(); },
  [&]{ return check_distance_to_SF( config.min_distance_from_foil ); },
  [&]{ return check_distance_to_MW( config.min_distance_from_main_walls ); },
  [&]{ return check_distance_to_XW( config.min_distance_from_X_walls ); }
};
```

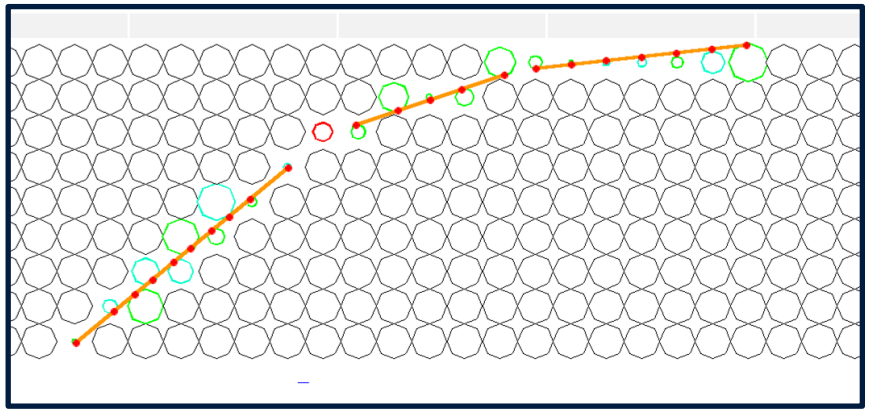
2. “Endpoints middle” criteria set:

```
// constructing a list of criteria
std::initializer_list<Criterion> criteria = {
  [&]{ return check_are_ends_close_3D( config.max_trajectory_endpoints_distance ); },
  [&]{ return check_close_hits_2D( config.max_tracker_hits_distance ); },
  [&]{ return check_middle_point_distance( config.max_trajectories_middlepoint_distance ); },
  [&]{ return check_angle_3D_after( config.min_trajectory_connection_angle, config.max_trajectory_connection_angle ); },
};
```

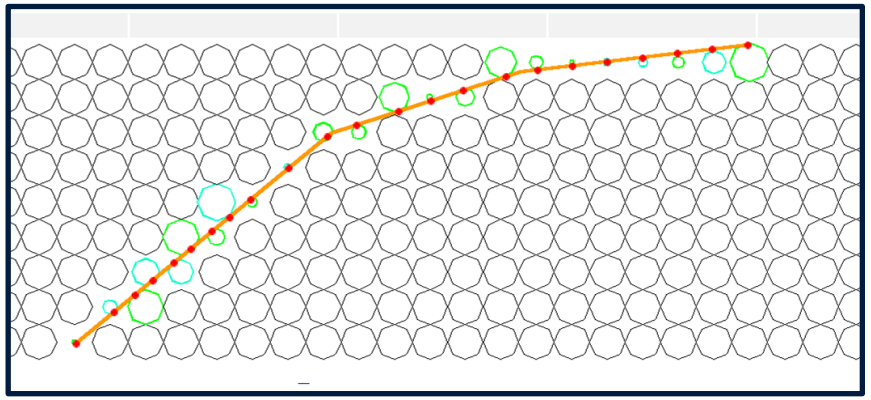
Refinements

We changed the fits. What broke?

