

Many problems in computer vision can be formulated as the **matching between two graphs**



Contribution 1: bistochastic normalization enhances **distinctive matches**.

Focus matching on salient points, without explicit saliency detection.

Contribution 2: SMAC
Spectral method for graph Matching with **Affine Constraints**

Spectral Matching with Affine Constraints

$$\max_x \frac{x^T W x}{x^T x} \quad \text{s.t.} \quad Cx = b$$

EQUIVALENT to IQP for x binary

Linear Constraint: $Cx = 0 \implies$ Yu and Shi, 2001

Affine Constraint: $Cx = b \iff \sum_{i'} x_{ii'} = 1$ and $\sum_i x_{ii'} = 1$

Inequality Constraint? $Cx \leq b$ NP-HARD (cf AISTATS 07, submitted)

Solution

1. rewrite as $\max_{x,t} \frac{x^T W x}{x^T x}$ s.t. $Cx = tb$ linear, but ill defined: denominator is not $(x,t)^T(x,t)$

2. introduce $C_{eq} = I_{k-1,k}(C - (1/b_k)bC_k)$ $P = I - C_{eq}^T(C_{eq}C_{eq}^T)^{-1}C_{eq}$

3. solve $P \cdot W \cdot P \quad x = \lambda x$

Efficient computation with Sherman-Morrison formula

Optimality bounds (cf AISTATS 07, submitted)

A general graph matching cost:

$$\epsilon_{GM}(M) = \sum_{ii' \in M, jj' \in M} W(i, i', j, j')$$

$x_{ii'} = 1$ for a match $ii' \in M$

Integer Quadratic Programming (IQP) formulation:

$$\max \epsilon(x) = x^T W x \quad \text{s.t.} \quad Cx \leq b, \quad x \in \{0, 1\}^{nm'}$$

$Cx \leq b$: degree constraint (1-1, 1-many,...)

W encodes how well a **match** (i,i') between 2 graphs G, G' is **compatible** to another **match** (j,j') (see figure below)

In image matching, $W(i,i',j,j')$ is high if
1) feature point i is similar to i' , j is similar to j' , and
2) Spatial distance $\text{dist}(i,j) \approx \text{dist}(i',j')$

$W(i,i',j,j')$ can be reordered (permuting indexes) into $S(i,j,i',j')$ to reflect the similarity between edges (ij) and $(i'j')$

