

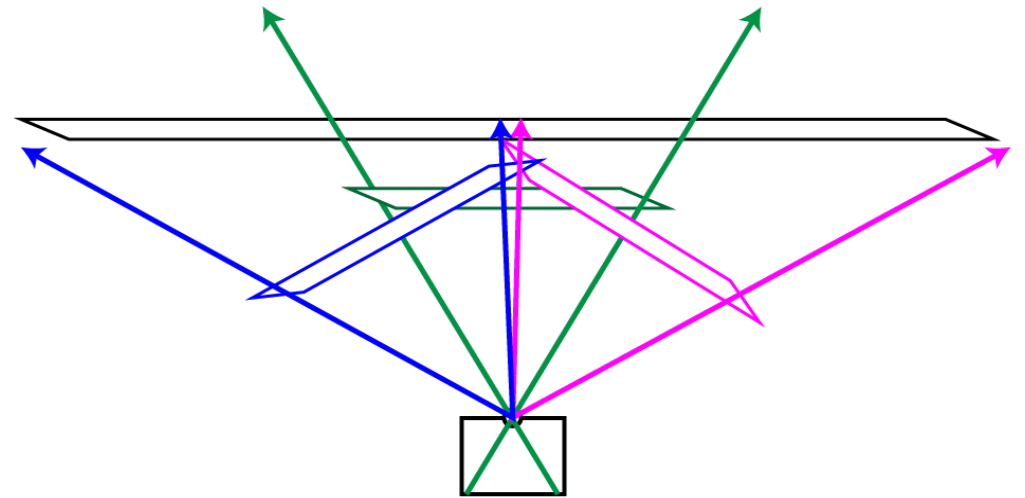
RANSAC Algorithm

AIG Talk 2/22/21

Ryan Levy

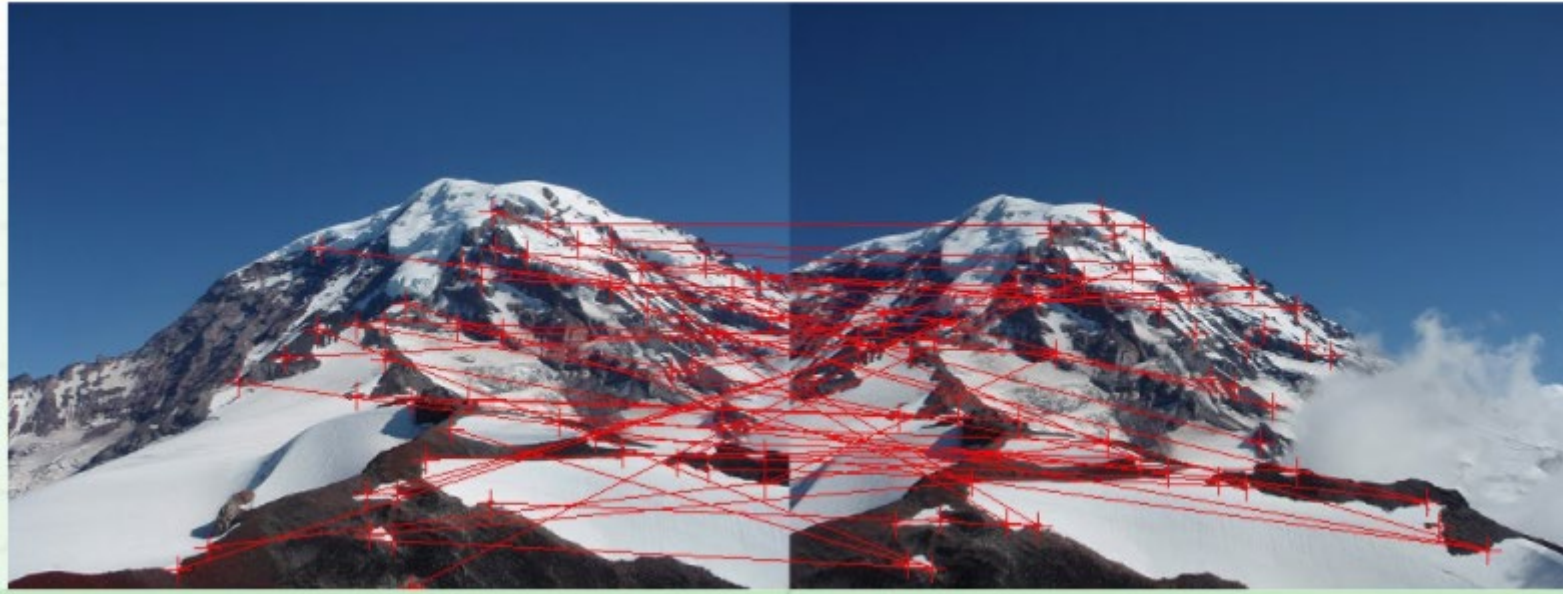
Context – Computer Vision

- Often two images will come from the same projection plane but with different transformation
 - Panorama Stitching

