

L09. Data Association

* Summary of L10 SLAM : Online SLAM using EKF

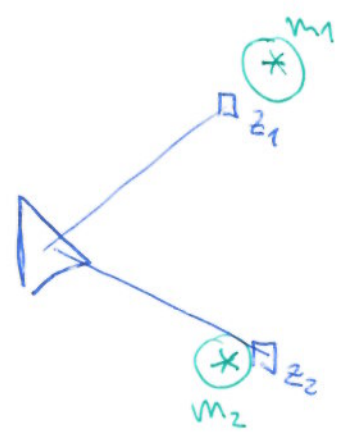
$$p(\underline{x}_t, m | \underline{z}, \mathcal{K})$$

$$g(y_t, \mu_t) = \begin{bmatrix} g^x \\ m \\ \vdots \\ m_N \end{bmatrix}, \quad z_t = h(y_t, c_t)$$

$$\bar{m}_{new} = h^{-1}(x_t, \bar{z}_t) |_{\bar{\mu}_t} \quad \mu_t = \begin{bmatrix} \mu_t \\ \mu_{new} \end{bmatrix} \quad \bar{z}_t = \begin{bmatrix} \text{square} \\ \text{square} \end{bmatrix} z_{new}$$

$$H = [H^1, 0, \dots, 0, H^j, 0, \dots, 0]$$

* Euclidean nearest neighbour



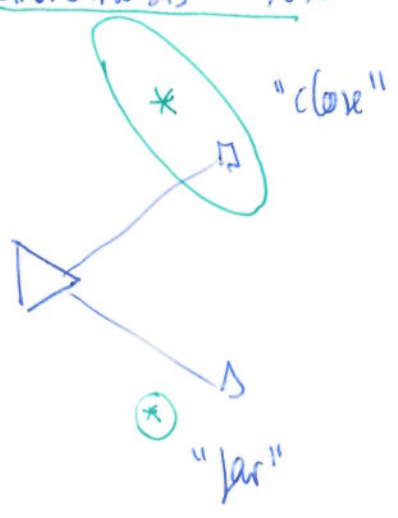
$$c_t^i = \text{argmin} \| m_j - z_t^i \|_2$$

$$\begin{bmatrix} \text{for } i = 1, \dots, K \quad (z \text{ obs}) \\ \left[\begin{array}{l} \text{for } j = 1, \dots, N \\ c_t^j = \min (\| m_j - z_t^i \|_2) \end{array} \right] \end{bmatrix}$$

$$O(K \cdot N)$$

- ✓ ✓ Match each observation to closest landmark
- ✓ Easy and fast $\nexists O(KN)$
- ✗ Greedy data association.

* Mahalanobis NN



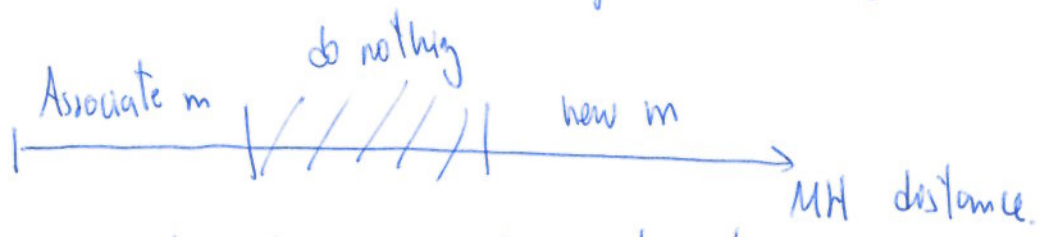
or $h(\mu_t)$

$h^{-1}(z^i, y_t)$

$$d_{ij}^z = \|m_j - z^i\|_Z^2$$

$$= (m_j - z^i)^T Z^{-1} (m_j - z^i)$$

MH captures uncertainty.



New landmarks \rightarrow need confirmation over several obs.

- ✓ More robust to noise.
- ✓ Easy and fast $O(KN)$
- ✗ Still greedy

* Maximum likelihood (ML)

from the Bayes filter, we should calculate the distribution of correspondences:

$$p(c_{1:t} | x_{t+1}, m_{t+1})$$

very complicated! \rightarrow sequence of all correspondences should be re-evaluated constantly for all observations.

* Approximation 1: Solve DA incrementally

$$p(c_t | z_t, y_t)$$

The history of correspondences $c_{1:T}$ only depends on the last ~~most~~ correspondence.

Assume previous correspondences were correct.

$$p(c_t | z_t, y_t) \propto p(z_t | c_t, y_t)$$

posterior

likelihood for a given c_t

$$c_t^* = \underset{c_t}{\operatorname{argmax}} \left\{ p(z_t | c_t, y_t) \right\}$$

7 param.

