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► Metropolis-Hastings (MH) Sampling

C – configuration (of all variable values)

Here $C = \mathbf{F}$ and $p(C) = p(\mathbf{F} | X, Y, D)$

Goal: Generate a sequence of random samples $\{C_i\}$ from $p(C)$

- setup a Markov chain with a suitable transition probability function so that it generates the sequence

Sampling procedure

1. given C_i , generate random sample S from $q(S | C_i)$

q may use some information from C_i (Hastings)

2. compute acceptance ratio

the evidence term drops out

$$a = \frac{p(S)}{p(C_i)} \cdot \frac{q(C_i | S)}{q(S | C_i)}$$

3. generate random number u from unit-interval uniform distribution $U_{0,1}$
4. if $u < a$ then $C_{i+1} := S$ else $C_{i+1} := C_i$

'Programming' an MH sampler

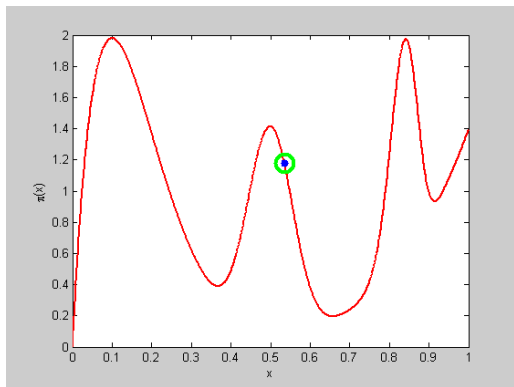
1. design a proposal distribution (mixture) q and a sampler from q
2. write functions $q(C_i | S)$ and $q(S | C_i)$ that are proper distributions

not always simple

Finding the mode

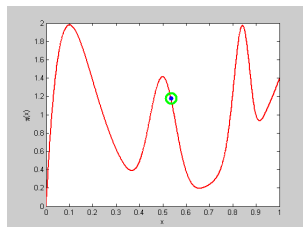
- remember the best sample fast implementation but must wait long to hit the mode
- use simulated annealing very slow
- start local optimization from the best sample good trade-off between speed and accuracy

MH Sampling Demo

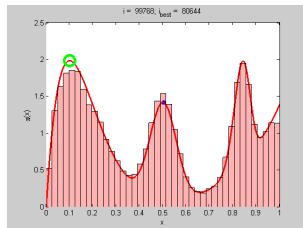


sampling process (video, 7:33, 100k samples)

- blue point: current sample
- green circle: best sample so far $\text{quality} = \pi(x)$
- histogram: current distribution of visited states
- the vicinity of modes are the most often visited states



initial sample



final distribution of visited states

Demo Source Code (Matlab)

```
function x = proposal_gen(x0)
% proposal generator q(x | x0)

T = 0.01; % temperature
x = betarnd((x0)/T+1, (1-x0)/T+1);
end

function p = proposal_q(x, x0)
% proposal distribution q(x | x0)

T = 0.01;
p = betapdf(x, x0/T+1, (1-x0)/T+1);
end

function p = target_p(x)
% target distribution p(x)

% shape parameters:
a = [2 40 100 6];
b = [10 40 20 1];

% mixing coefficients:
w = [1 0.4 0.253 0.50]; w = w/sum(w);
p = 0;
for i = 1:length(a)
    p = p + w(i)*betapdf(x,a(i),b(i));
end
end
```

```
%% DEMO script

k = 10000; % number of samples
X = NaN(1,k); % list of samples

x0 = proposal_gen(0.5);
for i = 1:k
    x1 = proposal_gen(x0);
    a = target_p(x1)/target_p(x0) * ...
        proposal_q(x0,x1)/proposal_q(x1,x0);
    if rand < a
        X(i) = x1; x0 = x1;
    else
        X(i) = x0;
    end
end

figure(1)
x = 0:0.001:1;
plot(x, target_p(x), 'r', 'linewidth',2);
hold on
binw = 0.025; % histogram bin width
n = histc(X, 0:binw:1);
h = bar(0:binw:1, n/sum(n)/binw, 'histc');
set(h, 'facecolor', 'r', 'facealpha', 0.3)
xlim([0 1]); ylim([0 2.5])
xlabel 'x'
ylabel 'p(x)'
title 'MH demo'
hold off
```

► From MH Sampling to RANSAC

- configuration = k -tuple of inlier correspondences
the minimization will be over a discrete set of epipolar geometries proposable from 7-tuples
- data-driven proposals q :
 1. select k -tuple from data independently and uniformly $q(S) = \binom{mn}{k}^{-1}$
 2. solve the minimal geometric problem \mapsto geometry proposal (e.g. \mathbf{F} from $k = 7$)
- independent sampling $a = \frac{p(S')}{p(S_i)} \cdot \frac{q(S_i)}{q(S')}$
 1. q uniform, then $a = \frac{p(S')}{p(S_i)}$ MAPSAC ($p(S)$ includes the prior)
 2. q dependent on descriptor similarity PROSAC (similar pairs are proposed more often)

