A Comparative Study of Multi-Objective Evolutionary Trace Transform Methods for Robust Feature Extraction

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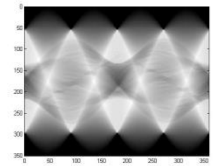
22nd March 2013

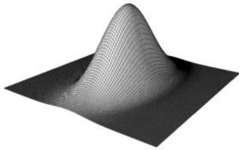
Outline

- Introduction



- Evolutionary Trace Transform – Method I

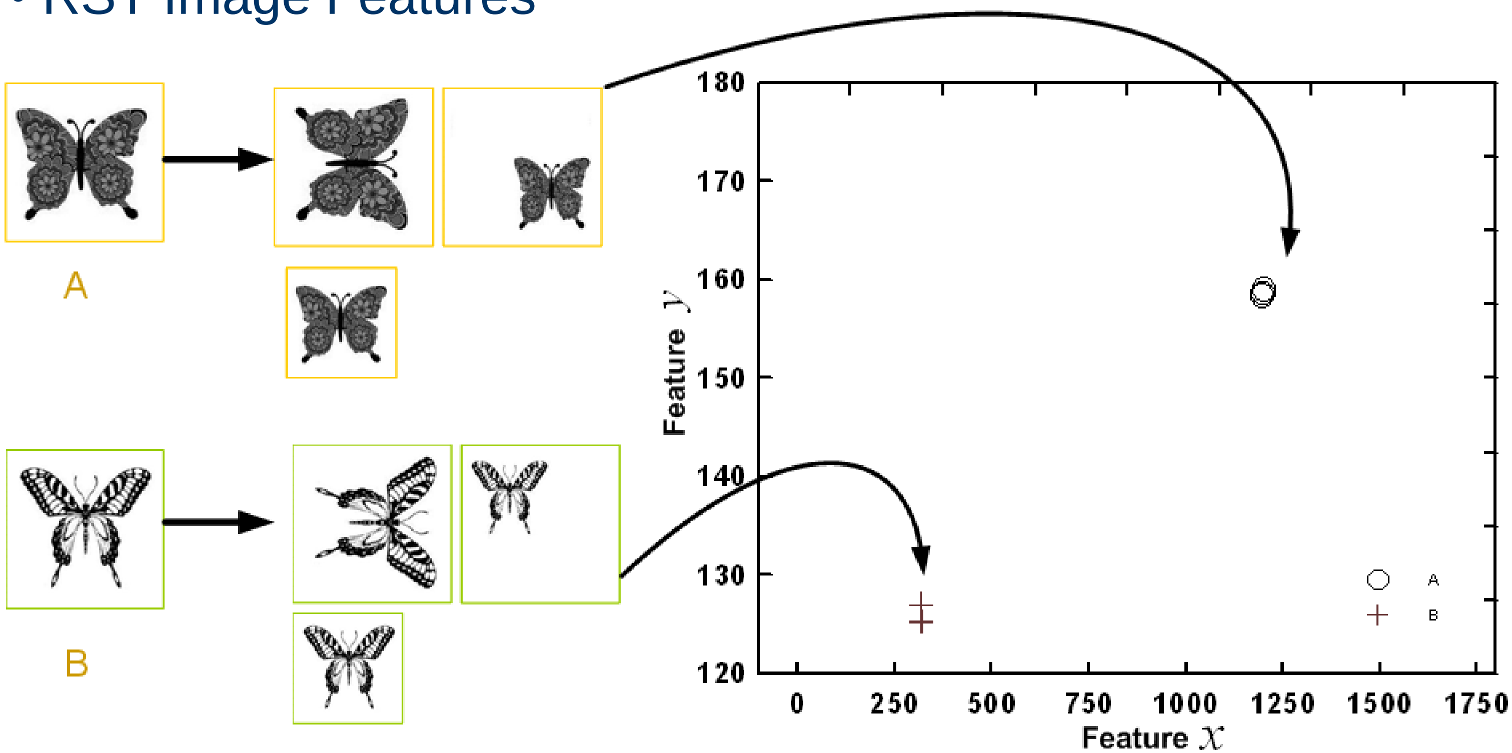
- Evolutionary Trace Transform – Method II
- Experiments