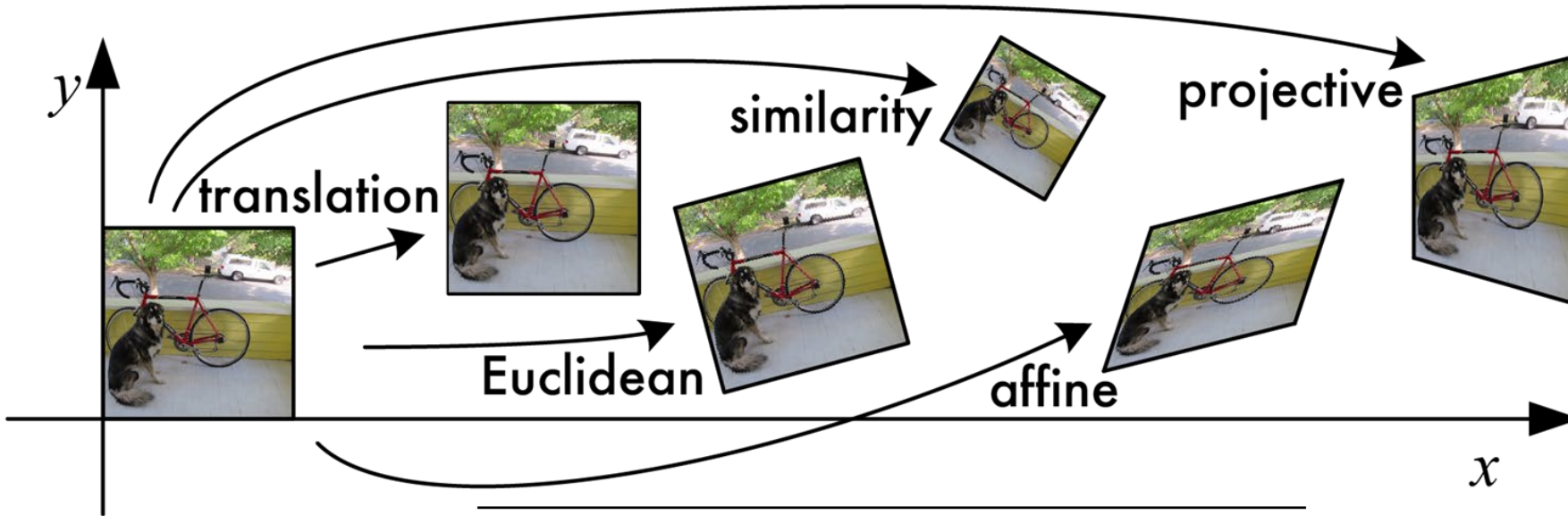


Context – Determine Transform

- Use (other) algorithms to perform pattern matching
 - Match 'unique' features
- Today's goal: Match corresponding features without outliers



Context – Transformations



Transformation	Matrix	# DoF	Preserves	Icon
translation	$\begin{bmatrix} \mathbf{I} & & \mathbf{t} \end{bmatrix}_{2 \times 3}$	2	orientation	
rigid (Euclidean)	$\begin{bmatrix} \mathbf{R} & & \mathbf{t} \end{bmatrix}_{2 \times 3}$	3	lengths	
similarity	$\begin{bmatrix} s\mathbf{R} & & \mathbf{t} \end{bmatrix}_{2 \times 3}$	4	angles	
affine	$\begin{bmatrix} \mathbf{A} \end{bmatrix}_{2 \times 3}$	6	parallelism	
projective	$\begin{bmatrix} \tilde{\mathbf{H}} \end{bmatrix}_{3 \times 3}$	8	straight lines	

$$v = \begin{pmatrix} v_x \\ v_y \\ w \end{pmatrix}$$

Math Background

$$v' = Hv$$

(overdetermined)

