Outline

- Data Association Scenarios
- Track Filtering and Gating
- Global Nearest Neighbor (GNN)
- Review: Linear Assignment Problem
- Murthy's k-best Assignments Algorithm
- Probabilistic Data Association (PDAF)
- Joint Probabilistic Data Assoc (JPDAF)
- Multi-Hypothesis Tracking (MHT)
- Markov Chain Monte Carlo DA (MCMCDA)

TODAY

Multi Target Tracking (MTT)

Scenario: Detect and Track

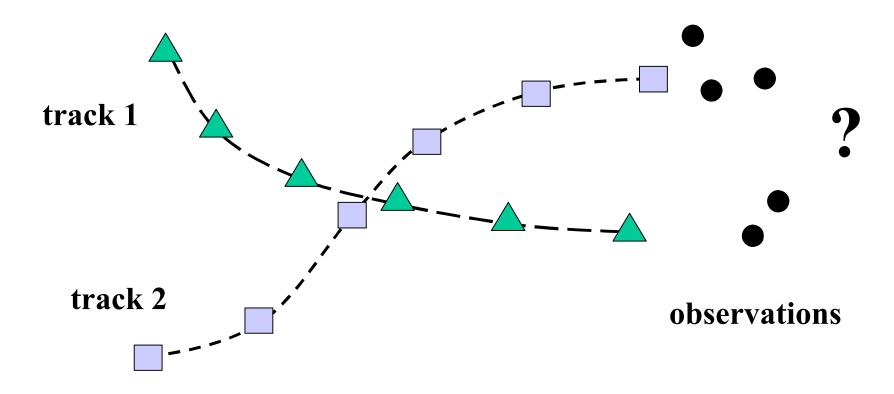
Given: N tracked target trajectories and M new sensor observations

Problem: deciding which target generated which observation

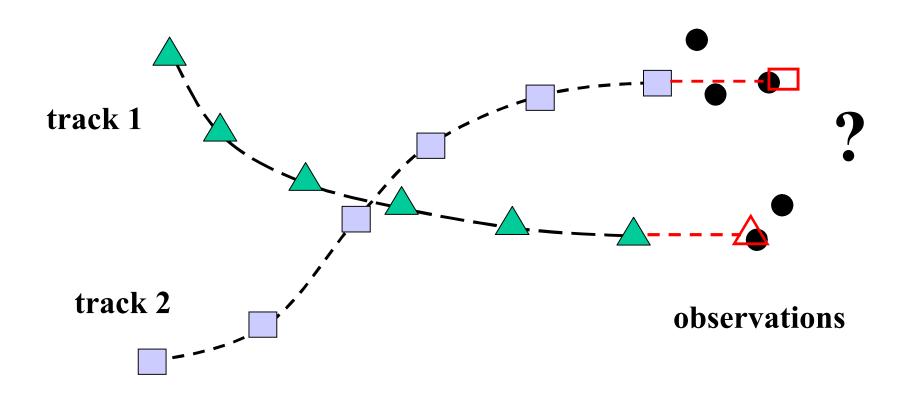
Data Association = assigning sensor responses to trajectories

Note: if assignment was always unambiguous, we could turn MTT into independent single-target tracking problems. However, when the association is ambiguous (multiple observations in one gating region; common observations in multiple gating regions), then the assignment decisions become coupled and much harder to solve.

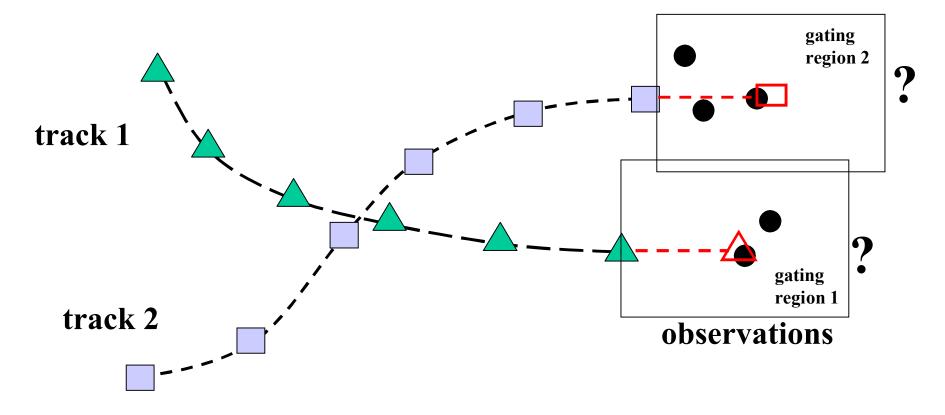
Multi-frame Matching (matching observations in a new frame to a set of tracked trajectories)