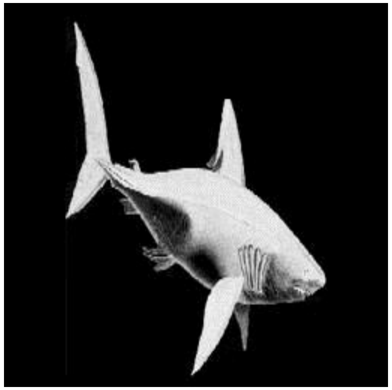
- Conclusion

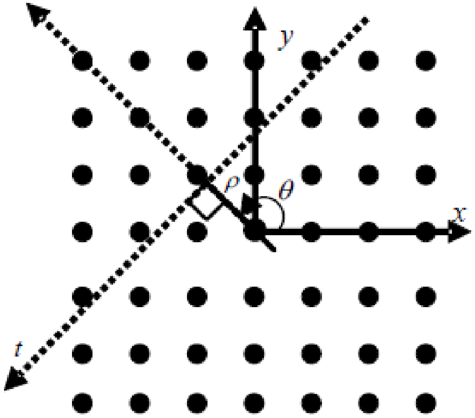
Introduction

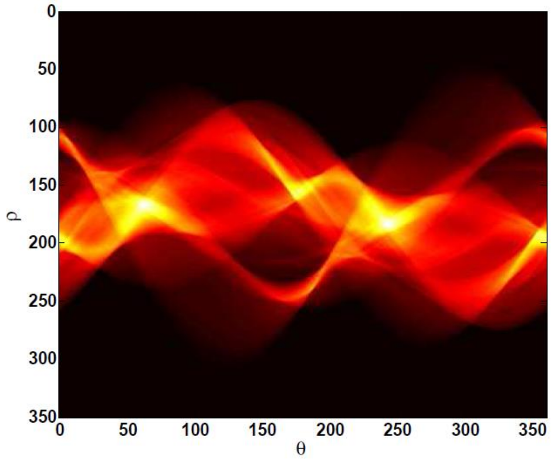
- RST Image Features



- Trace Transform[1] and Theory of Triple Features

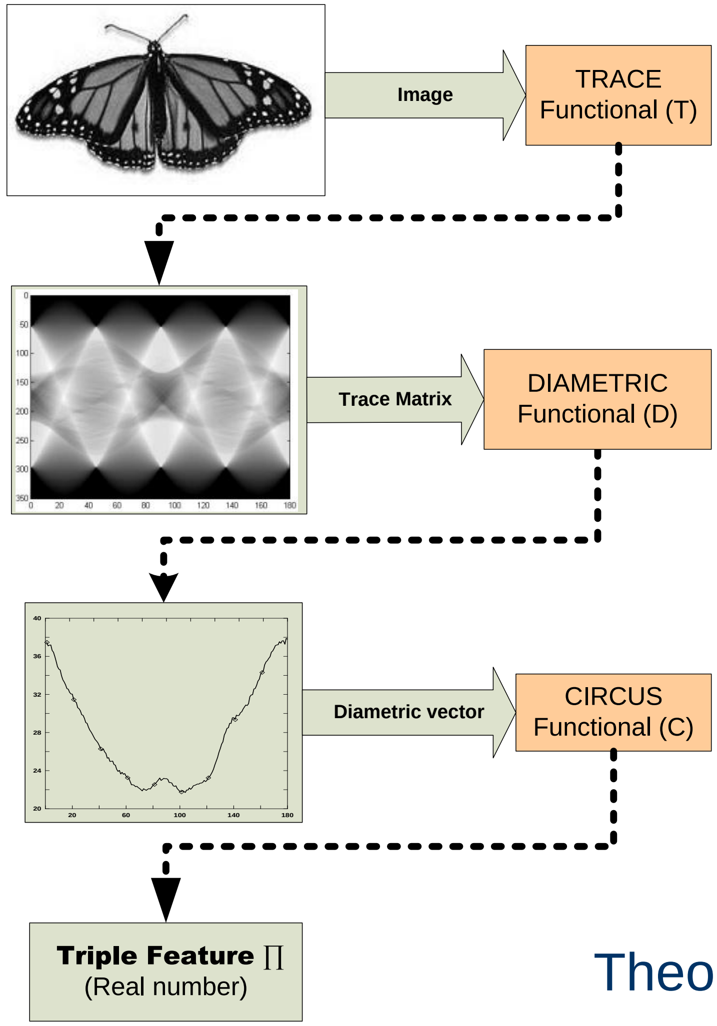






[1] Kadyrov, A., Petrou, M.: The trace transform and its applications. IEEE Transactions on Pattern Analysis and Machine Intelligence 23(8), 811–828 (2001)

Theory of Triple Features



[2] Albukhanajer, W.A., Jin, Y., Briffa, J.A., Williams, G.: Evolutionary Multi-Objective Optimization of Trace Transform for Invariant Feature Extraction. In: 2012 IEEE Congress on Evolutionary Computation, CEC, Brisbane, Australia, June.10-15, pp. 401–408 (2012)

• Evolutionary Trace Transform (ETT)[2]