Balanced Graph Matching

Given matching compatibility W , we want to S to be **bistochastic**

Step 1. Convert W to S : $S_{ij,i'j'} = W_{ii',jj'}$

Step 2. repeat until convergence

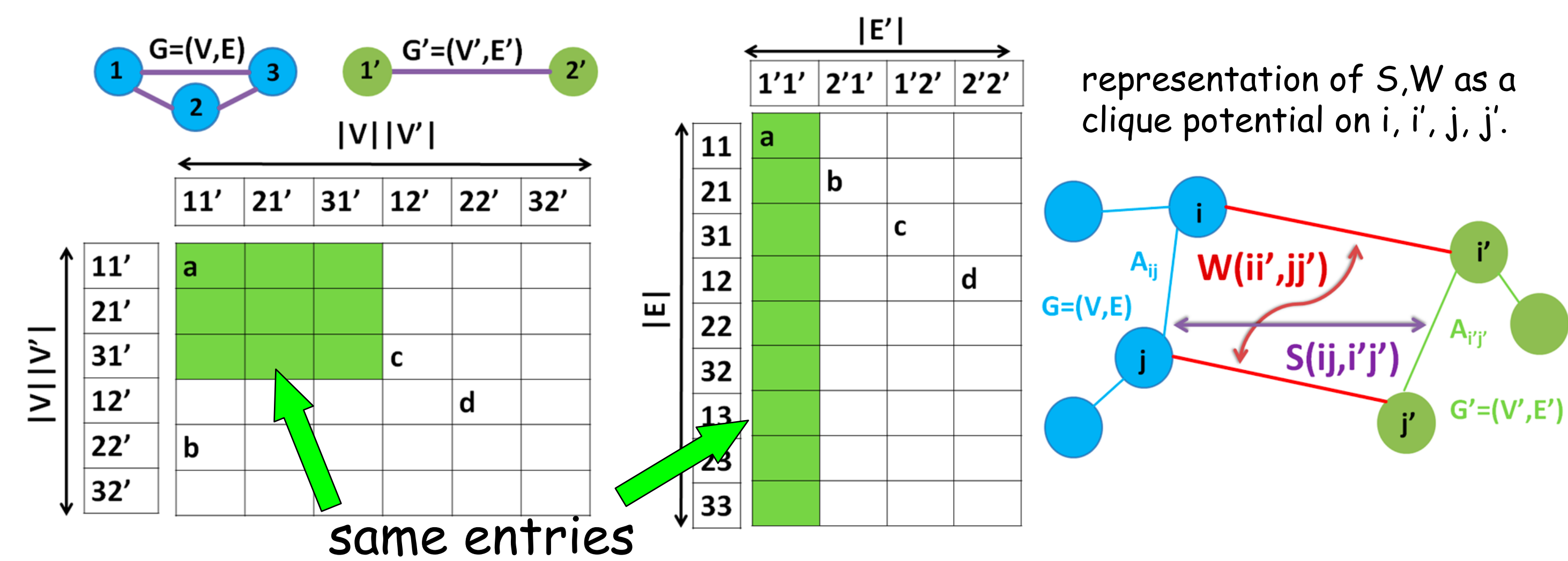
- (a) normalize the rows of S : $S_{ij,i'j'}^{t+1} := S_{ij,i'j'}^t / \sum_{k'} S_{ij,k'j'}^t$
- (b) normalize the columns of S : $S_{ij,i'j'}^{t+2} := S_{ij,i'j'}^{t+1} / \sum_{kl} S_{kl,i'j'}^{t+1}$

Theorem: iterated row & column normalization converges to **unique balancing weights** (D, D') s.t. DSD' **rectangular bistochastic**