Maximum likelihood estimator.

$$p(z_t | c_t, y_t) = p(z_t^1 | z_t^{2:k}, y_t, c_t)$$

$$\bullet p(z_t^2 | z_t^{3:k}, y_t, c_t)$$

$$\bullet p(z_t^3 | z_t^{4:k}, y_t, c_t)$$

⋮

$$p(z_t^k | y_t, c_t)$$

Approximation 2: Independence assumption

$$p(z_t | c_t, y_t) \approx \prod_i^k p(z_t^i | c_t^i, y_t) \quad \text{for each } z^i \text{ there is } 1 c^i \text{ single.}$$

$$c_t^* = \underset{c_t}{\operatorname{argmax}} \prod_i^k p(z_t^i | c_t^i, y_t)$$

$$\text{where, } c_t = \{ c_t^1 = m_{j1}, c_t^2 = m_{j2}, \dots, c_t^i = m_{ji}, \dots \}$$

Since c_t are independent:

$$\max \left(\prod_i^k p(z_t^i | c_t^i, y_t) \right) = \prod_i^k \max_{c_t^i} p(z_t^i | c_t^i, y_t)$$

evaluate c_t^i individually!

$$z_t^i \sim N(z_t^i; h(\bar{\mu}_t, c^i), H_t^i \bar{Z}_t H_t^{iT} + \Sigma_t)$$

New landmark: (Prob Rob 322)

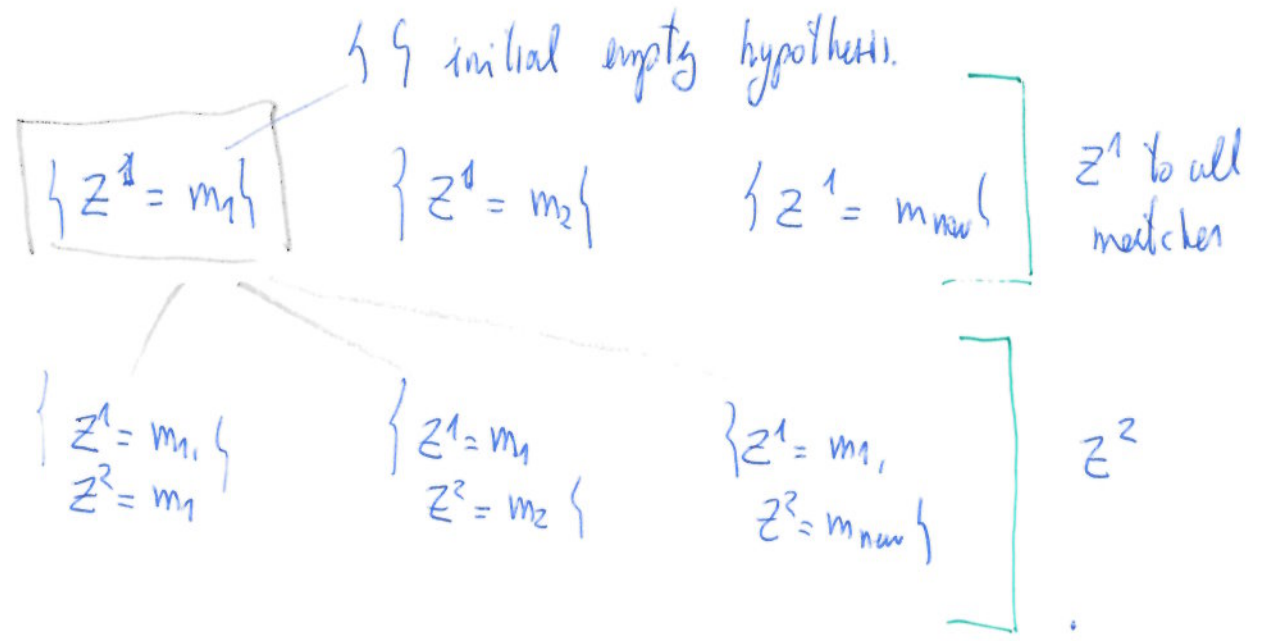
$$p(z_t^i | c_t^i = \text{new}, y_t) = \alpha$$

threshold value.
hard to tune.

If we don't set this L.H. to α , then the new landmark won't be created.

We create a landmark only if distance to all other landmarks is higher than α .