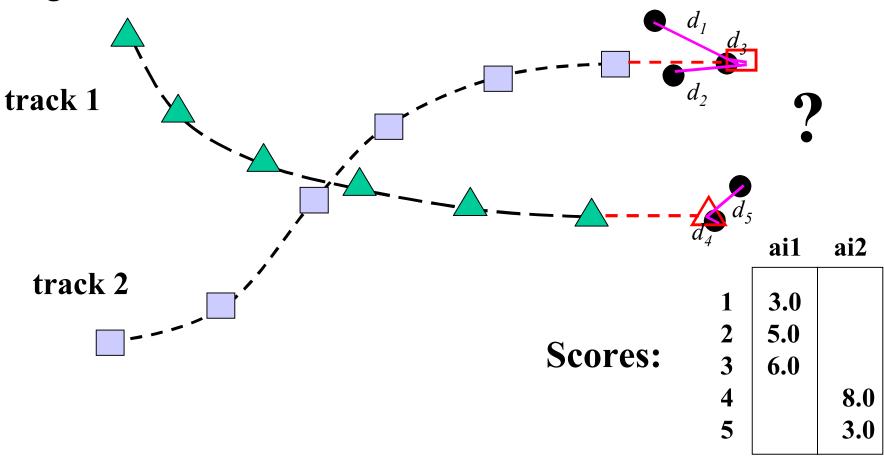
Predict next target position along each track.



Form a gating region around each predicted target location. This is a divide and conquer approach.

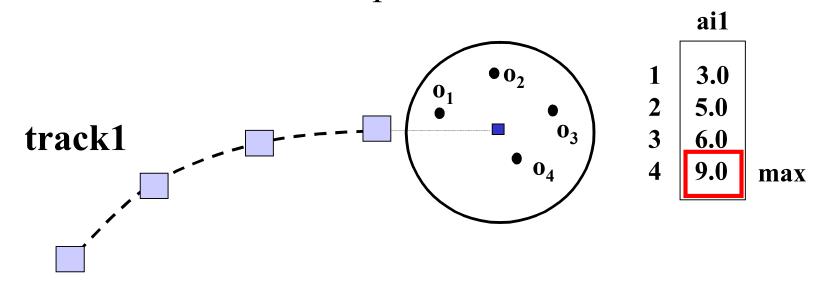


For each candidate matches (a track-to-data pairing), compute match score based on likelihood of the data given the track.



Recall: Global Nearest Neighbor

Evaluate each observation in track gating region. Choose "best" one to incorporate into track.



a_{i1} = score for matching observation i to track 1

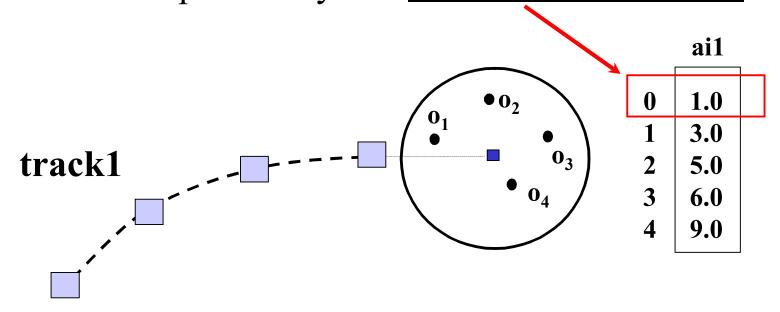
Choose best match $a_{m1} = \max\{a_{11}, a_{21}, a_{31}, a_{41}\}$

Probabilistic Data Association Filter

Updating single track based on new observations.

General idea: Instead of matching a single best observation to the track, we update based on all observations (in gating window), weighted by their likelihoods.

Consider all points in gating window. Also consider the additional possibility that <u>no observations match</u>.



 p_{i1} = "probability" of matching observation i to track 1

$$p_{i1} = \frac{a_{i1}}{\sum_{i=0}^{n} a_{i1}}$$

Kalman filter update is based on residual vector (diff between predicted location and observed location)

When using single best observation

$$\tilde{y}_k = o_{\text{max}} - H_k \, \hat{x}_{k|k-1}$$

PDAF uses weighted combination of observations

$$\tilde{y}_k = \sum_{i=1}^n p_{i1}(o_i - H_k \,\hat{x}_{k|k-1})$$

note: if we weren't consider the possibility of no match, this would exactly be the diff between the weighted center of mass of observations and the predicted location

Computation of Kalman posterior covariance must change too, to incorporate weighted matches and possibility of no match.

