L11: Data Association

* Summary of L10 SLAM: Online SLAM using EKF

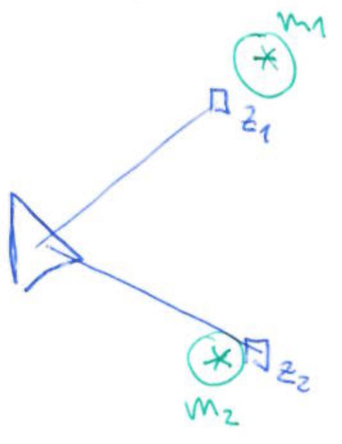
$$p(\underbrace{x_t, m}\mid Z, \mathcal{U})$$

$$g(y_t, u_t) = \begin{bmatrix} g^x \\ m_1 \\ \vdots \\ m_N \end{bmatrix}, \quad z_t = h(y_t, c_t)$$

$$\bar{m}_{new} = h^{-1}(x_t, z_t)\Big|_{\bar{\mu}_t} \qquad \mu_t = \begin{bmatrix} \mu_t \\ \mu_{new} \end{bmatrix} \qquad \bar{\Sigma}_t = \square \ \Sigma_{new}$$

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

* Euclidean nearest neighbour

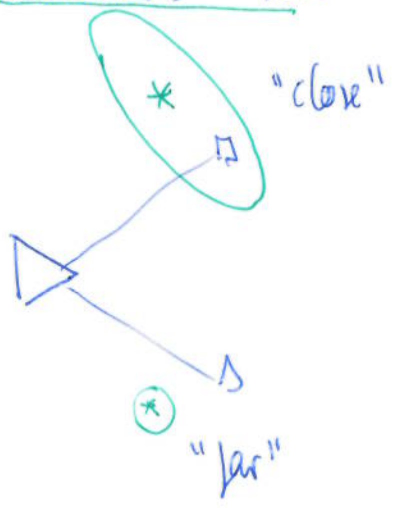


for $i = 1, \dots, K$ (z obs)
  for $j = 1, \dots, N$
    $c_t^j = \min(\|m_j - z_t^i\|_2)$

$O(K \cdot N)$

~ ✓ Matches each observation to closest landmark
✓ Easy and fast ∤ $O(KN)$
✗ Greedy data association.

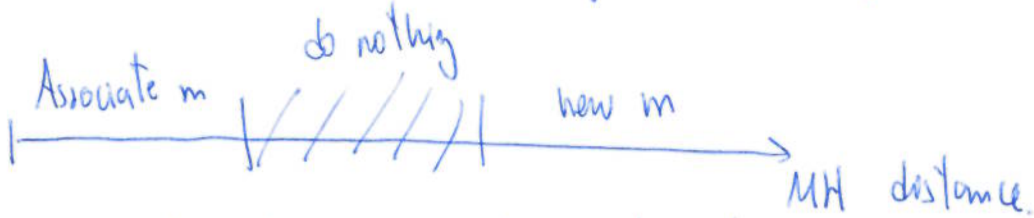
* Mahalanobis NN



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

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

MH captures uncertainty.



New landmarks → need confirmation over several obs.

✓ More robust to noise.

✓ Easy and fast $O(K \cdot N)$

✗ Still greedy

* Maximum likelihood (ML)

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

$$p(c_{1:t} \mid x_t, m, \mathcal{Z})$$

very complicated!

sequence of all correspondences should be re-evaluated constantly for all observations.

* Aproximation 1: Solve DA incrementally

$p(c_t \mid z_t, y_t)$ The history of correspondences $c_{1:T}$ only depends on the last ~~corresp~~ correspondence. Assumes previous correspondences were correct.

$$\underbrace{p(c_t \mid z_t, y_t)}_{\text{posterior}} \propto \underbrace{p(z_t \mid c_t, y_t)}_{\text{likelihood}} \quad \text{for a given } c_t$$

$$c_t^* = \arg\max_{c_t} \{ p(z_t \mid c_t, y_t) \}$$ Maximum likelihood estimator.

$$p(z_t \mid c_t, y_t) = p(z_t^1 \mid z_t^{2:K}, y_t, c_t) \cdot p(z_t^2 \mid z_t^{3:K}, y_t, c_t) \cdot p(z_t^3 \mid z^{4:K}, y_t, c_t) \cdots p(z_t^K \mid y_t, c_t)$$

Approximation 2: Independence assumption

$$p(z_t \mid c_t, y_t) \simeq \prod_i^K p(z_t^i \mid c_t^i, y_t)$$

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

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:

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

evaluate c_t^i individually!

