

# Lecture 09: Data Association

Gonzalo Ferrer

18 February 2021

# 1 Euclidean nearest neighbours

The data association problem consist of finding for each observation  $z^i$  to which landmark  $m_j$  it corresponds. In other words:

$$c_t = \{c_t^i\}, \ (z^i \to m_j)$$

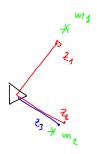


Figure 1: Euclidean nearest neighbours

$$c_t^i = \arg\min_j ||m_j - z_t^i||_2$$

#### Algorithm 1 Euclidean nearest neighbour

- 1: **for** i = 1 : K **do**
- 2: **for** j = 1 : N **do**
- 3:  $c_t^i = \min(||m_j z_t^i||_2)$
- 4: end for
- 5: end for

#### Pros:

- Match each  $z^i$  to closest  $m_j$
- Easy and Fast  $\mathcal{O}(K \cdot N)$

Cons: Greedy Data association.

# 2 Mahalanobis nearest neighbour

$$d_{ij}^2 = ||m_j - z^i||_{\Sigma}^2 = (m_j - z^i)^T \Sigma^{-1} (m_j - z^i)$$

MH captures uncertainty Pros:

• More robust to noise



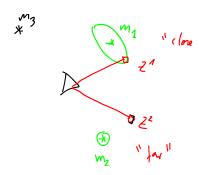


Figure 2: Mahalanobis nearest neighbours. The term "far" and "close" denote uncertainty for MH distances.

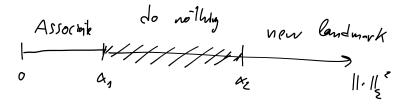


Figure 3: Decision Making for new observations. New landmarks might need conformation over several observations.

• Easy and fast  $\mathcal{O}(K \cdot N)$ 

Cons: Still greedy.

# 3 Maximum Likelihood (ML) Data Association

From the Bayes Filter we should calculate the distribution of correspondences:

$$p(x_{0:t}, c_{1:t}|Z, U) = (\text{product rule})$$
  
=  $p(c_{1:t}|x_{0:t}, Z, U)p(x_{0:t}|Z, U)$ 

Very complicated! Sequence of all correspondences should be re-calculated completely for all observations.

#### 3.1 Assumption I: Solve DA incrementally

 $p(c_t|z_t, y_t)$ . The history of correspondences  $c_{1:t}$  only depends on the last correspondence. Assume previous correspondences were correct.

$$p(c_t|z_t, y_t) = p(c_t|z_t, y_t, c_{1:t-1})$$

$$p(c_t|z_t, y_t) = \frac{p(z_t|c_t, y_t)p(c_t|y_t)}{p(z_t|y_t)} \propto p(z_t|c_t, y_t)$$

Posterior  $\propto$  likelihood for a given  $c_t$ .

$$c_t^* = \arg \max_{c_t} \{p(z_t|c_t, y_t)\}$$
 ML estimator



$$p(z_{t}|c_{t}, y_{t}) = p(z_{t}^{1}|z_{t}^{2:t}, y_{t}, c_{t})$$

$$\cdot p(z_{t}^{2}|z_{t}^{3:t}, y_{t}, c_{t})$$

$$\vdots$$

$$\cdot p(z_{t}^{K}|y_{t}, c_{t})$$

## 3.2 Assumption II: Independence

$$p(z_t|c_t, y_t) \simeq \prod_{i=1}^K p(z_t^i|c_t^i, y_t)$$

$$c_t^* = \arg\max_{c_t} \prod_{i=1}^K p(z_t^i | c_t^i, y_t),$$

where  $c_t = \{c_t^1 = m_{j_1}, c_t^2 = m_{j_2}, \dots, c_t^i = m_{j_i}, \dots\}$ Since  $c_t$  are independent:

$$\max_{c_t} \left( \prod_{i=1}^K p(z_t^i | c_t^i, y_t) \right) = \prod_{i=1}^K \max_{c_t^i} p(z_t^i | c_t^i, y_t)$$

Evaluate  $c_t^i$  individually!

$$z_t^i \sim \mathcal{N}(z_t^i; h(\bar{\mu}_t, c^i), H_t^i \bar{\Sigma}_t (H_t^i)^T + Q_t)$$

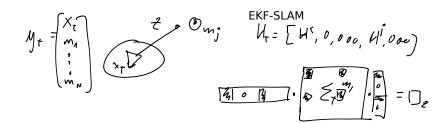


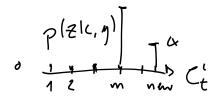
Figure 4: The Jacobian used to propagate he covariances of observations is the same as explained the the EKF-SLAM lecture.

New landmarks (ProbRob 322) under this method would not never be detected. Is for that reason that the hypothesis of being a new landmark should be considered:

$$p(z_t^i|c_t^i = new, y_t) = \alpha$$

where  $\alpha$  is a threshold value, hard to tune in practice.

We create a landmark only if distance to all other landmarks is higher than  $\alpha$ .





## 4 Joint DA

Efficient way to express DA: tree representation as seen in Fig. 5.