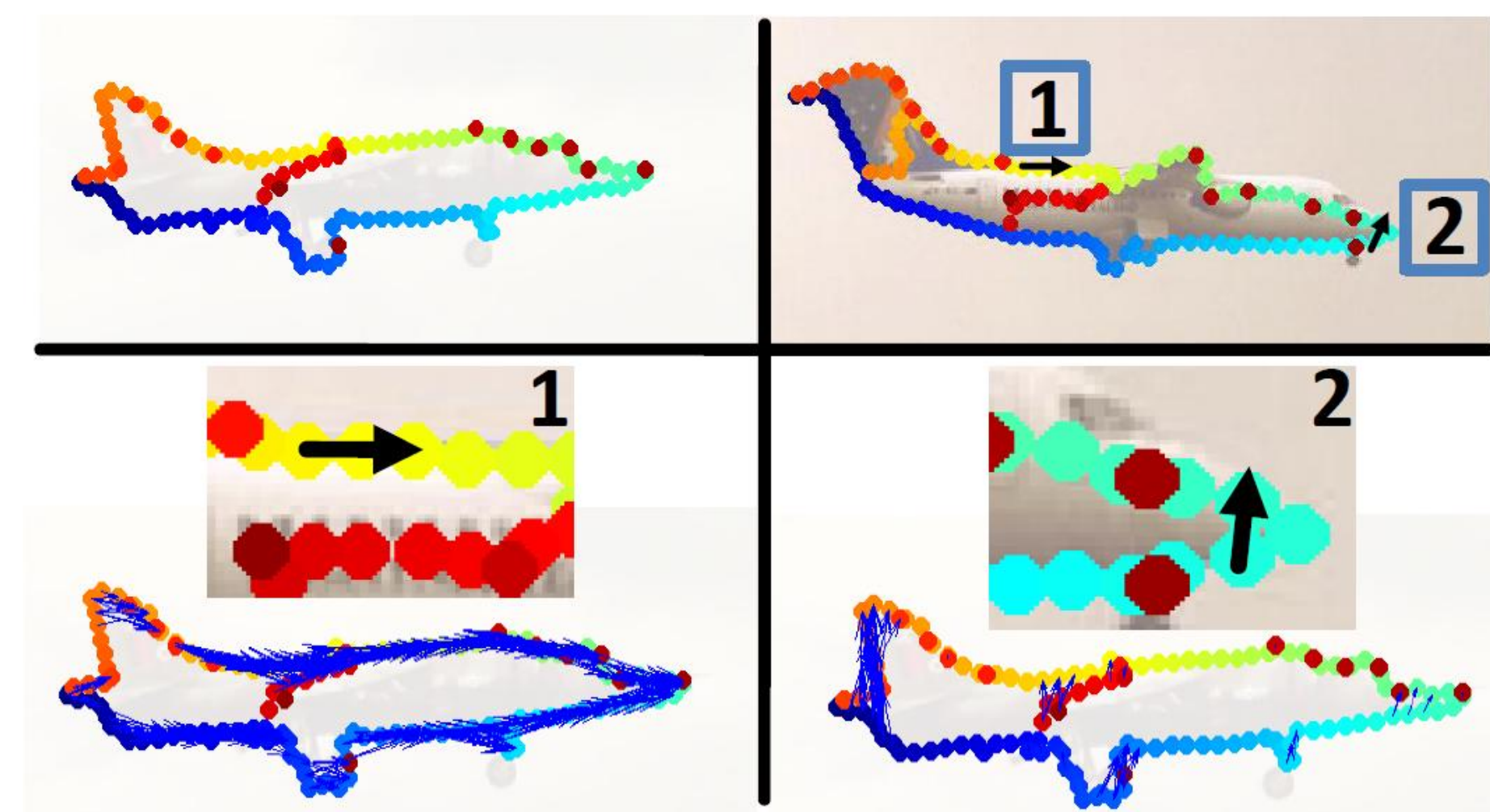
Step 3. Convert back S to W

Step 4. apply **SMAC** (or SDP, GA, or your favorite) to W

Dual representation: Matching Compatibility W vs. edge Similarity S



Representative cliques for graph matching. Blue arrows indicate edges with high similarity, showing 2 groups:

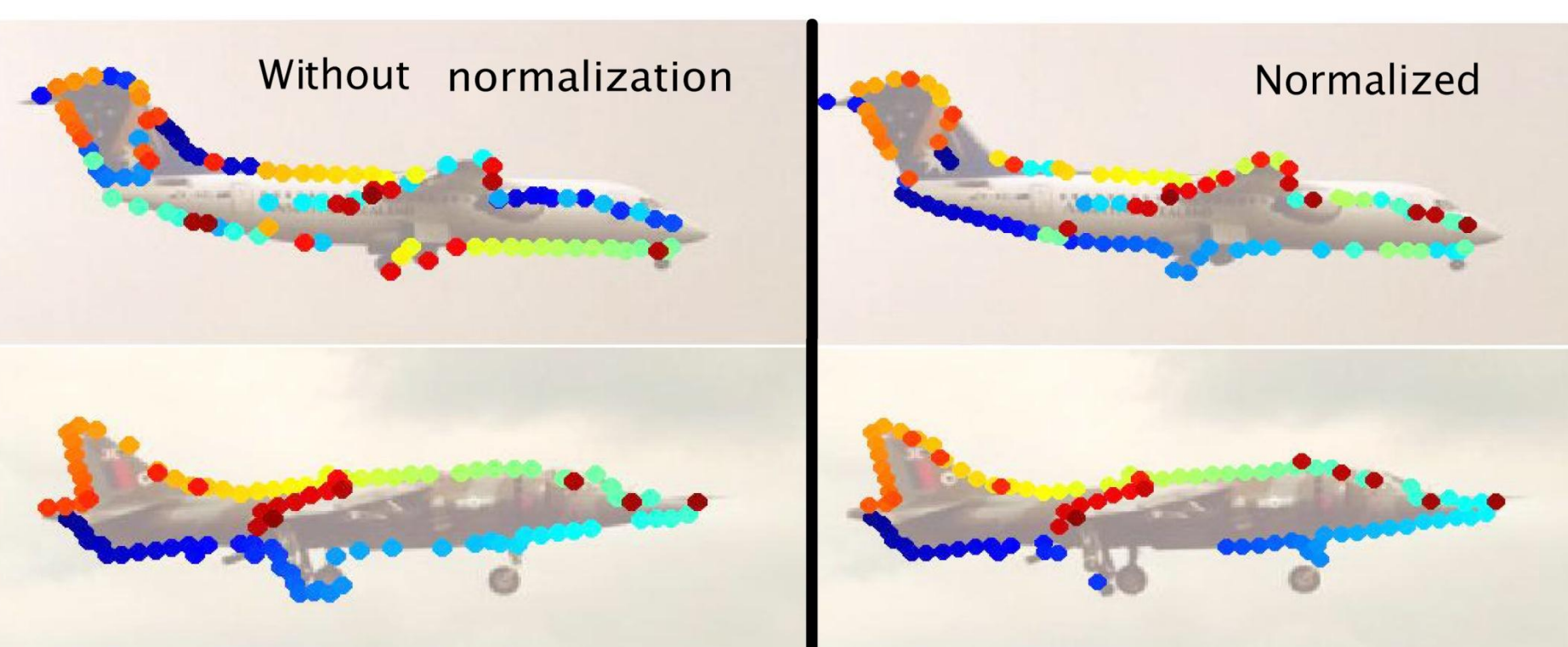


cliques of type 1 (pairing common edges in the 2 images) are **uninformative**