Typical computation when single match is used:

$$\mathbf{P}_{k|k} = (I - \mathbf{K}_k \mathbf{H}_k) \mathbf{P}_{k|k-1}$$

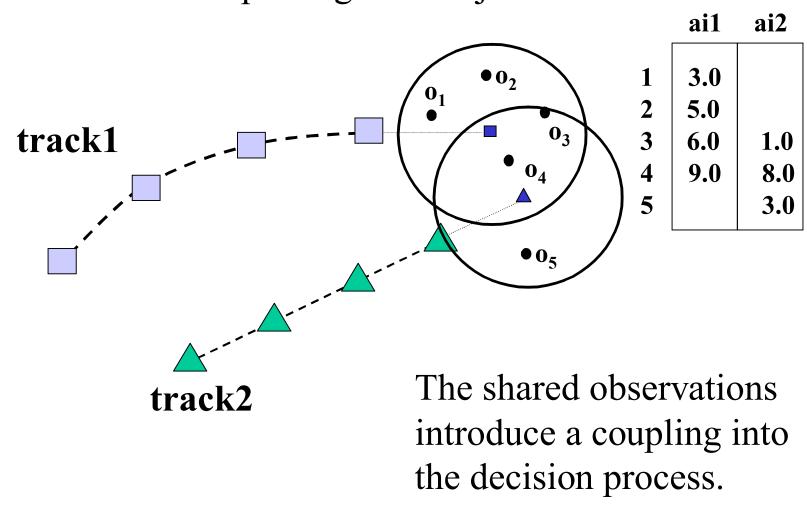
PDAF computation:

$$P_{k|k}=p_{01}\,P_{k|k-1}$$
 no match, no update $+(1-p_{01})[I-K_kH_k]P_{k|k-1}$ update if any match $+K_k\operatorname{Cov}(o_i-H_k\,\hat{x}_{k|k-1})\,K_k'$ correction term to reflect uncertain

correction term to reflect uncertain association (spread of possible matches or no match)

Problem

When gating regions overlap, the same observations can contribute to updating both trajectories.

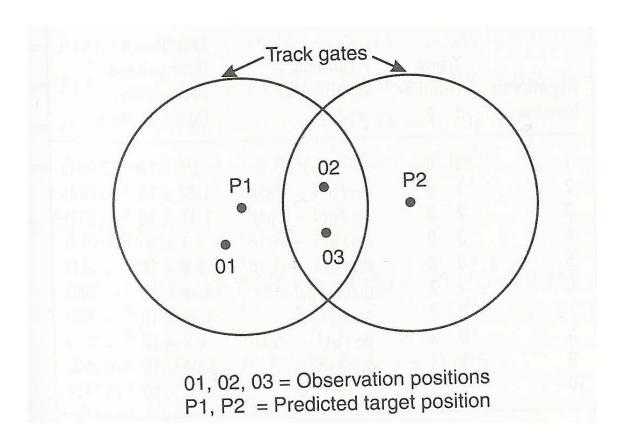


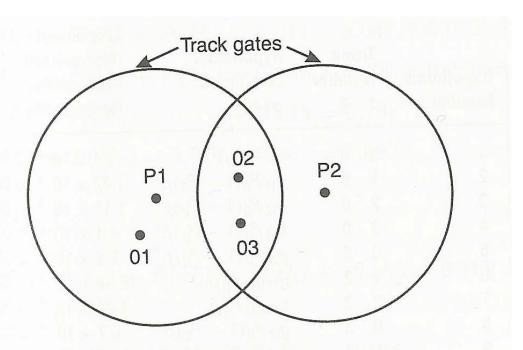
Joint Probabilistic Data Association Filter

If maintaining multiple tracks, doing PDAF on each one independently is nonoptimal, since observations in overlapping gate regions will be counted more than once (contribute to more than one track).

JPDAF reasons over possible combinations of matches, in a principled way.

Example (from Blackman and Popoli).





Candidates:

track1: 0 1 2 3

track2: 0 2 3

01, 02, 03 = Observation positions + Oo = no match P1, P2 = Predicted target position

Possible assignments: (i,j) = assign i to track1, j to track2

(0,0)(1,0)(2,0)(3,0)

(0,2)(1,2)(2,2)(3,2)

(0,3)(1,3)(2,3)(3,3)

don't assign same observation twice

Each possible (non-conflicting) assignment becomes a hypothesis with an associated probability.