Least Squares Problem!

$$S = \sum_i (v'_i - Hv_i)^2$$

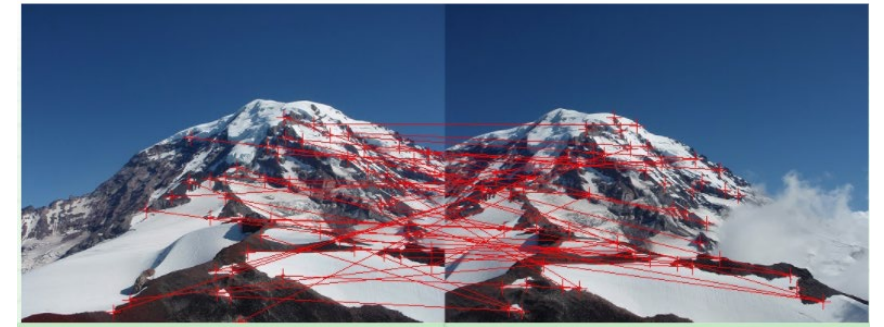
$$\frac{dS}{dH_{ij}} = -2v_i^T v'_i + 2v_i^T v_i H_{ij}$$
$$\Rightarrow H_{ij} = (v_i^T v_i)^{-1} v_i^T v'_i$$

$$H = \begin{pmatrix} h_{11} & h_{12} & h_{13} \\ h_{21} & h_{22} & h_{23} \\ h_{31} & h_{32} & 1 \end{pmatrix} \quad v = \begin{pmatrix} v_x \\ v_y \\ w \end{pmatrix}$$

8 free parameters

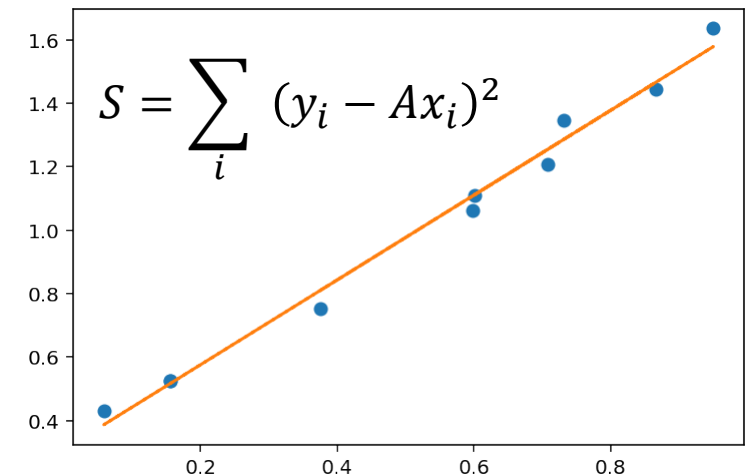
$$A = \begin{pmatrix} A_{11} & A_{12} & A_{13} \\ A_{21} & A_{22} & A_{23} \end{pmatrix}$$

6 free parameters



v'

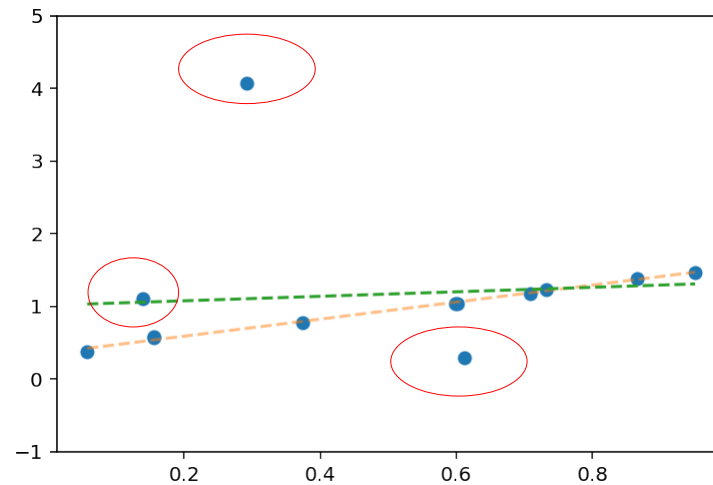
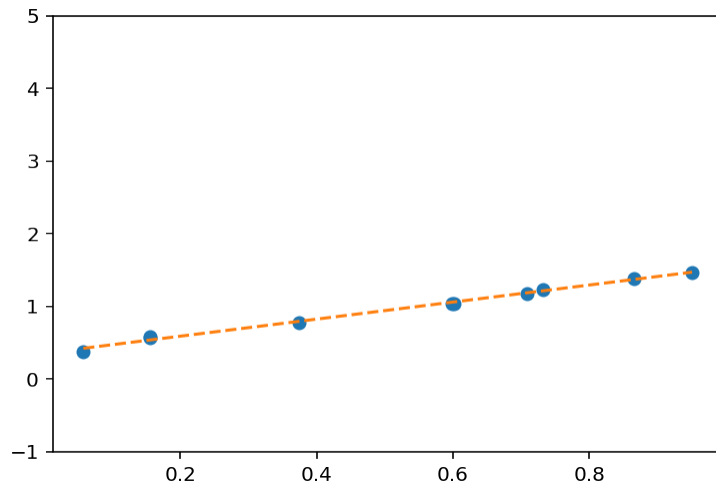
v