cliques of type 2 (pairing salient edges) are **distinctive**

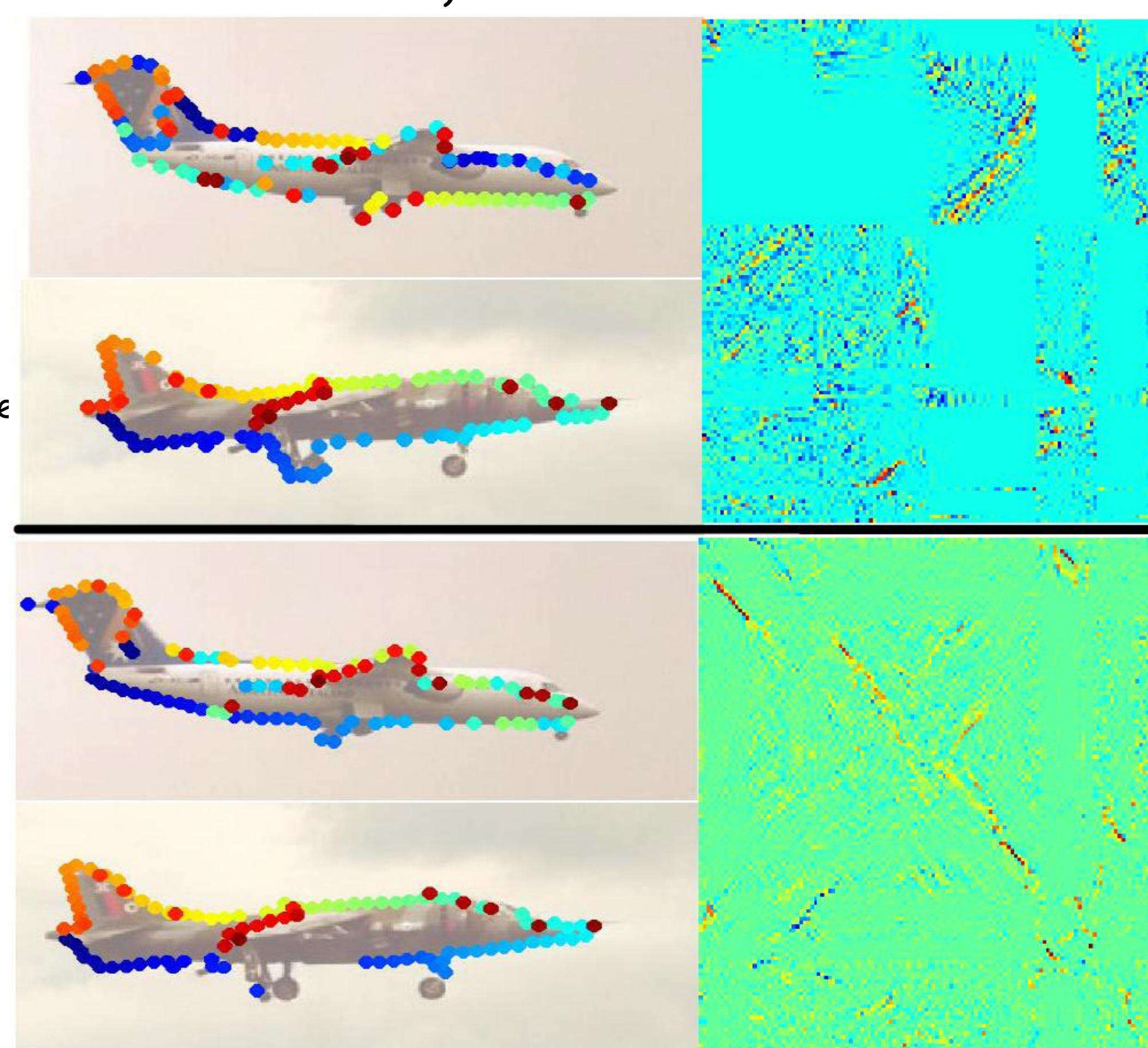
normalization **decreases** their influence