Table 6.8 Hypothesis Matrix for Example of Figure 6.3

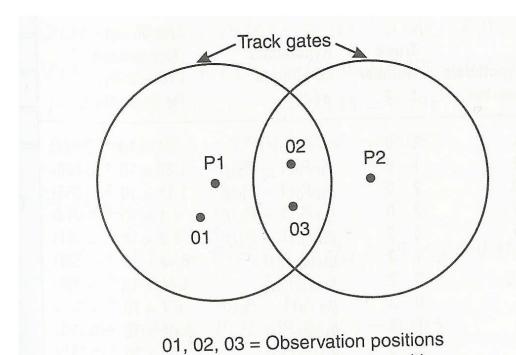
Hypothesis	Track Number		Hypothesis Likelihood	Likelihood (Normalized Probability)
Number	1	2	$p(H_i)$	for Example
1	0	0	$(1 - P_0)^2 \beta^3$	$2.4 \times 10^{-6} (0.011)$
2	1	0	$g_{11}P_{\rm D}(1-P_{\rm D})\beta^2$	$1.82 \times 10^{-5} (0.086)$
3	2	0	$g_{12}P_{\rm D}(1-P_{\rm D})\beta^2$	$1.11 \times 10^{-5} (0.053)$
4	3	0	$g_{13} P_{\rm D} (1 - P_{\rm D}) \beta^2$	$4.1 \times 10^{-6} (0.019)$
5 6	0	2	$g_{22} P_{\rm D} (1 - P_{\rm D}) \beta^2$	$8.6 \times 10^{-6} (0.041)$
6	1	2	$g_{11}g_{22}P_{0}^{2}\beta$	$6.47 \times 10^{-5} (0.306)$
7	3	2	$g_{13}g_{22}P_0^2\beta$	$1.44 \times 10^{-5} (0.068)$
8	0	3	$g_{23}P_{\rm D}(1-P_{\rm D})\beta^2$	$6.7 \times 10^{-6} (0.032)$
9	1	3	$g_{11}g_{23}P_{D}^{2}\beta$	$5.04 \times 10^{-5} (0.239)$
10	2	3	$g_{12}g_{23}P_{0}^{2}\beta$	$3.06 \times 10^{-5} (0.145)$

we will talk more about these in a moment

Now compute probability p_{ij} that each observation i should be assigned to track j, by adding probabilities of assignments where that is so. Example: p_{11} = prob that observation should be assigned to track 1.

Hypothesis Matrix for Example of Figure 6.3

Hypothesis	Track Number		Hypothesis Likelihood	Likelihood (Normalized Probability)	
Number	1	2	$p(H_i)$	for Example	
1	0	0	$(1-P_0)^2\beta^3$	$2.4 \times 10^{-6} \ (0.011)$	006
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P1, P2 = Predicted target position

Combined probabilities

Track1: Track2:

$$p_{10} = .084$$
 $p_{20} = .169$

$$p_{11} = .631$$
 $p_{21} = .0$

$$p_{12} = .198$$
 $p_{22} = .415$

$$p_{13} = .087$$
 $p_{23} = .416$

Continuing the example:

Track 1 probabilities

$$p_{01} = .084$$

$$p_{11} = .631$$

$$p_{21} = .198$$

$$p_{31} = .087$$



PDAF filter for track 1

Track 2 probabilities

$$p_{02} = .169$$

$$p_{12} = 0.0$$

$$p_{22} = .415$$

$$p_{32} = .416$$



PDAF filter for track 2

Note: running PDAF filters on each track independently is now OK because any inconsistency (double counting) has been removed.