Table 1. List of some Trace functional

No.	*Functional*	*Description*
1	$\int f(t)dt$	Radon transform
2	$\int \left\| f(t)' \right\| dt$	Integral of Gradient
3	$(\int \|f(t))\|^p dt)^q$	p-Norm, $p = 0.5, q = 1/p$
4	$max - min(\|f(x)\|)$	Maximum-minimum of the function

• Using NSGA-II[3] and Pareto front concept on Trace Functionals

[2] Albukhanajer, W.A., Jin, Y., Briffa, J.A., Williams, G.: Evolutionary Multi-Objective Optimization of Trace Transform for Invariant Feature Extraction. In: 2012 IEEE Congress on Evolutionary Computation, CEC, Brisbane, Australia, June 10-15, pp. 401–408 (2012)

[3] K. Deb, Multi-Objective Optimization using Evolutionary Algorithms, 1st ed. England: John Wiley & Sons. Ltd, 2002.

ETT – Method I

• Chromosome Structure (Integer):

T1	D1	C1	θ1

- T: Trace Functional
- D: Diametric Functional
- C: Circus Functional;
- Θ: Max number of Directions

•Using NSGA-II and Pareto front concept to search ‘good’ Trace Functionals combinations to minimise the fitness functions in 1D feature space (One triple feature).

• Fitness:

$$f_1 = S_w^I \tag{1a}$$

$$f_2 = 1/(S_b^I + \epsilon) \tag{1b}$$

where ϵ is a small quantity to avoid division by zero. S_w^I and S_b^I are the within-class variance and between-class variance defined in (2):

$$S_w^I = \sum_{k=1}^{K} \sum_{j=1}^{N_k} (x_{jk} - \mu_k^x)^2 \quad (2a)$$

$$S_b^I = \sum_{k=1}^{K} (\mu_k^x - \mu^x)^2 \quad (2b)$$

where

$$\mu_k^x = \frac{1}{N_k} \sum_{j=1}^{N_k} x_{jk}, \ \mu^x = \frac{1}{K} \sum_{k=1}^{K} \mu_k^x$$

and K: number of classes, N_k: number of samples in class k, μ_k^x: mean of class k of x triple features, x_{jk}: the j^{th} sample of class k of x triple features, and μ^x: mean of all classes of x triple features.

ETT – Method II

- Chromosome Structure (Integer):

T1	D1	C1	θ1	T2	D2	C2	θ2

Double length Chromosome

- Using NSGA-II and Pareto front concept to search ‘good’ Trace Functionals pair to minimise the fitness functions in 2D feature space (Two Triple features).

- Fitness:

$$f_1 = S_w^{II} \tag{3a}$$

$$f_2 = 1/(S_b^{II} + \epsilon) \tag{3b}$$

$$S_w^{II} = \sum_{k=1}^{K} \sum_{j=1}^{N_k} (x_{jk} - \mu_k^x)^2 + (y_{jk} - \mu_k^y)^2 \tag{4a}$$

$$S_b^{II} = \sum_{k=1}^{K} (\mu_k^x - \mu^x)^2 + (\mu_k^y - \mu^y)^2 \tag{4b}$$

where

$$\mu_k^x = \frac{1}{N_k} \sum_{j=1}^{N_k} x_{jk}, \mu_k^y = \frac{1}{N_k} \sum_{j=1}^{N_k} y_{jk}, \ \mu^x = \frac{1}{K} \sum_{k=1}^{K} \mu_k^x, \ \mu^y = \frac{1}{K} \sum_{k=1}^{K} \mu_k^y$$

and K: number of classes, N_k: number of samples in class k, μ_k^x: mean of class k of x triple features, μ_k^y: mean of class k of y triple features, x_{jk}: the j^{th} sample of class k of x triple features, y_{jk}: the j^{th} sample of class k of y triple features, μ^x: mean of all classes of x triple features and μ^y: mean of all classes of y triple features.

Experiments

Elitist NSGA-II operations: Method I&II

- Selection:
    1) *Tournament*
    2) *Pareto-front assignment*
    3) *Crowding Distance*
- Uniform Crossover
- Uniform Mutation

Table 2. Parameter Set-up for method I and II

Parameter	Value
Population size N_p	150
Mutation probability	0.125
Crossover probability	0.9
Number of generations	200
ϵ	10^{-5}

- The search space consists of

  1) *14 Trace Functionals (T)*
  2) *Six Diametric Functionals (D)*
  3) *Six Circus Functionals (C)*
  4) Θ takes a value between [180 - 360]

  for each chromosome in Method I &II.