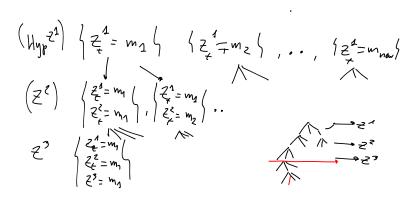


Figure 5: Joint Data Association. A tree structure captures all possible combinations of landmark-observation pairs.

#### 4.1 Individual compatibility test

 $\chi$  squared test ( $\alpha$  confidence level: 90, 95, 99%)

$$d_{11}^{2} = ||m_{1} - z^{1}||_{\Sigma} < \chi_{\alpha}^{2}$$

$$d_{12}^{2} < \chi_{\alpha}^{2}$$

$$d_{13}^{2} = ||m_{1} - z^{3}||_{\Sigma} \leqslant \chi_{\alpha}^{2}$$

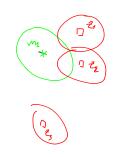


Figure 6: Individual compatibility

Fast filter to reject clearly incorrect hypothesis.

### 4.2 Joint Compatibility (JC) [1]

Content provides more accurate solutions. Set of hypothesis  $\rightarrow$  size exponential

$$\mathcal{H}_l = \{z_1 = m_1, z_2 = m_3, z_3 = m_{new}\}\$$

We will evaluate joint candidates based on their joint compatibility (JC)

if 
$$d_{\mathcal{H}_l}^2 < \chi_\alpha^2$$

For Individual compatibility (IC):

$$f_{ij}(y,z) = z^{i} - h(y,j)$$

For Joint compatibility:

$$f_{\mathcal{H}_{l}}(y,z) = \begin{bmatrix} f_{1,j_{1}}(y,z) \\ f_{2,j_{2}}(y,z) \\ \vdots \\ f_{l,j_{l}}(y,z) \end{bmatrix} = \begin{bmatrix} f_{\mathcal{H}_{l-1}}(y,z)f_{l,j_{l}}(y,z) \end{bmatrix}$$

$$\mathcal{H} = \{\underbrace{c^{1}}_{\mathcal{H}_{1}}, c^{2}, \dots, c^{K} \}$$

$$\underbrace{\mathcal{H}_{l}}_{\mathcal{H}_{l}}$$

If we rewrite  $f_{\mathcal{H}_{I}}(y,z)$  incrementally:

$$f_{\mathcal{H}_l}(y,z) = \begin{bmatrix} f_{\mathcal{H}_{l-1}}(y,z) \\ f_{l,j_l}(y,z) \end{bmatrix} \simeq f_{\mathcal{H}_l}(\bar{y},z) + G_{\mathcal{H}_l}(y-\bar{y}) + H_{\mathcal{H}_l}(z-\bar{z})$$

Covariance of the joint innovation

$$\begin{split} C_{\mathcal{H}_l^i} &= H_{\mathcal{H}_l^i} S H_{\mathcal{H}_l^i}^T + G_{\mathcal{H}_l^i} \Sigma G_{\mathcal{H}_l^i}^T \\ d_{\mathcal{H}_l^i}^2 &= f(\bar{y}, z)^T \cdot C_{\mathcal{H}_l^i}^{-1} \cdot f(\bar{y}, z) < \chi_{d, \alpha}^2, d = \dim(\mathcal{H}_l^i) \end{split}$$

This test is carried out incrementally.

#### 4.3 JC branch and Bound

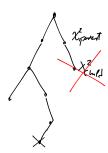


Figure 7: JCBB

Knowing that evaluating branched with the JC test allows us to discard branches without evaluating, since

$$\chi^2_{parent} < \chi^2_{child}$$

 $C_{H_l^i}$  captures cross-correlations of the observations while ML doesn't (assumed independence). More accurate and probabilistically more complete.

Slow (not exponential but it is on the worst case).

## References

[1] Neira, José, and Juan D. Tardós. "Data association in stochastic mapping using the joint compatibility test." IEEE Transactions on robotics and automation 17.6 (2001): 890-897.



# 5 Summary

$$c^i = \arg\min_j \|m_j - z^i\|_z$$
 – Euclidean Nearest Neighbor 
$$c^i = \arg\min_j \|m_j - z^i\|_{\Sigma_j}$$
 – Mahalanobis Nearest Neighbor 
$$c^*_t = \arg\max_j \{p(z_t|c_t,y_t)\}$$
 – Maximum Likelihood 
$$z_t = \{z^1,z^2,\dots,z^k\}$$
 Assumption:  $z$  independent 
$$\max(\prod p(\cdot)) = \prod(\max_j p(\cdot))$$
 – is equivalent to Mahalanobis Nearest Neighbor

## 5.1 JCBB: Joint Compatibility Branch and Bound

Evaluates hypothesis recursively and eliminates branches.  $d_{\mathcal{H}_l^i}^z < \chi_{d_i\alpha}^z$ , where  $\alpha$  – confidence level,  $d = \dim(f_{\mathcal{H}_l^i})$  – dimensionality.