Hypothesis Likelihoods

Table 6.8
Hypothesis Matrix for Example of Figure 6.3

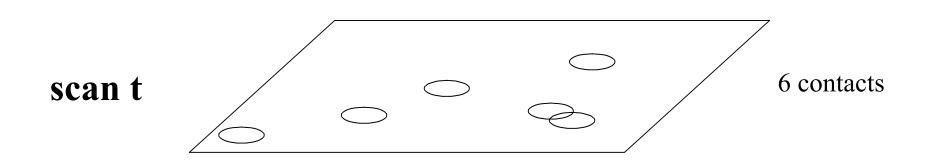
Hypothesis Number	N	ack imber 2	Hypothesis Likelihood $p(H_i)$	Likelihood (Normalized Probability) for Example
1	0	0	$(1 - P_0)^2 \beta^3$	$2.4 \times 10^{-6} (0.011)$
2	1	0	$g_{11}P_{0}(1-P_{0})\beta^{2}$	$1.82 \times 10^{-5} (0.086)$
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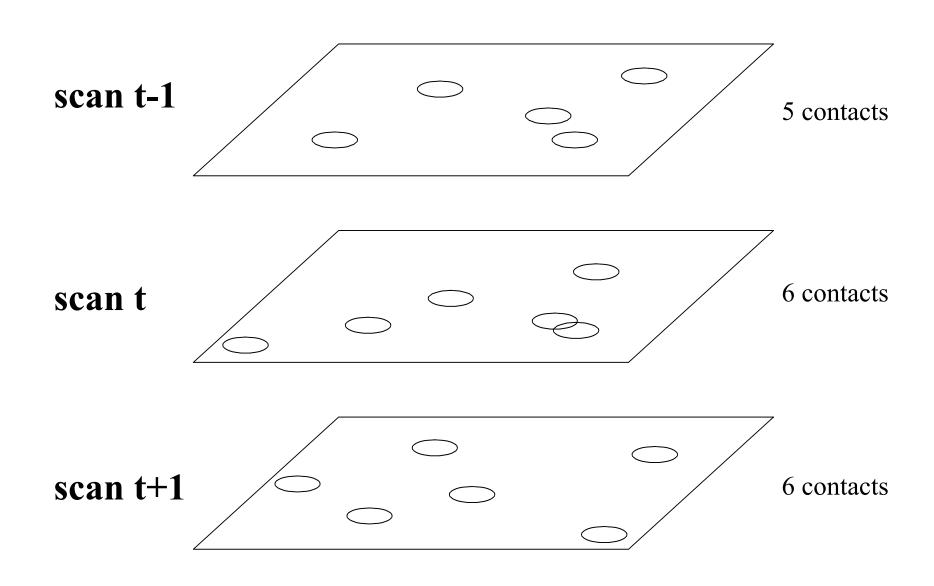
P_D is prob of detect
B is prob of false alarm
g_{ij} likelihood of observe j
given track i

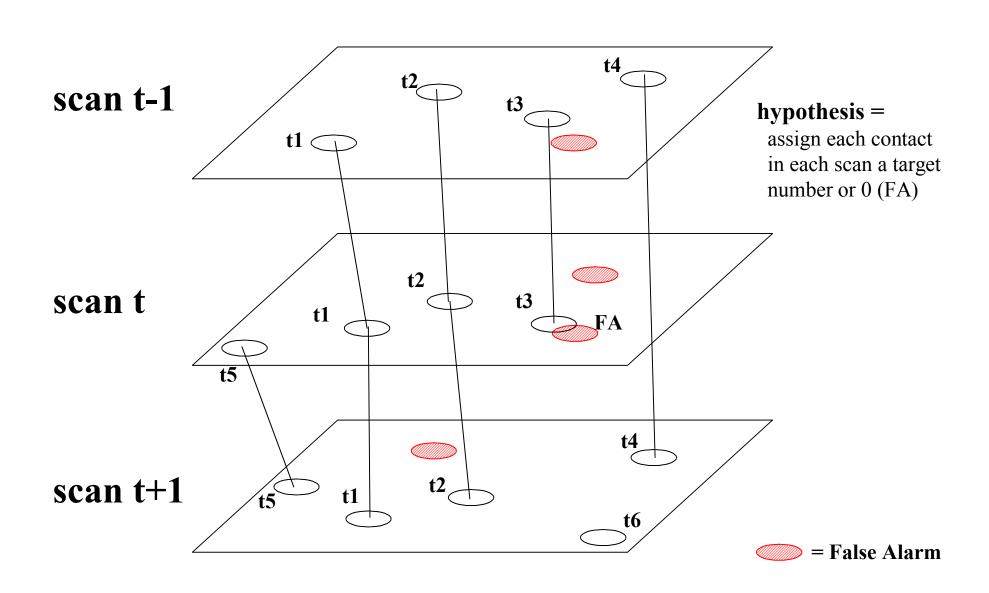
$$P(H) = \prod_{\substack{\text{Track i assigned} \\ \text{to observation j}}} g_{ij} P_D \prod_{\substack{\text{Tracks assigned} \\ \text{to no match (0)}}} (1-P_D) \prod_{\substack{\text{Unassigned} \\ \text{observations}}} B$$