normalization **increases** their influence



matches (discretized solution to SMAC)

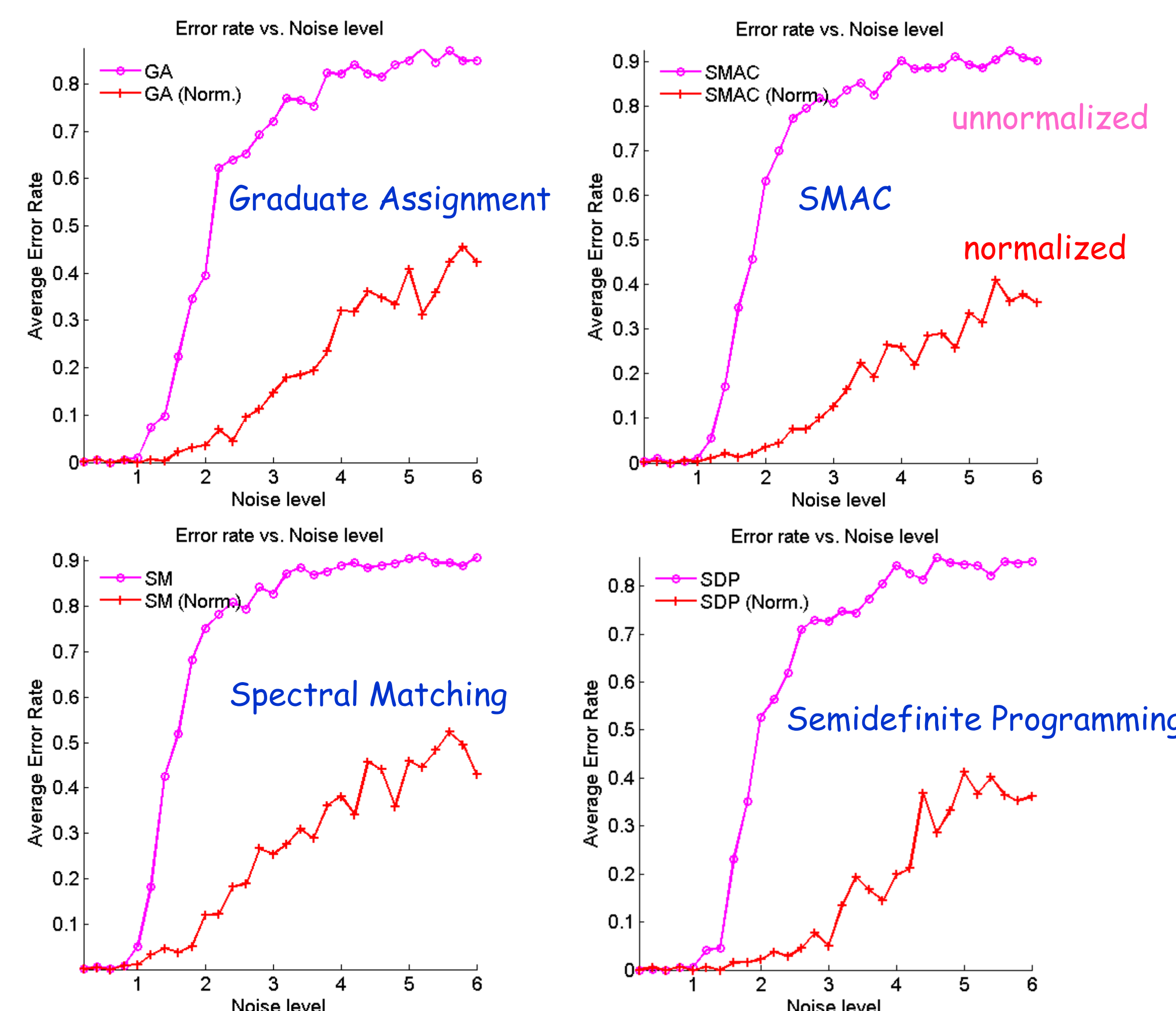
eigenvectors (soft solution to SMAC)