Problem - Outliers



- Naïve matching has lots of outliers
- Study RANSAC with linear fits



RANSAC

- Big idea: Try a bunch of fits, the one that is the best is the best!
 - Inliers vs outliers
 - **RAN**dom **SA**mple **C**onsensus

```
1 for n in range(numTrials):
2     pick random set of points
3     solve the model using those parameters
4     count number of inliers
5 pick the model with the most inliers
```

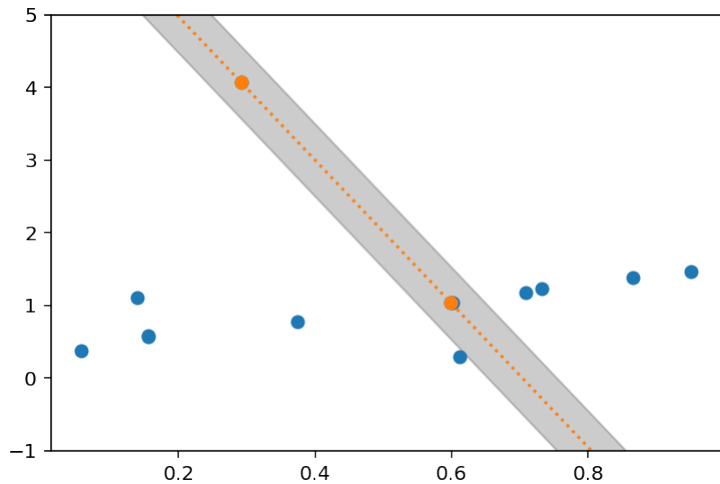
Random Sample Consensus: A Paradigm for Model Fitting with Applications to Image Analysis and Automated Cartography

Martin A. Fischler and Robert C. Bolles
SRI International

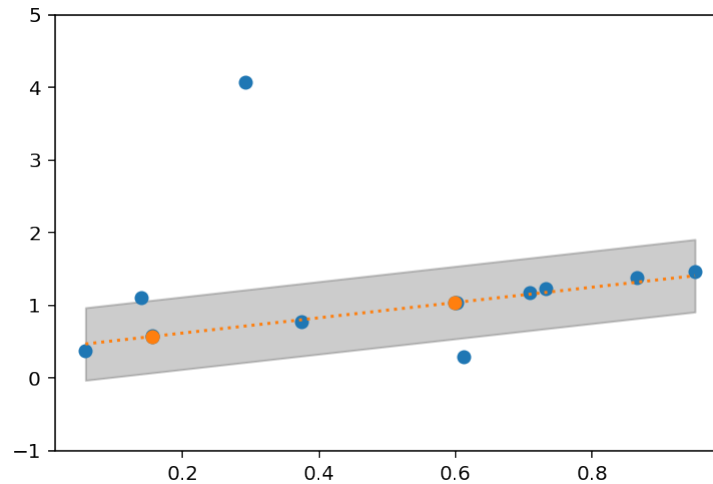
A new paradigm, Random Sample Consensus (RANSAC), for fitting a model to experimental data is introduced. RANSAC is capable of interpreting/smoothing data containing a significant percentage of gross errors, and is thus ideally suited for applications in automated image analysis where interpretation is based on the data provided by error-prone feature detectors. A major portion of this paper describes the application of RANSAC to the Location Determination Problem (LDP): Given an image depicting a set of landmarks with known locations, determine that point in space from which the image was obtained. In response to a RANSAC requirement, new results are derived on the minimum number of landmarks needed to obtain a solution, and algorithms are presented for computing these minimum-landmark solutions in closed form. These results provide the basis for an automatic system that can solve the LDP under difficult viewing