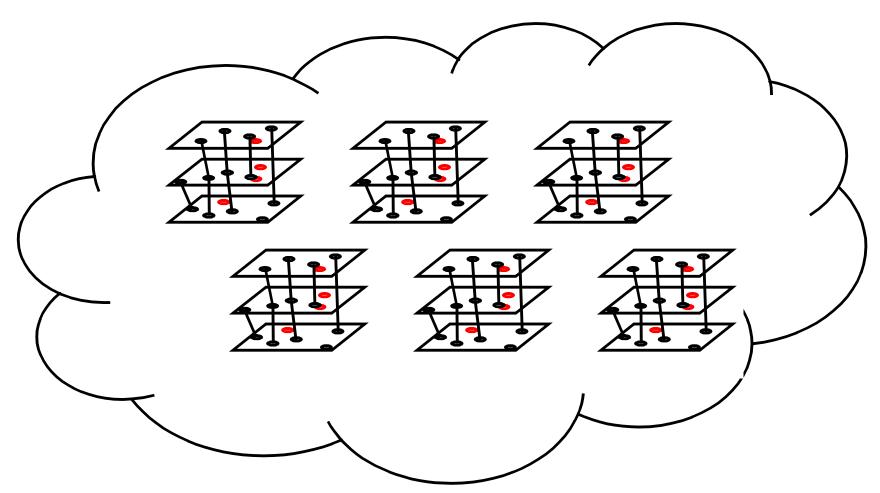
Basic idea: instead of collapsing the 10 hypotheses from the last example into two trajectory updates, maintain and propagate a subset of them, as each is a possible explanation for the current state of the world.

This is a delayed decision approach. The hope is that future data will disambiguate difficult decisions at this time step.







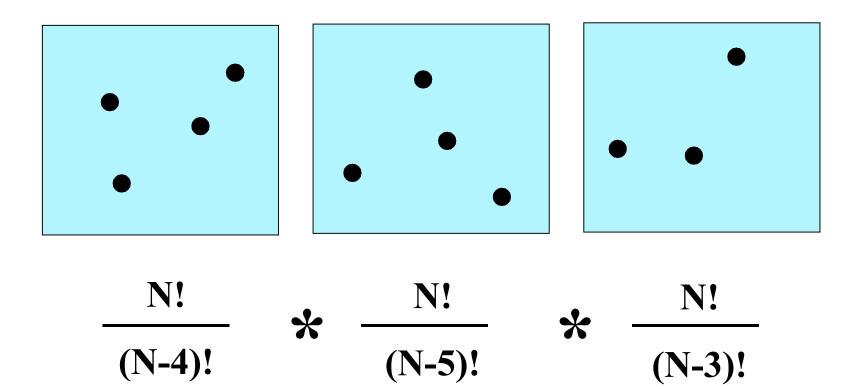


We maintain a set of such hypotheses. Each is one possible set of assignments of observations to targets or false alarms.

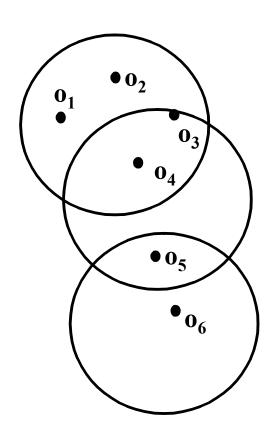
Combinatorial Explosion

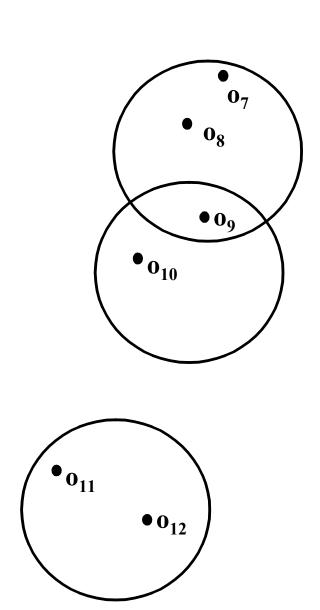
Rough order of magnitude on number of hypotheses:

Let's say we have an upper bound N on number of targets and we can associate each contact in each scan a number from 1 to N. (we are ignoring false alarms at the moment)