Refinements – wrong associations

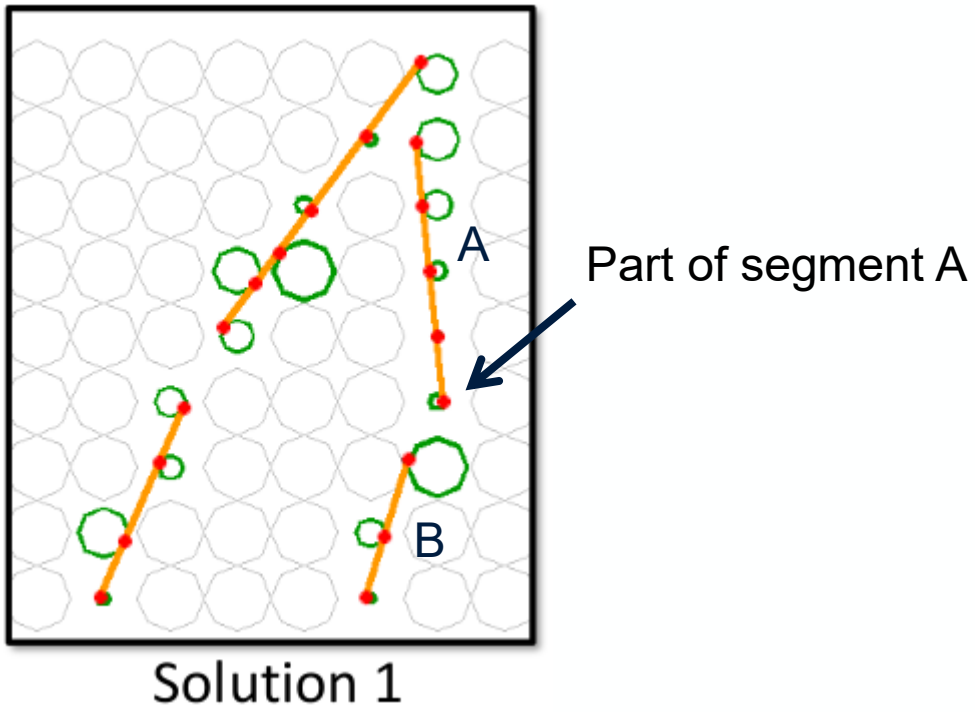


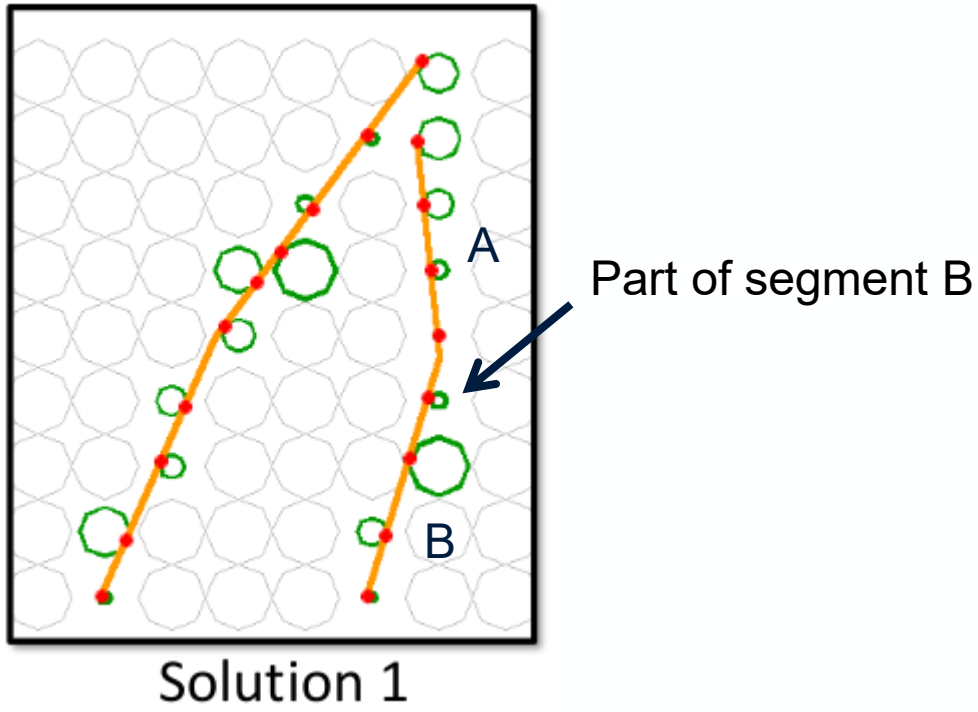
Missed completely



Can be added after connection (the fits changed)

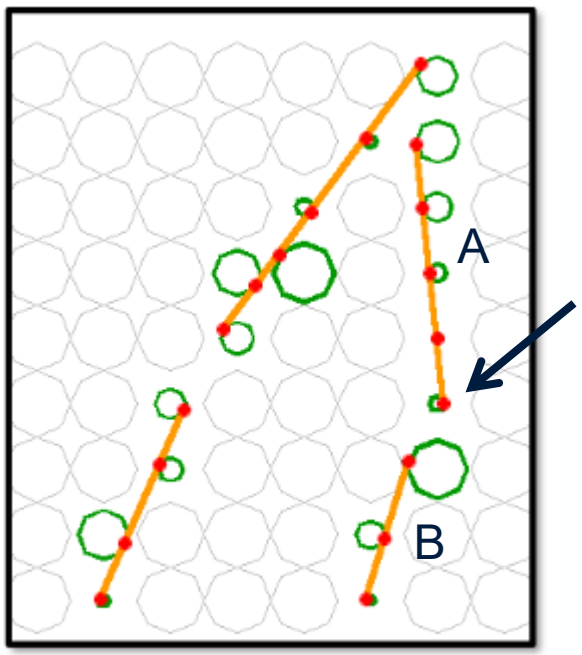
Refinements – wrong associations





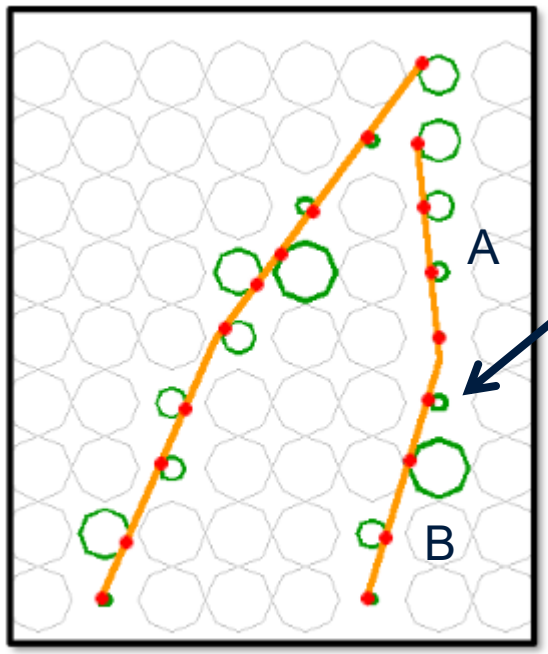
Refinements – wrong associations

- Reevaluating all associations to segments
- Updating all association points (changes χ^2…)



Part of segment A

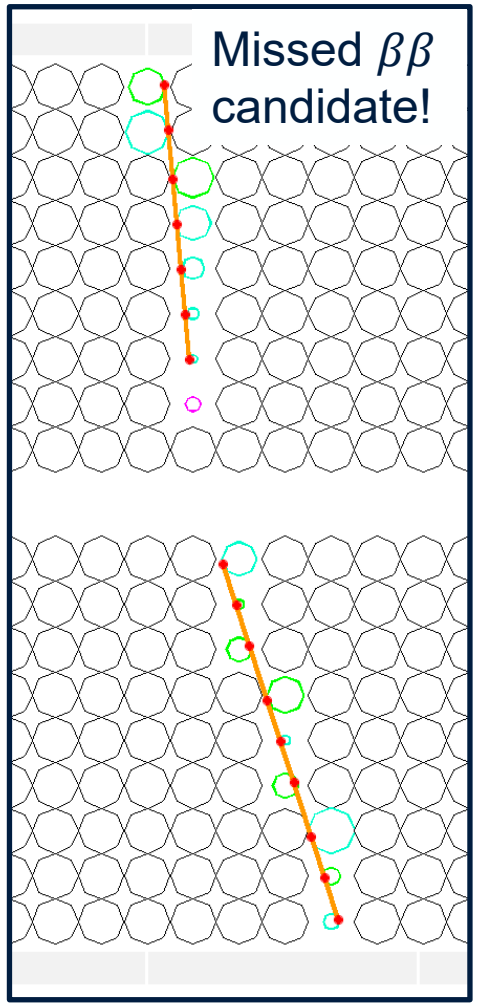
Solution 1

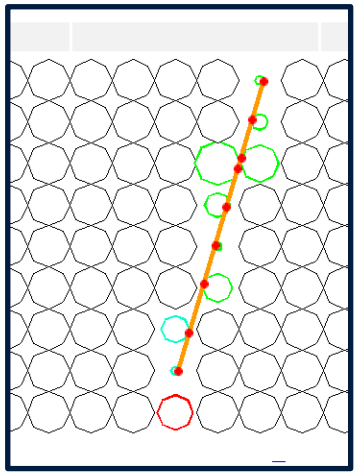


Part of segment B

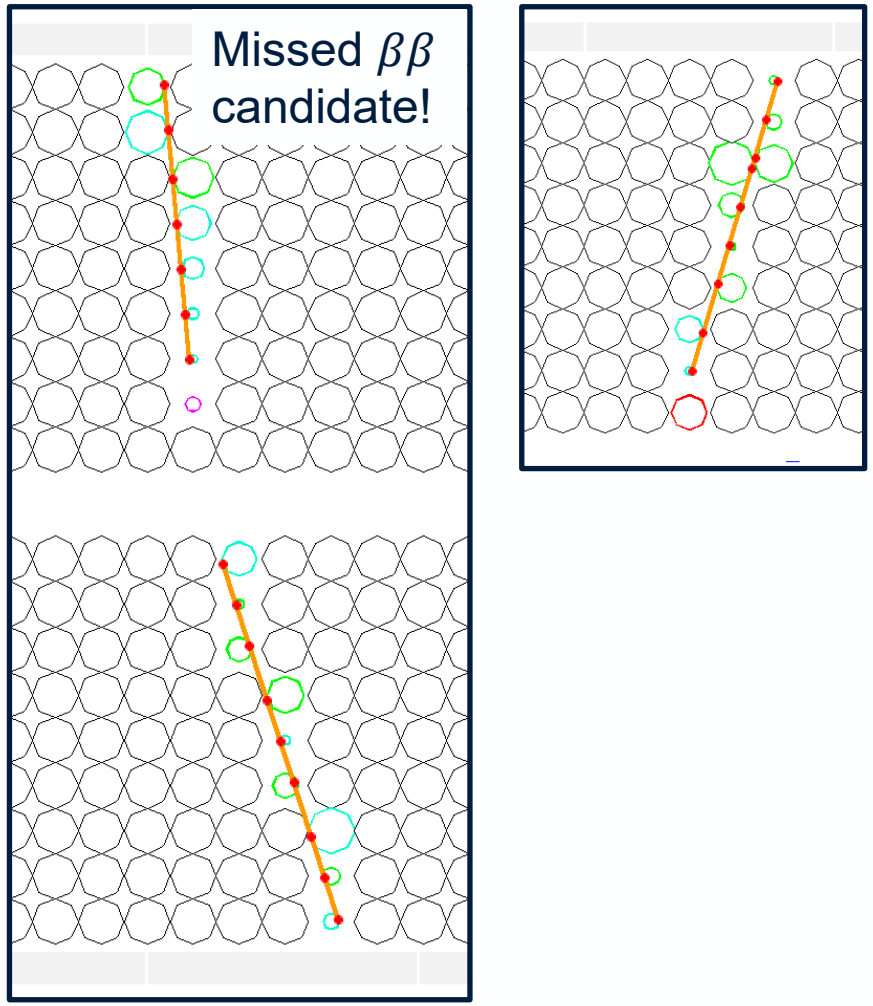
Solution 1

Refinements – trajectory extension