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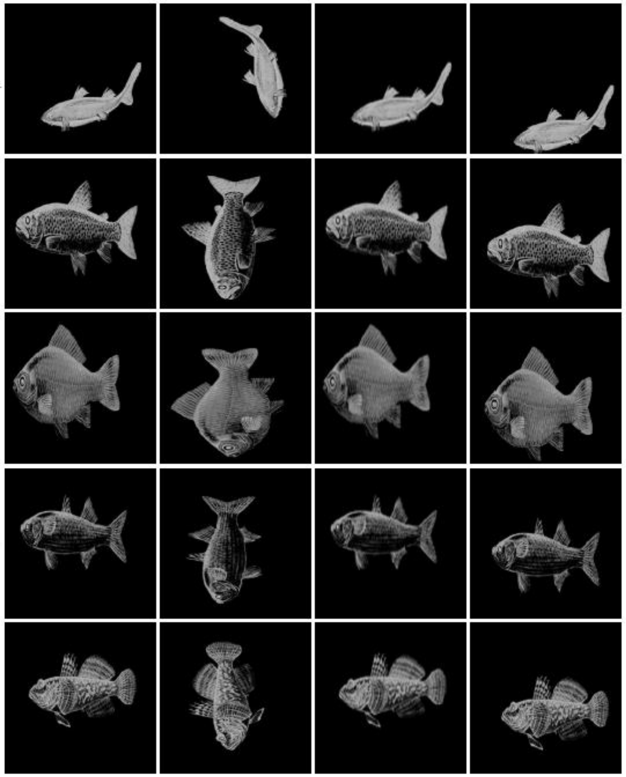
- Five images of low resolution (64x64) from fish database plus their rotated, scaled and translated versions are used during the evolutionary stage

- Offline Evolution: 200 generations.

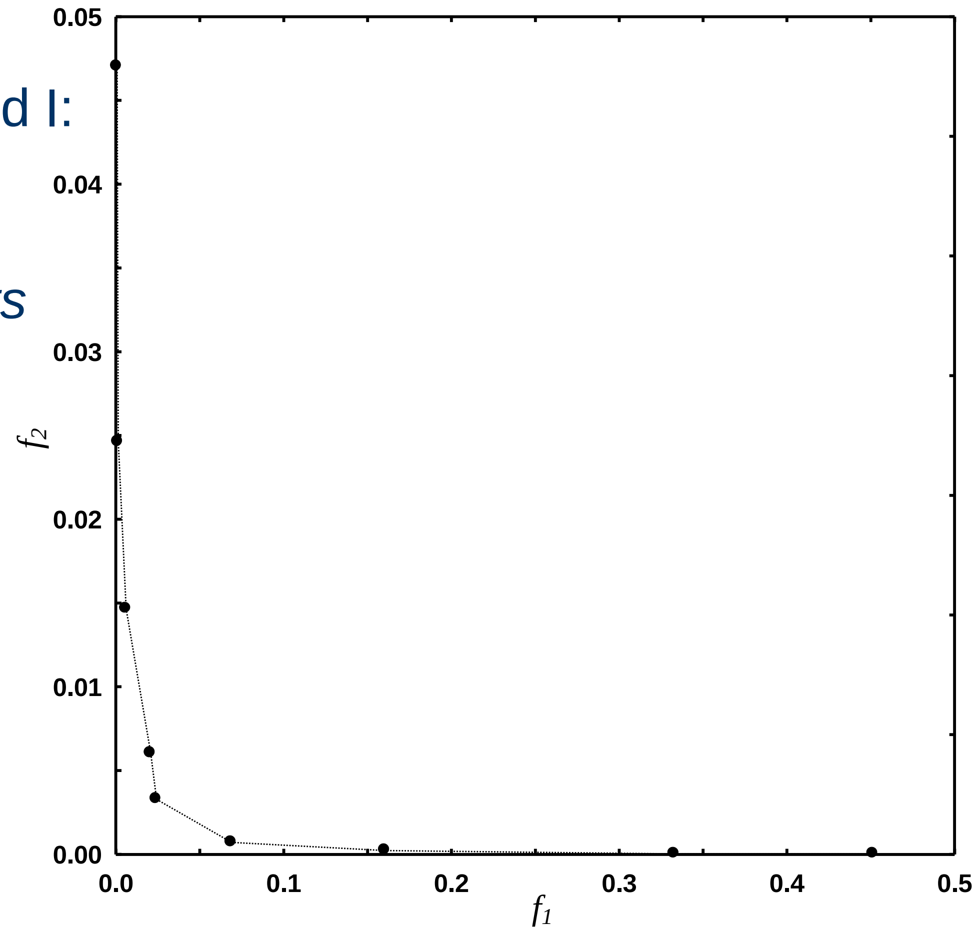
- NSGA-II implemented using SHARK Machine Learning Library[4]



[4] Christian Igel, Verena Heidrich-Meisner, and Tobias Glasmachers. Shark. Journal of Machine Learning Research 9, pp. 993-996, 2008