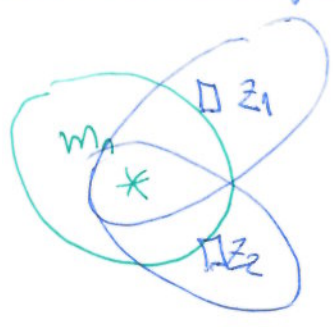
Efficient way to express DA: tree representation.



Best first exploration (from graph search). Greedy but efficient

True dimensionality of the tree: exponential $O((K+1)^K)!!$.

* Individual compatibility



$\square Z_3$

χ^2 squared test. (α confidence level $90, 95, 99, \dots$)

$$d_{11}^2 = \|m_1 - Z^1\|_Z < \chi_\alpha^2 \quad \checkmark$$

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

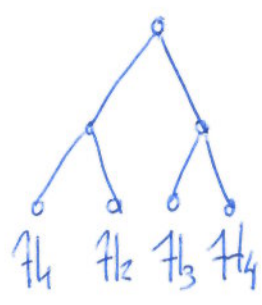
$$d_{13}^2 = \|m_1 - Z^3\|_Z \not< \chi_\alpha^2 \quad \times$$

put filter to reject clearly incorrect hypothesis.

* Joint Compatibility (JC) (Neira and Tardós 2001)

Context provides more accurate solutions

Ex: Stars vs constellations



Set of hypotheses \rightarrow size exponential (later)

$$H_i = \{ z_1 = m_1, z_2 = m_2, z_3 = m_{new} \}$$

$(c^1) \quad (c^2) \quad (c^3)$

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

if $\boxed{d_{H_i}^2 < \chi_k^2}$

\rightarrow for Individual compatibility: (IC)

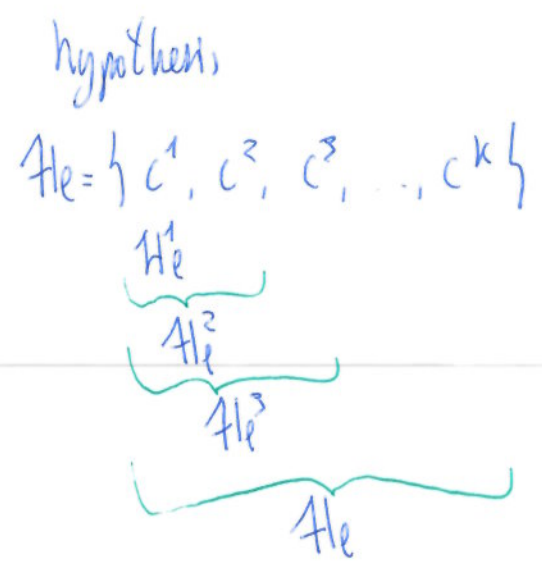
$$f_{ij}(y, z) = z^i - h(y, j)$$

\swarrow state \nwarrow obs

Innovation vector ^{LO5}
(ideally 1, 0)

\rightarrow JC

$$t_{H_i}(y, z) = \begin{bmatrix} f_{H_i^1}(y, z) \\ f_{H_i^2}(y, z) \\ \vdots \\ f_{H_i^k}(y, z) \end{bmatrix}$$



If we rewrite $f_{H_e}(y, z)$ incrementally:

$$f_{H_e^i}(y, z) = \begin{bmatrix} f_{H_e^{i-1}}(y, z) \\ f_{H_e^i}(y, z) \end{bmatrix}$$

$$\approx f_{H_e^i}(\bar{y}, \bar{z}) + G_{H_e^i}(y - \bar{y}) + H_{H_e^i}(z - \bar{z})$$

($H \neq H \Rightarrow$ from paper)

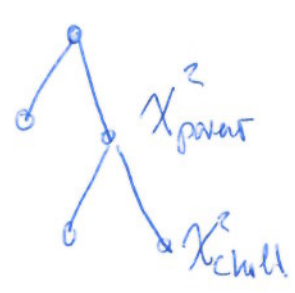
Covariance of the joint innovation

$$C_{H_e^i} = H_{H_e^i} S H_{H_e^i}^T + G_{H_e^i} \Sigma G_{H_e^i}^T$$

$$\Rightarrow d_{H_e^i}^2 = f(\bar{y}, \bar{z})^T C_{H_e^i}^{-1} f(\bar{y}, \bar{z}) < \chi_{d, \alpha}^2, \quad d = \dim(H_e^i)$$

this test is carried out incrementally (see paper)

* IC branch and Bound.



$$X_{parent}^z < X_{child}^z$$

this allows us to discard branches without evaluating!

$C_{H_e^i}$ captures crosscorrelations of the observations, while M_e doesn't (assumed independence).

More accurate and probabilistically more complete

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

↳ more filler!