LO-MAPSAC

1. generate random sample S_b from $q(S)$
2. set initial $N := \binom{mn}{k}$
3. repeat N -times:
 - a. generate random sample S' from $q(S)$
 - b. if $p(S') > p(S_b)$ then
 - i. $S_b := S'$
 - ii. threshold-out inliers using e_T from (23)
 - iii. start local optimization from S_b and update S_b with the result
 - iv. re-estimate N from inlier counts using the standard formula for RANSAC termination, see Slide 117
4. output S_b

• see the [MPV course for RANSAC details](#)

see also [Fischler & Bolles 1981], [25 years of RANSAC]

► Stopping RANSAC

Principle: what is the number of proposals N that are needed to hit an all-inlier sample?

$$N \geq \frac{\log(1 - P)}{\log(1 - (1 - w)^s)}$$

- $(1 - w)^s$ – proposal does not contain an outlier
- $1 - (1 - w)^s$ – proposal contains at least one outlier
- $1 - P =$ all proposals contained an outlier $= (1 - (1 - w)^s)^N$

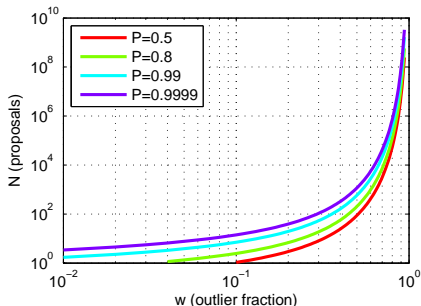
P – probability that at least one sample is all-inlier

w – the fraction of outliers among tentative correspondences

s – sample size (7 in 7-point algorithm)

N for $s = 7$

w	P	
	0.8	0.99
0.5	205	590
0.8	$1.3 \cdot 10^5$	$3.5 \cdot 10^5$
0.9	$1.6 \cdot 10^7$	$4.6 \cdot 10^7$

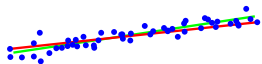


- N can be re-estimated using the current estimate for w (if there is LO, then after LO)
the quasi-posterior estimate for w is the average over all samples generated so far
- for $w \rightarrow 1$ we gain nothing over the standard MH-sampler stopping criterion

► The Difference between RANSAC and a General MH Sampler

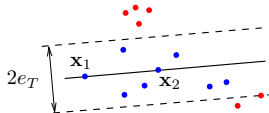
RANSAC = five ideas: [Fischler & Bolles 1981]

1. proposal distribution is given by the empirical distribution of data sample:



- pairs of points define line distribution from $p(\mathbf{n} | X)$ (left)
- random correspondence tuples drawn uniformly propose samples of \mathbf{F} from a data-driven distribution $q(\mathbf{F} | X, Y)$

2. stopping based on the probability of mode-hitting → Slide 117
3. standard RANSAC replaces probability maximization with consensus maximization



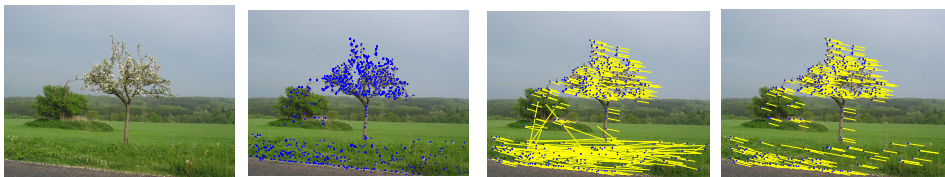
the e_T is the inlier/outlier threshold from (23)

4. when counting inliers, do not work with all m_{ij} but with a set of tentative correspondences that form a matching, e.g. selected by stable matching:

- a. find a pair m_{ij} of greatest $p_1(d_{ij})$ and remember it
- b. remove row i and column j from the matching table (needs some bookkeeping and reindexing)
- c. repeat Steps a–c until the table is empty
- d. return the remembered set

5. each time a new best sample occurs, start local optimization from inliers
or LO weighted by posterior $p(m_{ij})$ [Chum et al. 2003]
LM optimization with Sampson error (and re-weighting)

Example Matching Results for the 7-point Algorithm with RANSAC



input images

interest points (ca. 3600) tentative corresp. (416)

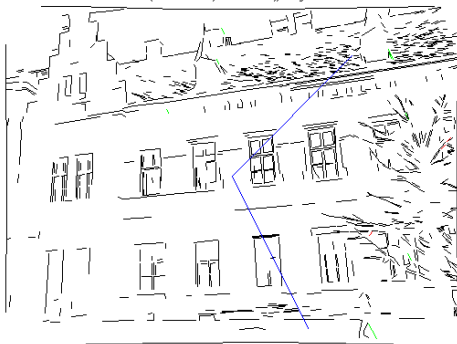
matching (340)
notice wrong matches

- the minimization is over a discrete set of epipolar geometries proposable from 7-tuples