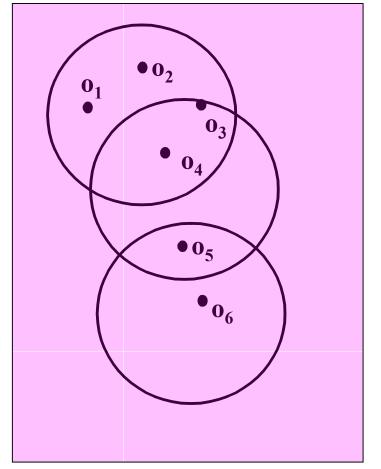


Clustering

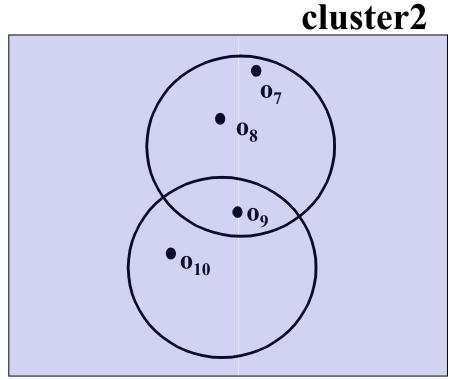


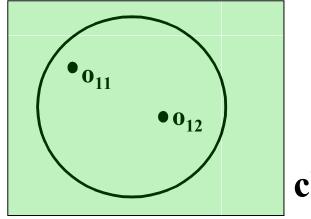


Clustering: can analyze each cluster independently (e.g. on a separate processor)



cluster1





cluster3

Track Merging

merge similar trajectories (because this might allow you to merge hypotheses)

- •common observation history (e.g two tracks having the last N observations in common)
- •similar current state estimates (e.g same location and velocity in Kalman Filter)

Pruning: Discard low probability hypotheses

For example, one hypothesis that is always available is that every contact ever observed has been a false alarm! However, that is typically a very low probability event.

One of the most principled approaches to this is by Cox and Hingorani (PAMI'96). They combine MHT with Murty's k-best assignment algorithm to maintain a fixed set of k best hypotheses at each scan.

MHT with Murty's k-best

One way to avoid combinatorial explosion is to fix the number of hypotheses maintained at each frame, and use Murty's method for k-best assignments to find the k best hypotheses.

Example: let's say we want 5 hypotheses at each stage:

Given the 5 old hypotheses from time t-1, perform Hungarian algorithm to find best assignment of the observations in the current frame to each of them, forming new hypotheses at time t. Rank order them by hypothesis likelihood and put them in a priority queue: {H1,H2,H3,H4,H5}.

MHT with Murty's k-best

Now perform Murty's method using H1, to find the k highest variants of H1. Let's say k=3, and those variants are H_{11} , H_{12} , H_{13} .

By insertion sort, put them in with the original list of hypotheses, bumping out any hypotheses as necessary to keep a total list length of 5.

For example, we might now have $\{H1,H_{11},H2,H3,H_{12}\}$, where H4, H5 and H_{13} have been discarded

Now perform Murty's method on the next item in the list, which is H_{11} , and so on. If H_{11} had been less than H2 in score, then Murty's would have been performed on H2 instead.

Idea: use Markov Chain Monte Carlo (MCMC) to sample from / explore the huge combinatorial space of hypotheses.

S. Oh, S. Russell, and S. Sastry, 2004. Markov Chain Monte Carlo data association for general multiple-target tracking problems. In Proc. IEEE Int. Conf. on Decision and Control, pages 735–742, 2004.

Yu, G. Medioni, and I. Cohen, 2007. Multiple target tracking using spatio-temporal Markov Chain Monte Carlo data association. In Proc. IEEE Int. Conf. on Computer Vision and Pattern Recognition, pages 1–8, 2007.

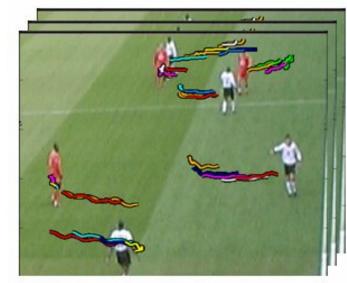


W.Ge and R.Collins, 2008, "Multi-target Data Association by Tracklets with Unsupervised Parameter Estimation," British Machine Vision Conference (BMVC'08), University of Leeds, September 2008, pp. 935-944.

Rather than use detections in each frame, first extract a set of "tracklets" by tracking detections through short subsequences of

the original video.

For example, detection "seeds" at every 10th frame are tracked through the next 30 frames (1 second) of video.