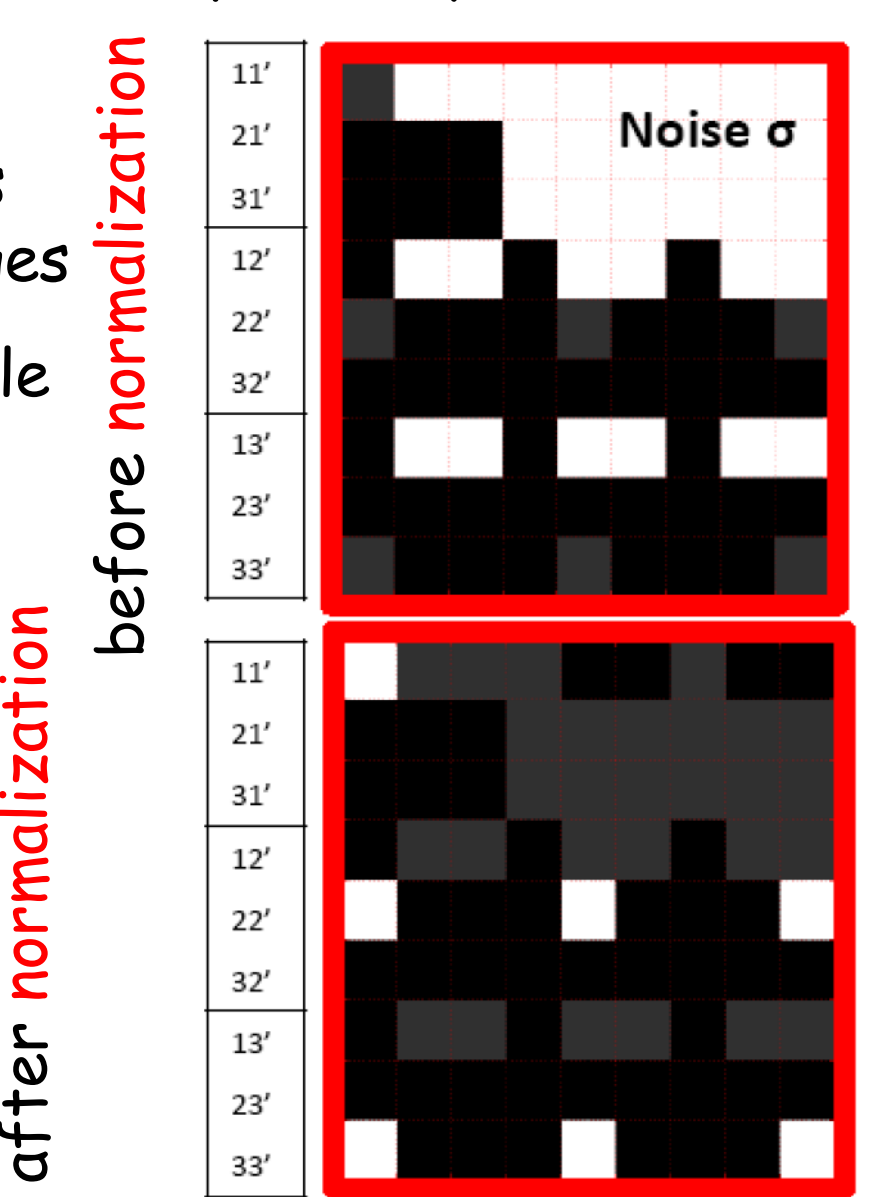
Experiments on 1-1 matchings with random graphs