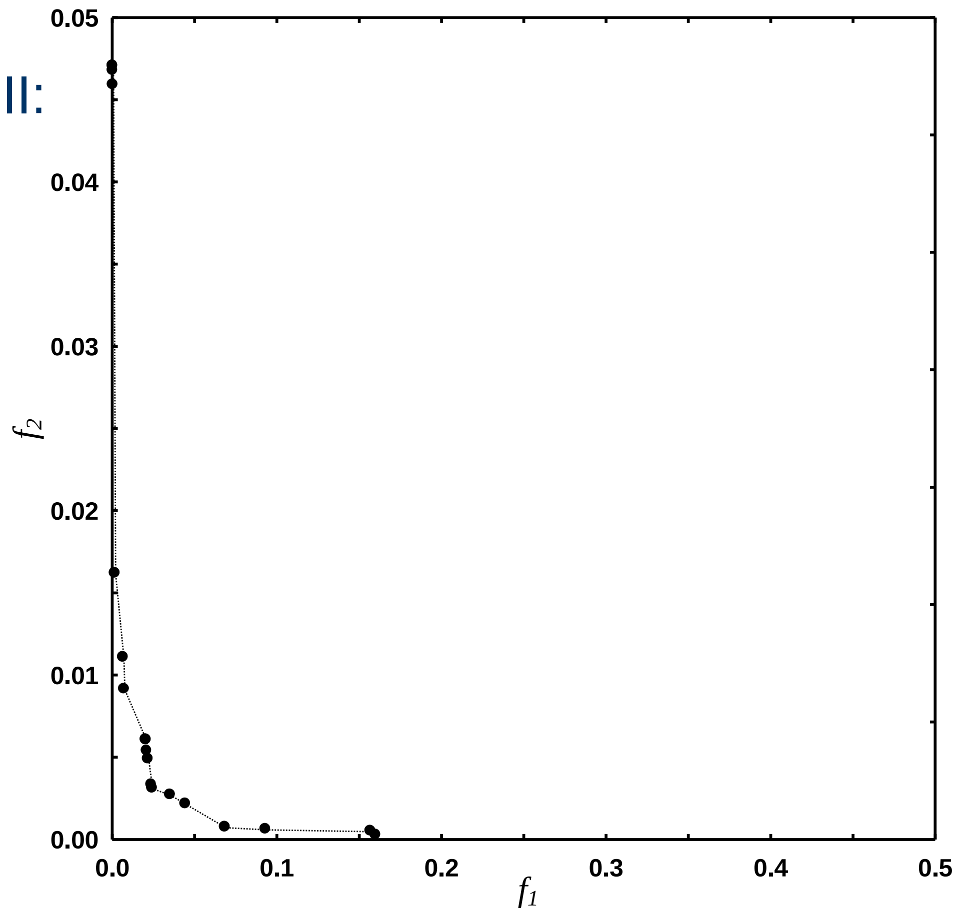
http://image.diku.dk/shark

- Resulting Pareto-front, Method I:
  - *Nine solutions,*
  - *Each solution represents a triple feature (1D).*



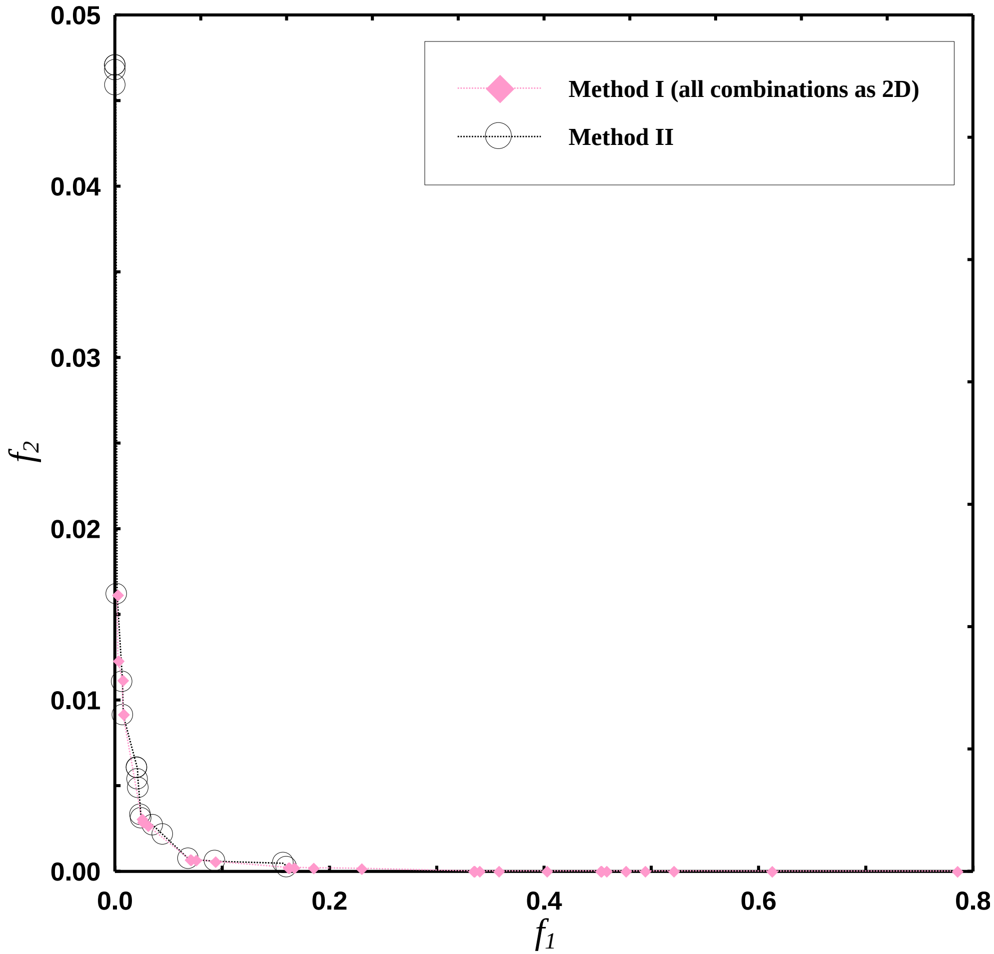
- Resulting Pareto-front, Method II:
    - *19 solutions,*
    - *Each solution represents*