RANSAC

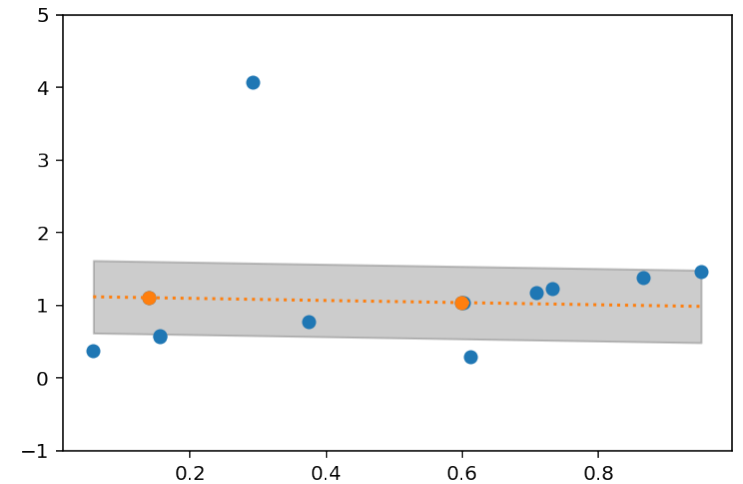
```
1 for n in range(numTrials):  
2     pick random set of points  
3     solve the model using those parameters  
4     count number of inliers  
5 pick the model with the most inliers
```



1 inliers



8 inliers

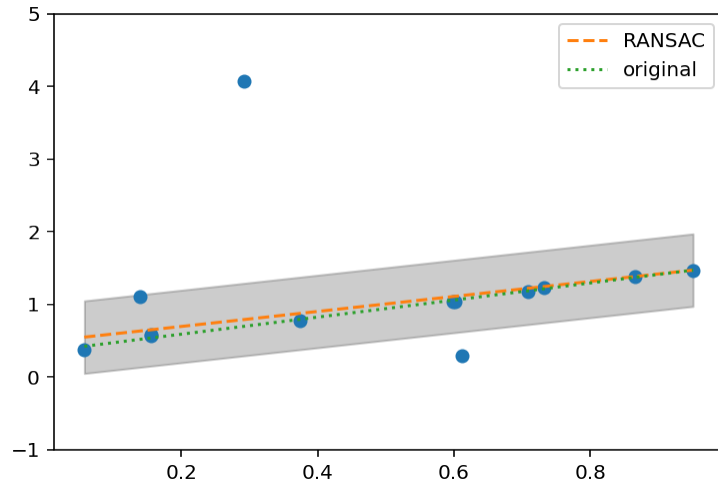


8 inliers

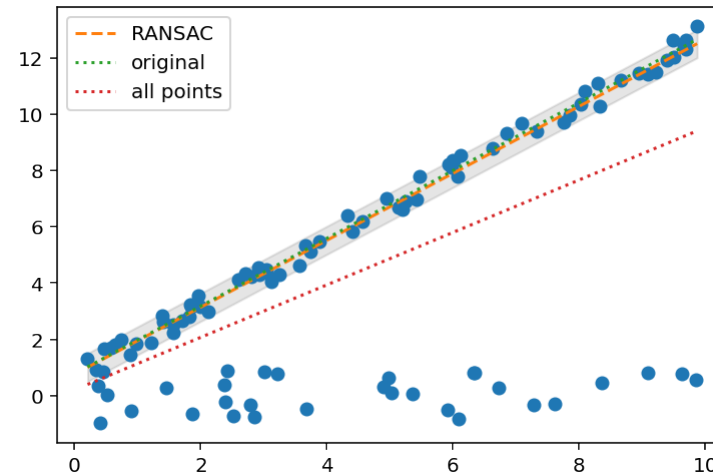
Here total possible trials:

