BetaSAC: A New Conditional Sampling For RANSAC

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We present a new strategy for RANSAC [2] sampling named BetaSAC, in reference to the beta distribution. Our proposed sampler builds a hypothesis set incrementally, selecting data points conditional on the previous data selected for the set. Such a sampling is shown to provide more suitable samples in terms of inlier ratio but also of consistency and potential to lead to an accurate parameters estimation. The algorithm is presented as a general framework, easily implemented and able to exploit any kind of prior information on the potential of a sample. As with PROSAC [1] and GroupSAC [4], BetaSAC converges towards RANSAC in the worst case. The benefits of the method are demonstrated on the homography estimation problem.

1 Objective

As shown in Figure 1, an uncontaminated sample is not always able to lead to a good estimation of the searched model parameters. The aim of BetaSAC is to generate more suitable samples than previous methods.

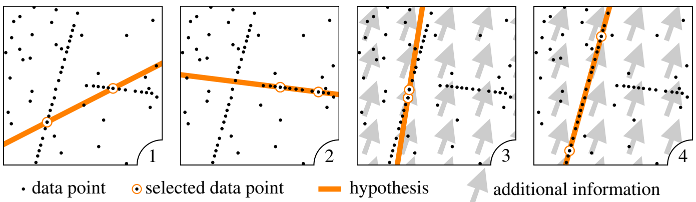


Figure 1: Different types of inlier samples for the line fitting problem. 1) *inlier sample* (all sample points belong to a line). 2) *consistent sample*. 3) *sample consistent with additional information*. 4) *suitable sample*. Thanks to its conditional sampling, BetaSAC is able to generate *suitable samples* earlier than RANSAC and PROSAC would do.

2 Algorithm

Given an iteration count t, a draw of a complete sample s of size m with our conditional random variable is presented in Algorithm 1.

Algorithm 1 Generation of one sample s of m data points.

1: $s \leftarrow \{\emptyset\}$
2: **for** $l = 0$ to $m-1$ **do**
3: Select n data points at pure random
4: Rank the n data points with respect to s
5: Find d, the $i_l(t)^{th}$ among the n data points in the ranking
6: $s \leftarrow s \cup d$
7: **end for**

With the use of a linear selection algorithm for step 5, the computational complexity of this sampling procedure is only $O(m.n)$, with n typically equal to 10.

Which ranking function to use ? It is possible to use any kind of information about how well one data point would complement a current partial hypothesis sample. This includes inlier priors but also consistency and non-degeneracy criteria.

What is the value of $i_l(t)$? $i_l(t)$ evolves during the iterations in a way that satisfies two properties introduced in [1]:

- Most probable samples are drawn in the first iterations.
- After T_N iterations, each sample has had the same chance of being formed.

These properties allow to guide the sampling while preventing from an impairing of the randomization.

3 Results

We tested our approach on the homography estimation problem in presence of outliers. In this context, a data point d is a correspondance between two images.

The use of BetaSAC requires the definition of a scoring function q (line 4 of Algorithm 1). We tried two different functions. The first, $q_{matching}(d)$, is simply the matching score of the correspondence d. This is the function used in PROSAC. Let P_d, P'_d and A_d be two end points and the associated affine matrix of a correspondence d obtained with an affine invariant key point detector (we used [3]). Given a partial hypothesis set $s = \{s_1, \ldots, s_{|s|}\}$ and for any correspondence d, the second scoring function, $q_{affine}(d,s)$, is defined in Equation 1. As it depends on s, it could not be used in the PROSAC framework.

$$q_{affine}(d,s) = \begin{cases} q_{matching}(d) & \text{if } |s| = 0 \\ -\left(\|P'_{s_1} - A_d P_{s_1}\| + \|P'_d - A_{s_1} P_d\|\right) & \text{otherwise} \end{cases} \quad (1)$$

Results on four image pairs are presented in Figure 3. BetaSAC with scoring function q_{affine} is always significantly faster than RANSAC and PROSAC, which prove the benefit of a conditional sampling.

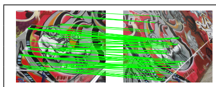
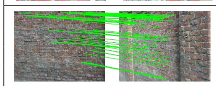
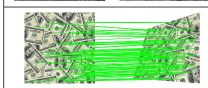
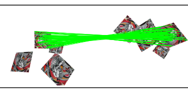
	Sampling algorithm	Mean iters.	Time (ms)	Speed-up
	RANSAC	8181.9	1595.5	1
	PROSAC	1709.9	333.3	4.79
	BetaSAC with $q_{matching}$	1548.6	289.3	5.51
	BetaSAC with q_{affine}	287.0	55.51	**28.74**
	RANSAC	15858.5	1447.4	1
	PROSAC	6445.6	587.5	2.46
	BetaSAC with $q_{matching}$	6414.0	602.3	2.4
	BetaSAC with q_{affine}	636.9	63.8	**22.69**
	RANSAC	1302.8	1293.0	1
	PROSAC	1533.6	1523.1	0.85
	BetaSAC with $q_{matching}$	678.2	677.9	1.91
	BetaSAC with q_{affine}	30.8	30.9	**41.85**
	RANSAC	687.2	198.0	1
	PROSAC	329.7	94.9	2.09
	BetaSAC with $q_{matching}$	242.8	71.0	2.79
	BetaSAC with q_{affine}	7.1	2.12	**93.41**

Figure 2: Results obtained on the homography estimation problem using two different ranking functions, $q_{matching}$ and q_{affine}.

4 Main References

[1] Ondrej Chum and Jiri Matas. Matching with prosac " progressive sample consensus. In *CVPR '05: Proceedings of the 2005 IEEE Computer Society Conference on Computer Vision and Pattern Recognition (CVPR'05) - Volume 1*, pages 220–226, Washington, DC, USA, 2005. IEEE Computer Society. ISBN 0-7695-2372-2. doi: http://dx.doi.org/10.1109/CVPR.2005.221.

[2] Martin A. Fischler and Robert C. Bolles. Random sample consensus: A paradigm for model fitting with applications to image analysis and automated cartography. *Communications of the ACM*, 24(6): 381–395, 1981.

[3] Krystian Mikolajczyk and Cordelia Schmid. Scale & affine invariant interest point detectors. *Int. J. Comput. Vision*, 60(1):63–86, 2004. ISSN 0920-5691. doi: http://dx.doi.org/10.1023/B:VISI.0000027790.02288.f2.

[4] Kai Ni, Hailin Jin, and Frank Dellaert. Groupsac: Efficient consensus in the presence of groupings. In *ICCV09*, Kyoto;Japan, October 2009. URL `http://frank.dellaert.com/pubs/Ni09iccv.pdf`.