    A pair of Triple features (2D).



- Pareto fronts of Method I&II
  - *Nine solutions Method II,*
  - *39 Solutions Method I (combined)*

- 36 Possible combinations of Triple features pairs can be formed to implement 2D feature space: $\binom{9}{2} = \frac{9!}{2(9-2)!}$



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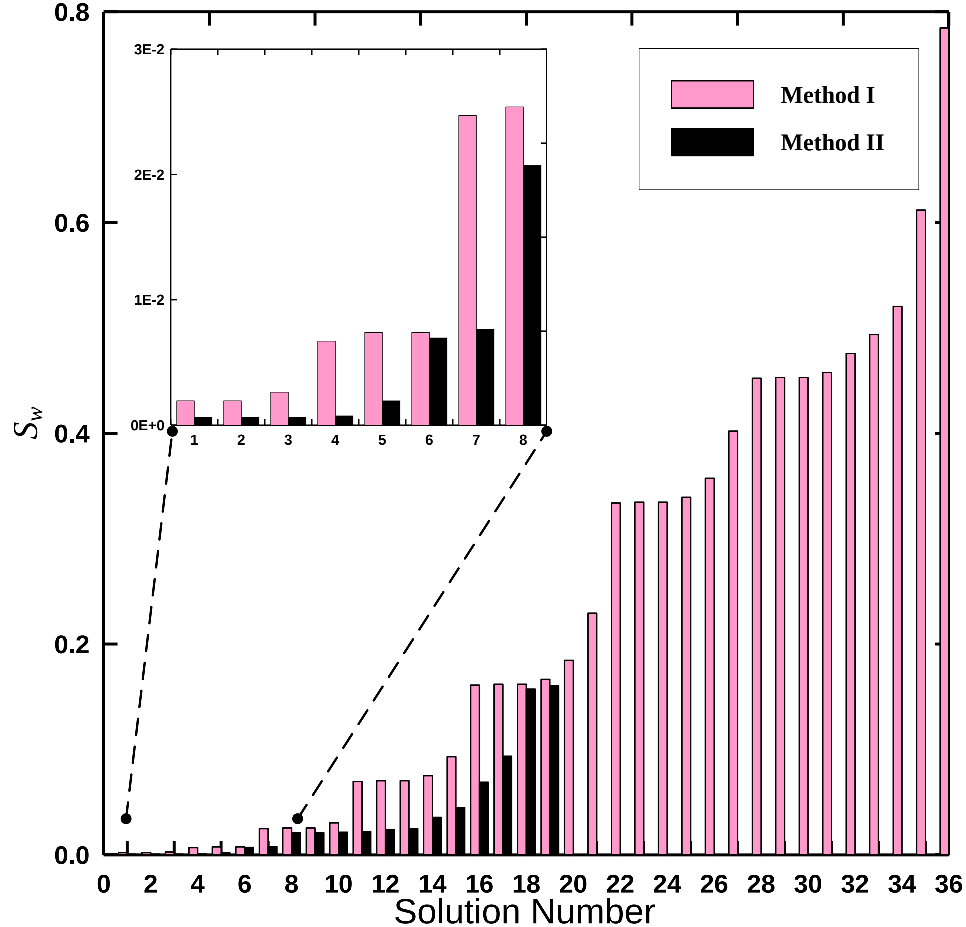
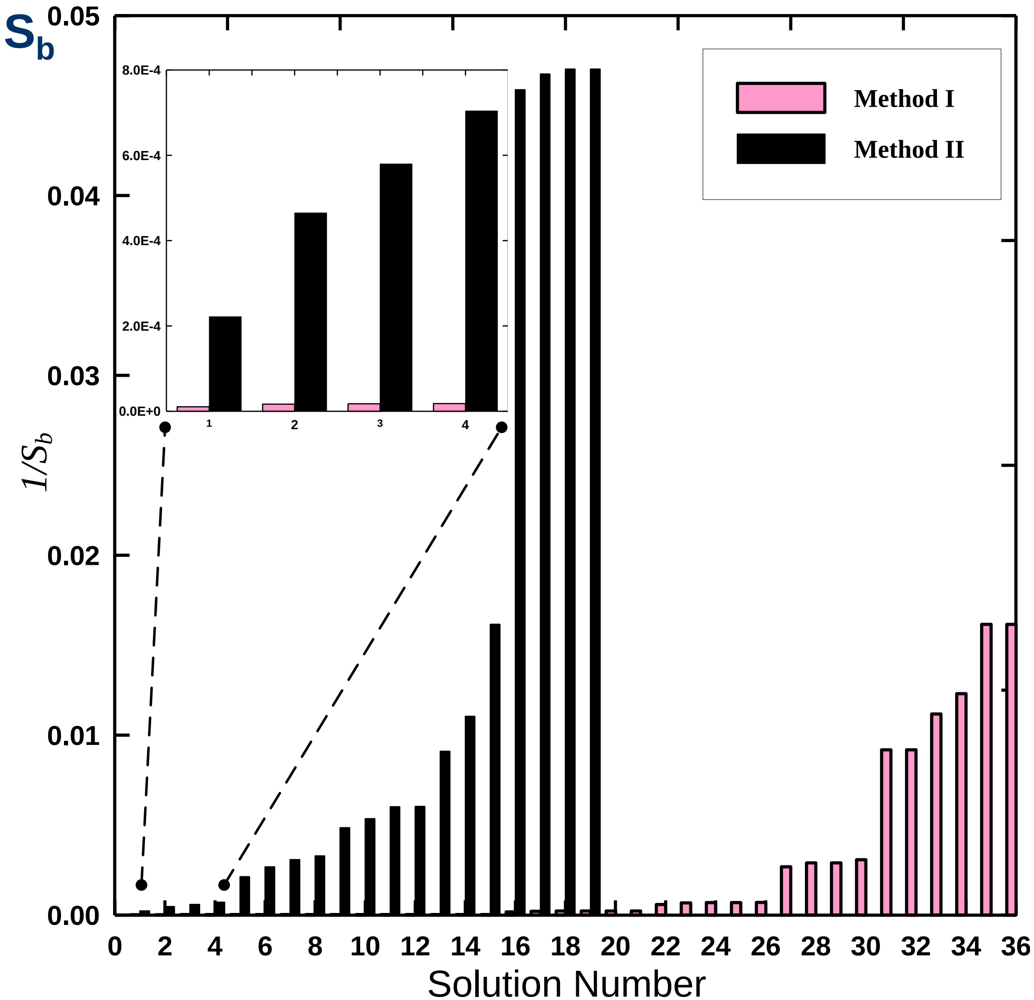
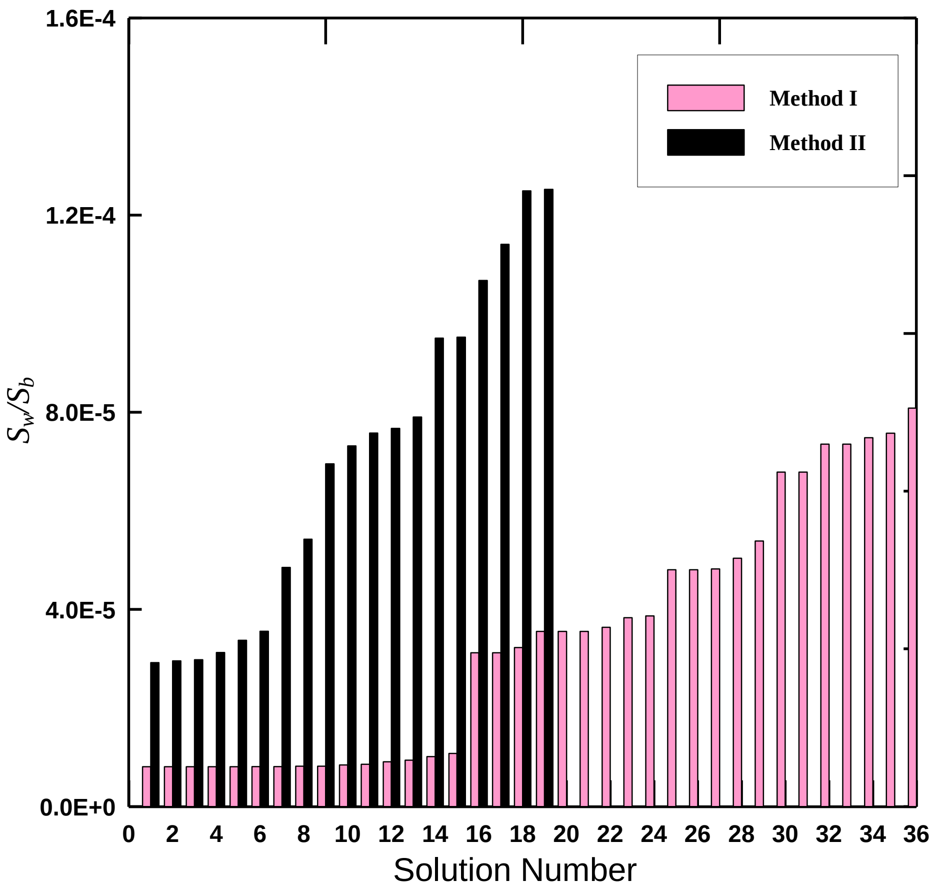
• **Within-class scatter S_w**