$$\binom{13}{2} = 78$$

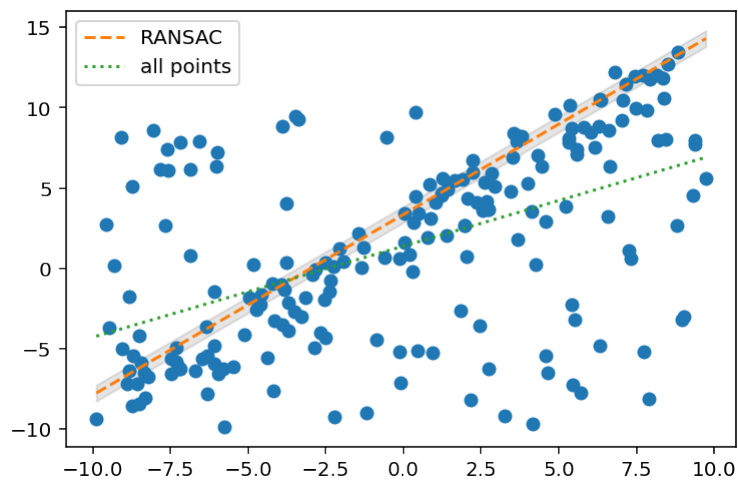
RANSAC Example



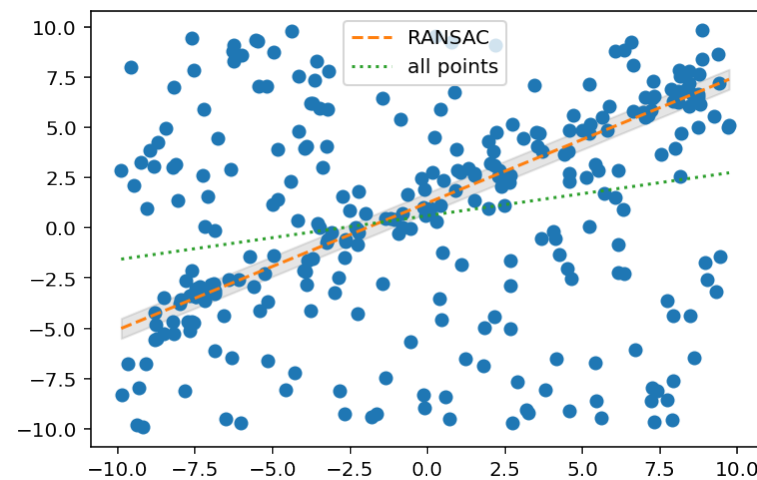
nTrials = 100
Delta = 0.5
N = 13
N_out = 3



nTrials = 100
Delta = 0.5
N = 100
N_out = 30



nTrials = 100
Delta = 0.5
N = 200
N_out = 100



nTrials = 100
Delta = 0.5
N = 300
N_out = 200

That was too easy?

- Pros

- Simple/straightforward
- Very fast
- Handles large number of outliers
- # of datapoint insensitive

- Cons

- KNOBS
 - Inlier/outlier selection
 - (secretly: model choice)
 - Number of trials
 - Computational time(!)

- Trial Selection:

- $N_{trials} \geq \frac{\log[1-p_s]}{\log[1-(p_g)^s]}$

- p_s – probability of success (~0.99)
 - p_g - probability of good points (% inliers)
 - s - # parameters