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

New landmark: (ProbRob 322)

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

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.

{ } initial empty hypothesis.

$\boxed{\{z^1 = m_1\}}$ $\quad \{z^1 = m_2\} \quad \{z^1 = m_{new}\}$ — z^1 to all matches

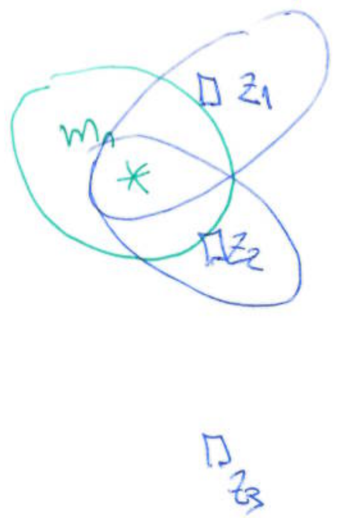
$\{z^1 = m_1, z^2 = m_1\} \quad \{z^1 = m_1, z^2 = m_2\} \quad \{z^1 = m_1, z^2 = m_{new}\}$ — z^2

⋮

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

True dimensionality of the tree: exponential $O((N+1)^k)$!!

* Individual compatibility



xi squared test. (α confidence level 90, 95, 99...)

$d_{11}^2 = \| m_1 - z^1 \|_\Sigma < \chi^2_\alpha$ ✓

$d_{12}^2 < \chi^2_\alpha$ ✓

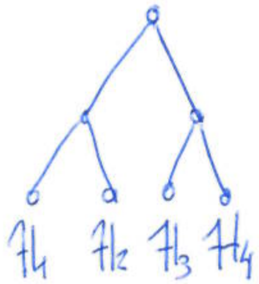
$d_{13}^2 = \| m_1 - z^3 \|_\Sigma \nless \chi^2_\alpha$ ✗

fast filter to reject clearly incorrect hypothesis.

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

Context provides more accurate solutions

Ex: Stars vs constellations



Set of hypothesis → size exponential (later)

$H_i = \{ z_1 = m_1, \; z_2 = m_3, \; z_3 = m_{new} \}$
$\quad (c^1) \quad (c^2), \quad (c^3)$

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

if $\boxed{d^2_{\mathcal{H}_e} < \chi^2_\alpha}$

→ for Individual compatibility: (IC)

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

state, obs

Innovation vector (ideally → 0) L05

→ JC

$$f_{\mathcal{H}_e}(y,z) = \begin{bmatrix} f_{\mathcal{H}_e^1}(y,z) \\ f_{\mathcal{H}_e^2}(y,z) \\ \vdots \\ f_{\mathcal{H}_e}(y,z) \end{bmatrix}$$

hypothesis

$$\mathcal{H}_e = \{ \underbrace{\underbrace{\underbrace{c^1, c^2}_{\mathcal{H}_e^1}, c^3}_{\mathcal{H}_e^2}, \ldots}_{\mathcal{H}_e^3}, c^k \}$$
$$\underbrace{\qquad\qquad\qquad\qquad}_{\mathcal{H}_e}$$

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

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

$$\simeq f_{\mathcal{H}_e^i}(\hat{y},\hat{z}) + G_{\mathcal{H}_e^i}(y-\hat{y}) + H_{\mathcal{H}_e^i}(z-\hat{z})$$

($H \neq \mathcal{H}$ =) from paper

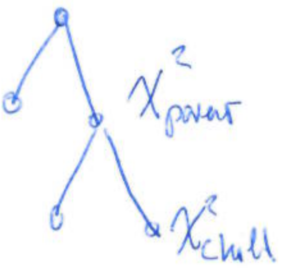
Covariance of the joint innovation

$$C_{\mathcal{H}_e^i} = H_{\mathcal{H}_e^i} S H_{\mathcal{H}_e^i}^T + G_{\mathcal{H}_e^i} \Sigma G_{\mathcal{H}_e^i}$$

$$\Rightarrow d^2_{\mathcal{H}_e^i} = f(\hat{y},z)^T C_{\mathcal{H}_e^i}^{-1} f(\hat{y},z) < \boxed{\chi^2_{d,\alpha}}$$, $d = \dim|\mathcal{H}_e^i|$

this test is carried out incrementally (see paper)

* JC branch and Bound.



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

this allows us to discard branches without evaluating!

$C_{\mathcal{H}_e}$ captures crosscorrelations of the observations, while NL doesn't (assumed independence)

More accurate and probabilistically more complete

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

↳ pre filter!