Comparison of matching performance with **normalized** and **unnormalized** W

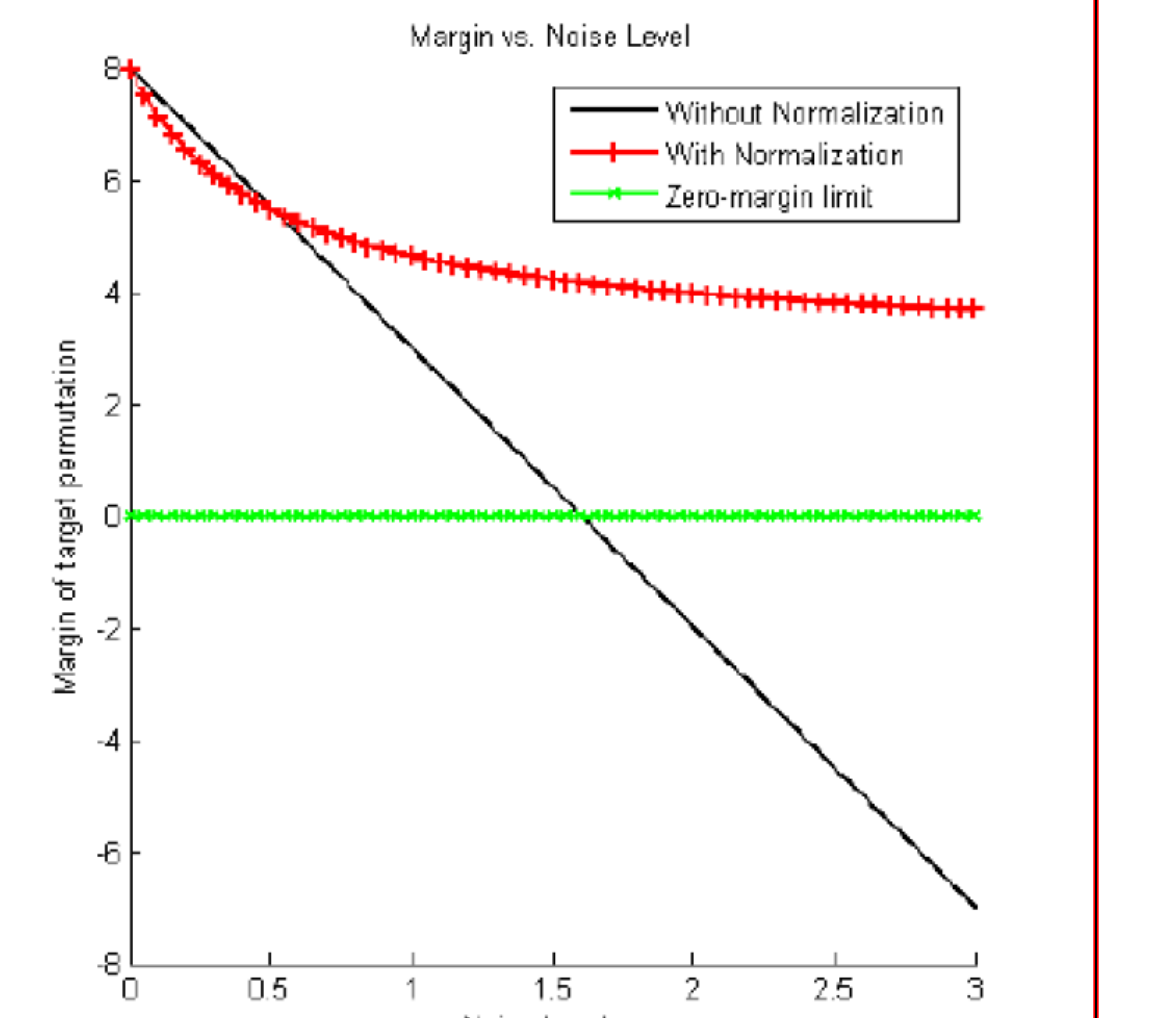
Axes are error rate vs. noise level



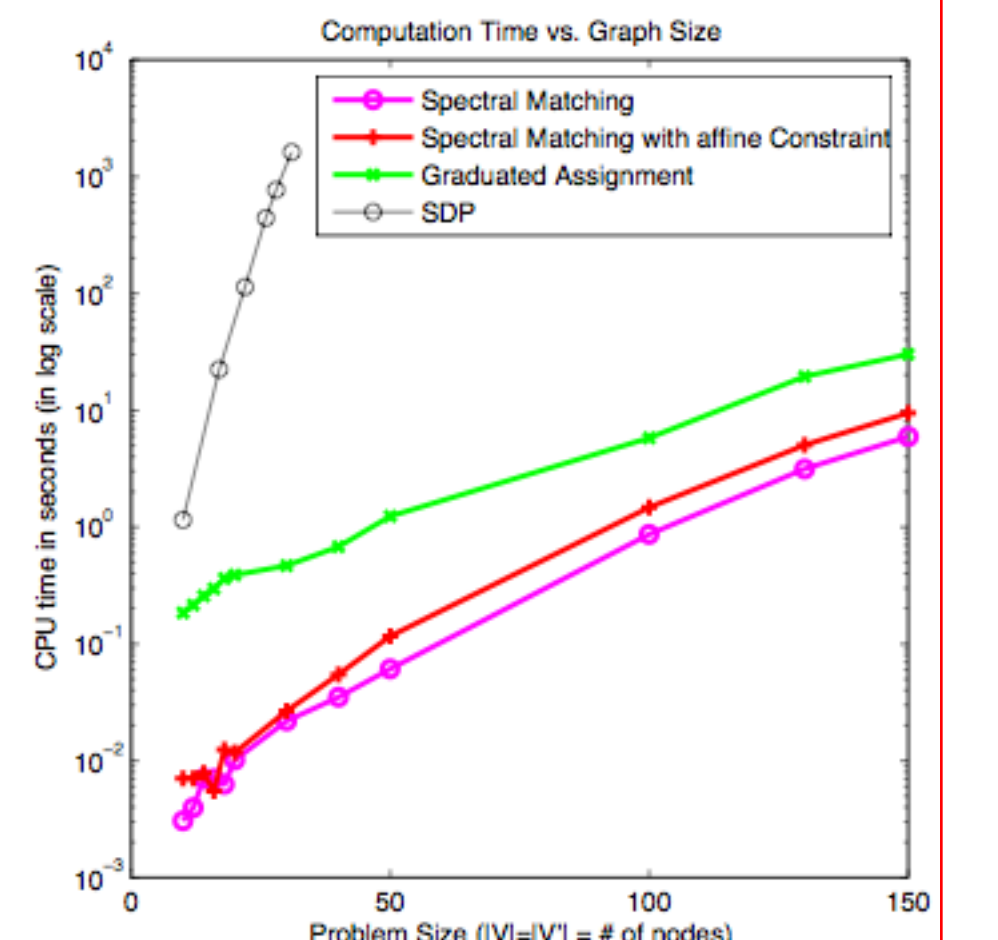
compatibility matrices W



margin as a function of **noise** (difference between correct matching score and best runner-up score).



Running on GA, SDP, SM, SMAC



error rate across algorithms