- We had $s = 2$, and at worst $p_g = \frac{1}{3}$

$$N_{trials} \geq 39$$

- Now imagine $s = 6$ with $p_g = \frac{1}{3}$

$$N_{trials} \geq 3355(!)$$

	$s = 6$		
p_g	95%	75%	50%
N_{trials}	4	24	293

Enhancements

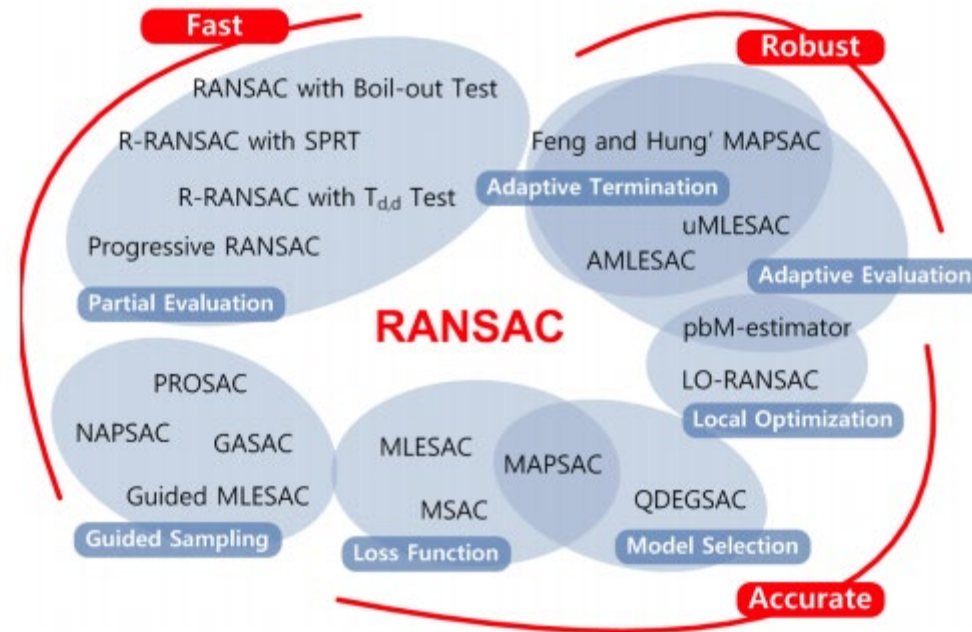


Figure 1: RANSAC Family

Guided Sampling

- PROSAC

- Big idea: Group similar points together to get inliers
- Sort all points by “quality”, always start with high quality points and expand afterward
 - Increases speed

- GASAC

- Big idea: use a Genetic algorithm to select groups

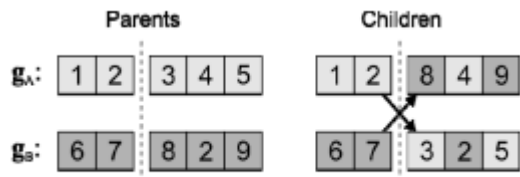


Figure 3: Exchange of chromosome parts using cross-over

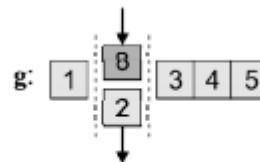


Figure 4: Modification of genes by mutation

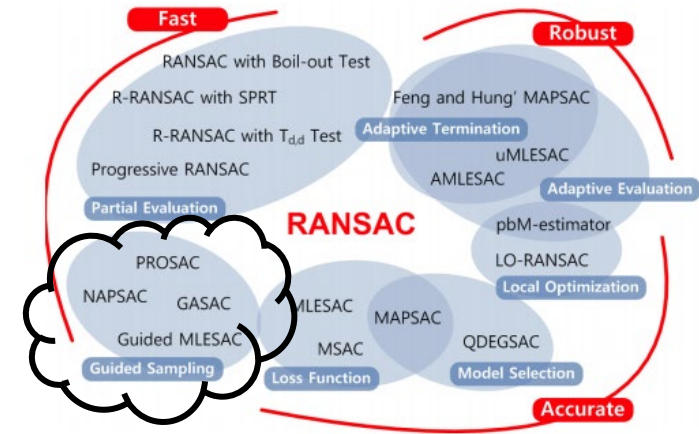


Figure 1: RANSAC Family

Partial Evaluation

- $T_{d,d}$ test
 - Big idea: randomly check $d \ll N$ points to confirm model
 - Randomly select $d \ll N$ points, see if considered inlier to currently model
 - If yes, stop
 - $d = 1$ seems optimal
- Boil-out Test - ?
- Bail-out Test
 - Big idea: Discard models that have too few inliers
 - Fit your model and randomly select points to do an inlier/outlier check
 - Ignore your model if there's too few inlier according to probability distributions

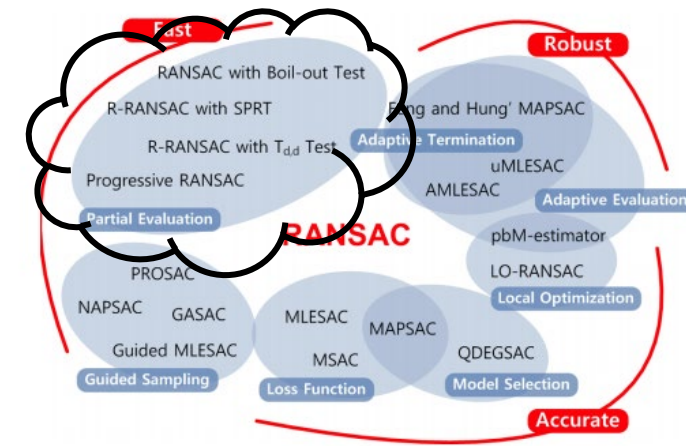


Figure 1: RANSAC Family

Likelihood Extensions

- MLESAC
 - Big idea: instead of inliers choose maximum likelihood
- MAPSAC
 - Big idea: MLESAC + Bayesian update, i.e., posterior probability maximization
- uMLESAC
 - Big idea: use ideas from MAPSAC with adaptive termination
 - Uses $T_{d,d}$ test