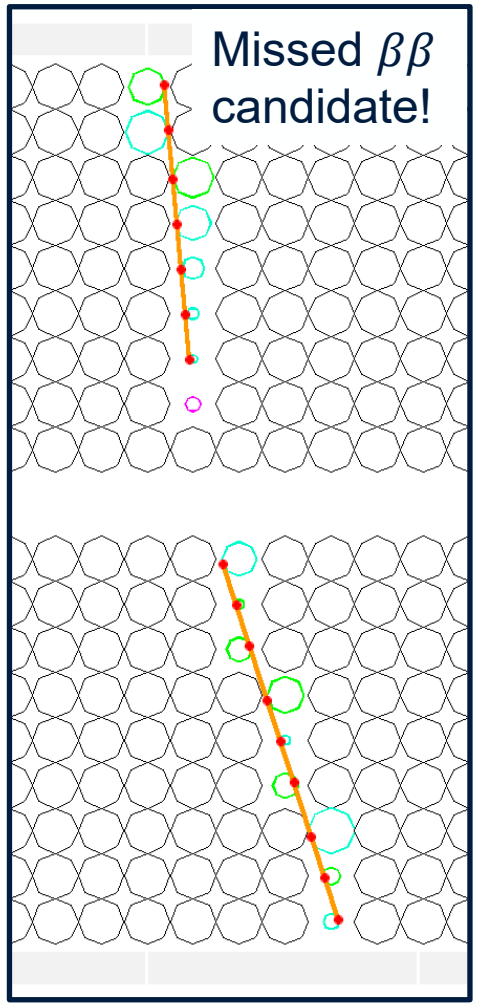


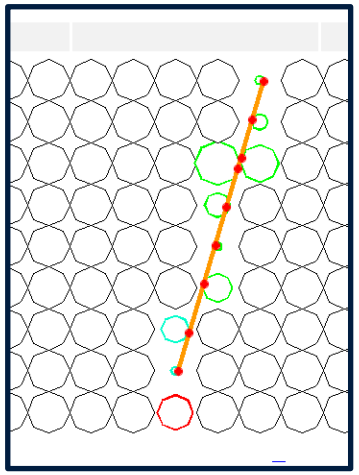
Refinements – trajectory extension



- Extending the trajectories (up to certain length)
- Recovers missed hits at the ends
- Higher mismatch tolerance

Refinements – trajectory extension





- Extending the trajectories (up to certain length)
- Recovers missed hits at the ends
- Higher mismatch tolerance

```
########################
# Trajectory extension #
########################

# Maximum allowed length to prolong the track to include previously unassociated or incorrectly associated hit
polylines.max_extention_distance : real as length = 120.0 mm