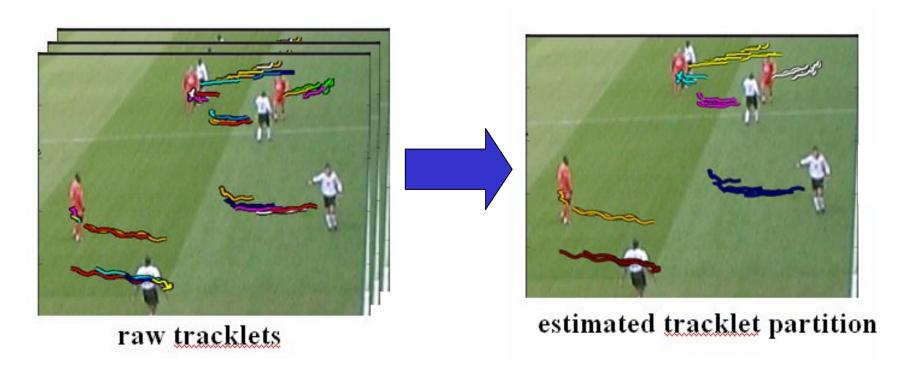


raw tracklets

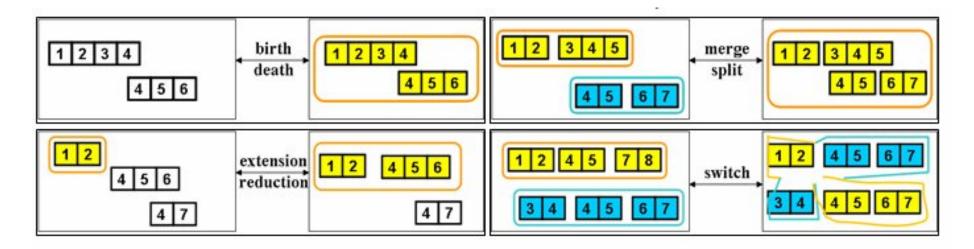
Why?

- •tracklets provide more spatial/temporal context than raw detections
- •short tracklets can be generated by simple (fast) trackers
- •less prone to drift/occlusion than longer tracks

Problem we are trying to solve: Find a partition of the set of overlapping tracklets such that tracklets belonging to the same object are grouped together. They could obviously be merged after that by a postprocessing stage.



Recall that MCMC stochastically explores the search space (of tracklet partitions, in this example) by proposing a set of "moves" from the current state to a new state.



MCMC moves

MCMC then decides whether or not to accept the proposal based, in part, on the ratio of likelihoods of the current state and the proposed state.

Z=observed tracklets

$$\omega^* = \underset{\omega}{\operatorname{arg\,max}}(p(\omega|Z)) \overset{\text{Bayes' rule}}{\longleftrightarrow} \underset{\omega}{\operatorname{arg\,max}}(p(Z|\omega)p(\omega))$$
likelihood prior

The likelihood and prior are calculated as functions of 8 features:

Likelihood features Prior features

Color Appearance False Alarm Rate

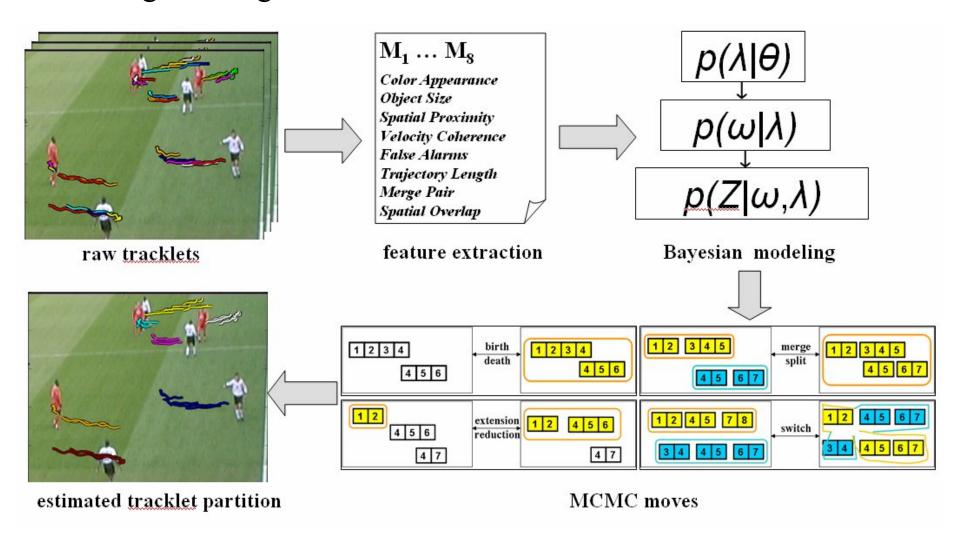
Object Size Trajectory Length

Spatial Proximity Merge Pair (encourage merging rather than starting new tracks)

Velocity Coherence Spatial Overlap (discourage overlaps between diff tracks)

note, she actually solved a harder problem of also inferring hyperparameters from the data

Putting it all together:



input tracklets

hypothesized tracks (at some time)