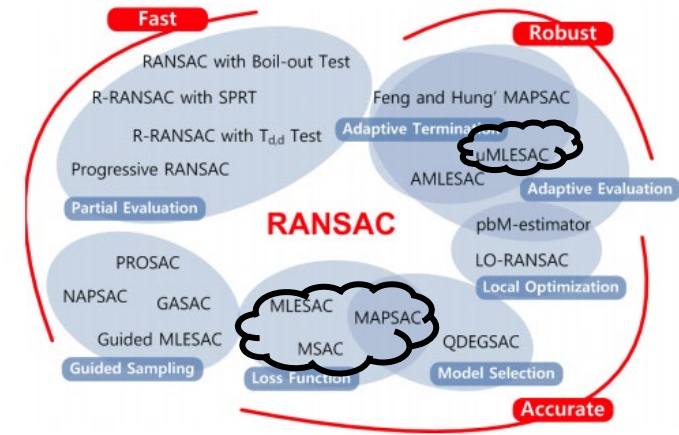


Figure 1: RANSAC Family

Summary

- RANSAC is an algorithm for solving least squares problems with outliers
 - Robust, fast, and simple algorithm
- Many improvements, focused on speed as well as accuracy

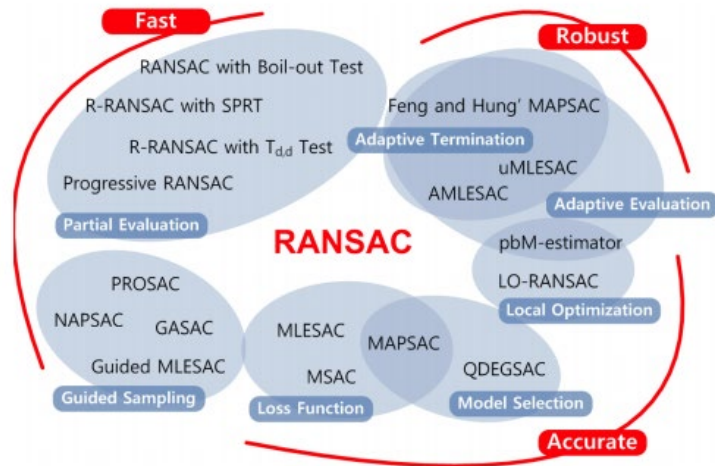
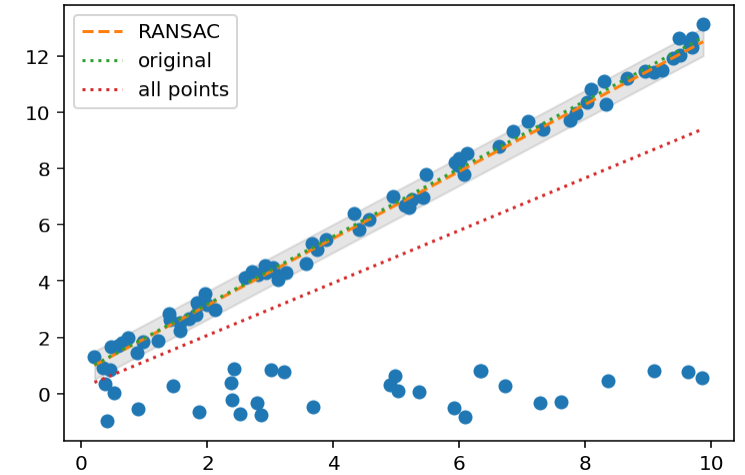


Figure 1: RANSAC Family

References

- Ancient Secrets of Computer Vision
- Richard Szeliski (2007), "Image Alignment and Stitching: A Tutorial", Foundations and Trends® in Computer Graphics and Vision: Vol. 2: No. 1, pp 1-104.
<http://dx.doi.org/10.1561/06000000009>
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