# Maximum distance to associate tracker hit to a track during extension
polylines.hit_association_distance : real as length = 12.0 mm
```

What's missing?

1. **TCD input/output conflict**

What's missing?

1. **TCD input/output conflict**
2. **TrajectoryBuilder:**
   - Better control through config
     (on/off switch for individual strategies, better option names…)
   - Make official release (Cimrman 1.2.0)
   - Do we want to reuse the code?

What's missing?

1. **TCD input/output conflict**
2. **TrajectoryBuilder:**
   - Better control through config
     (on/off switch for individual strategies, better option names…)
   - Make official release (Cimrman 1.2.0)
   - Do we want to reuse the code?
3. **Alpha tracking:**
   - No upgrade since last Collaboration meeting
   - Lack of feedback (Antoine is using TrackFit)
   - More testing needed
   - Communication with official drift model

What's missing?

4. **Solutions in PTD bank?**
   - At least a module dedicated for decision making


SUPER NEMO
Source = ββ Isotope = ^{82}Se
Drift cells (Geiger mode)
e⁻
Calorimeter energy
Drift hits
Reconstructed track
Vertex (ββ decay)
DON'T PANIC
It's not just a detector. It's a trip.
CIMRMAN RECONSTRUCTION MODULE
CIMRMAN
Turning hits into understanding.
Mostly harmless.

Thank you