Example: MH Sampling for a More Complex Problem

Task: Find two vanishing points from line segments detected in input image.

iter: 10 (acc TOT=0.0%, HMC=NaN%); Eavg = 14.597



video

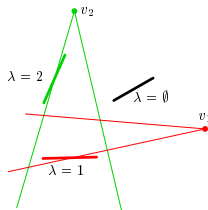
simplifications

- vanishing points restricted to the set of all pairwise segment intersections
- mother lines fixed by segment centroid

Model

- principal point known, square pixel
- explicit variables
 1. two unknown vanishing points v_1, v_2
- latent variables
 1. each line has a vanishing point label $\lambda_i \in \{\emptyset, 1, 2\}$, \emptyset represents an outlier
 2. 'mother lines' passing through vanishing points

$$\arg \min_{v_1, v_2, \Lambda, L} V(v_1, v_2, \Lambda, L | S)$$



Beyond RANSAC

Note that by simplification in (18) on Slide 106 we have lost constraints on M (eg. uniqueness). One can choose a better model when not marginalizing:

$$p(M, \mathbf{F}, X, Y, D) = \underbrace{p(X, Y | M, \mathbf{F})}_{\text{geometric error}} \cdot \underbrace{p(D | M)}_{\text{similarity}} \cdot \underbrace{p(M)}_{\text{constraints}} \cdot \underbrace{p(\mathbf{F})}_{\text{prior}}$$

this is a global model: decisions on m_{ij} are no longer independent!

In the MH scheme

- one can work with full $p(M, \mathbf{F} | X, Y, D)$, then $S = (M, \mathbf{F})$
 - explicit labeling m_{ij} can be done by, e.g. sampling from

$$q(m_{ij} | \mathbf{F}) \sim ((1 - \alpha_0) p_1(e_{ij} | \mathbf{F}), \alpha_0 p_0(e_{ij} | \mathbf{F}))$$

when $p(M)$ uniform then always accepted, $a = 1$

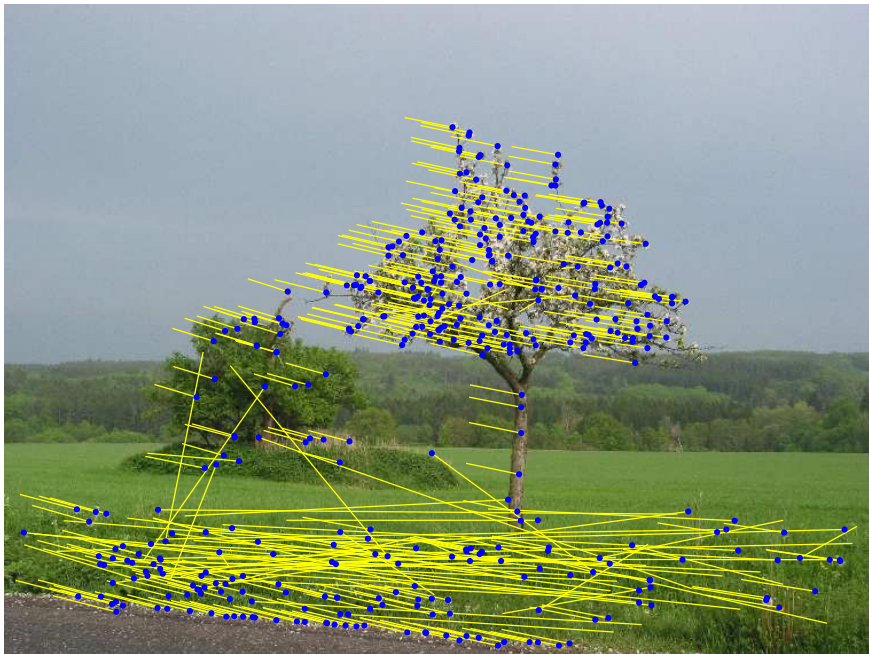
⊛ derive

- additional proposals from $q(\mathbf{F} | M)$ are possible, with explicit inliers Hybrid Monte Carlo
- we can compute the posterior probability of each match $p(m_{ij})$ by histogramming m_{ij} over $\{S_i\}$
- local optimization can then use explicit inliers and $p(m_{ij})$
- error can be estimated for elements of \mathbf{F} from $\{S_i\}$ does not work in RANSAC!
- large error indicates problem degeneracy this is not directly available in RANSAC
- good conditioning is not a requirement we work with the entire distribution $p(\mathbf{F})$
- one can find the most probable number of epipolar geometries by reversible jump MCMC (homographies or other models)

if there are multiple models explaining data, RANSAC will return one of them randomly

Thank You









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