• **Inverse between-class scatter S_b**



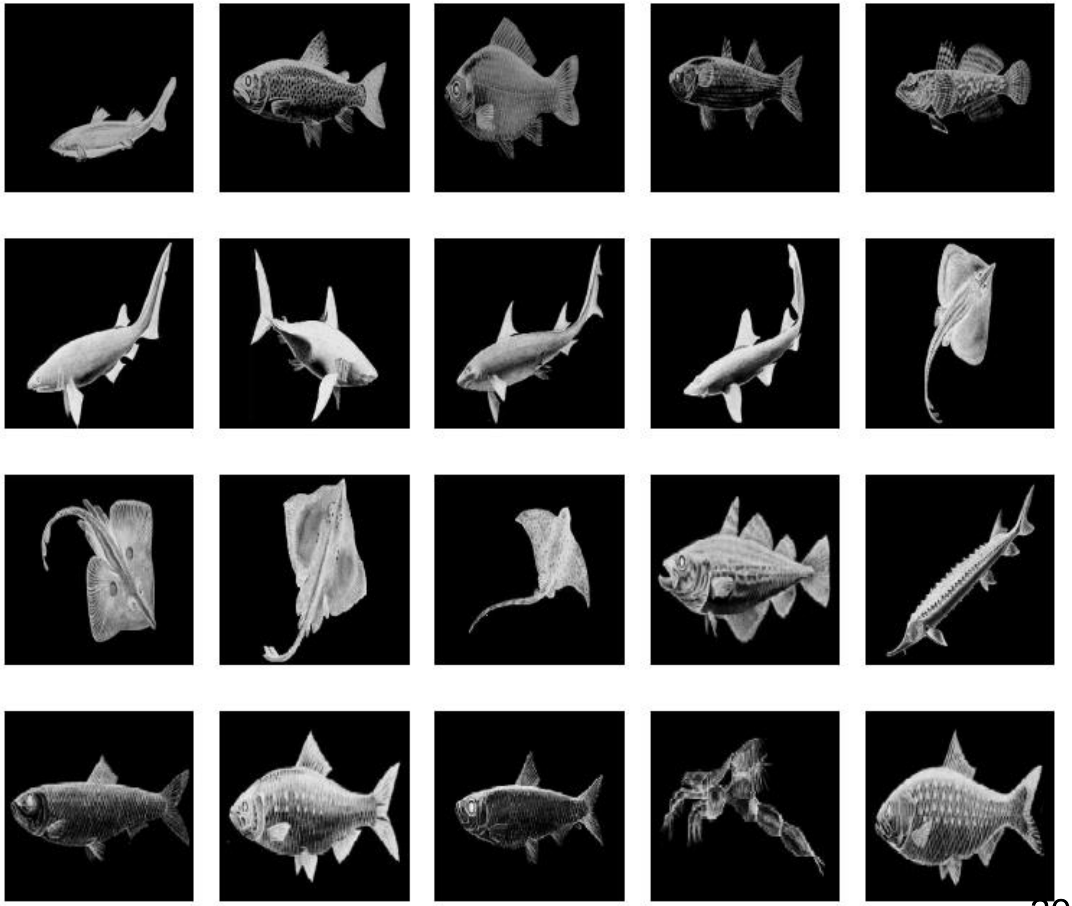
• **Ratio S_w/S_b**



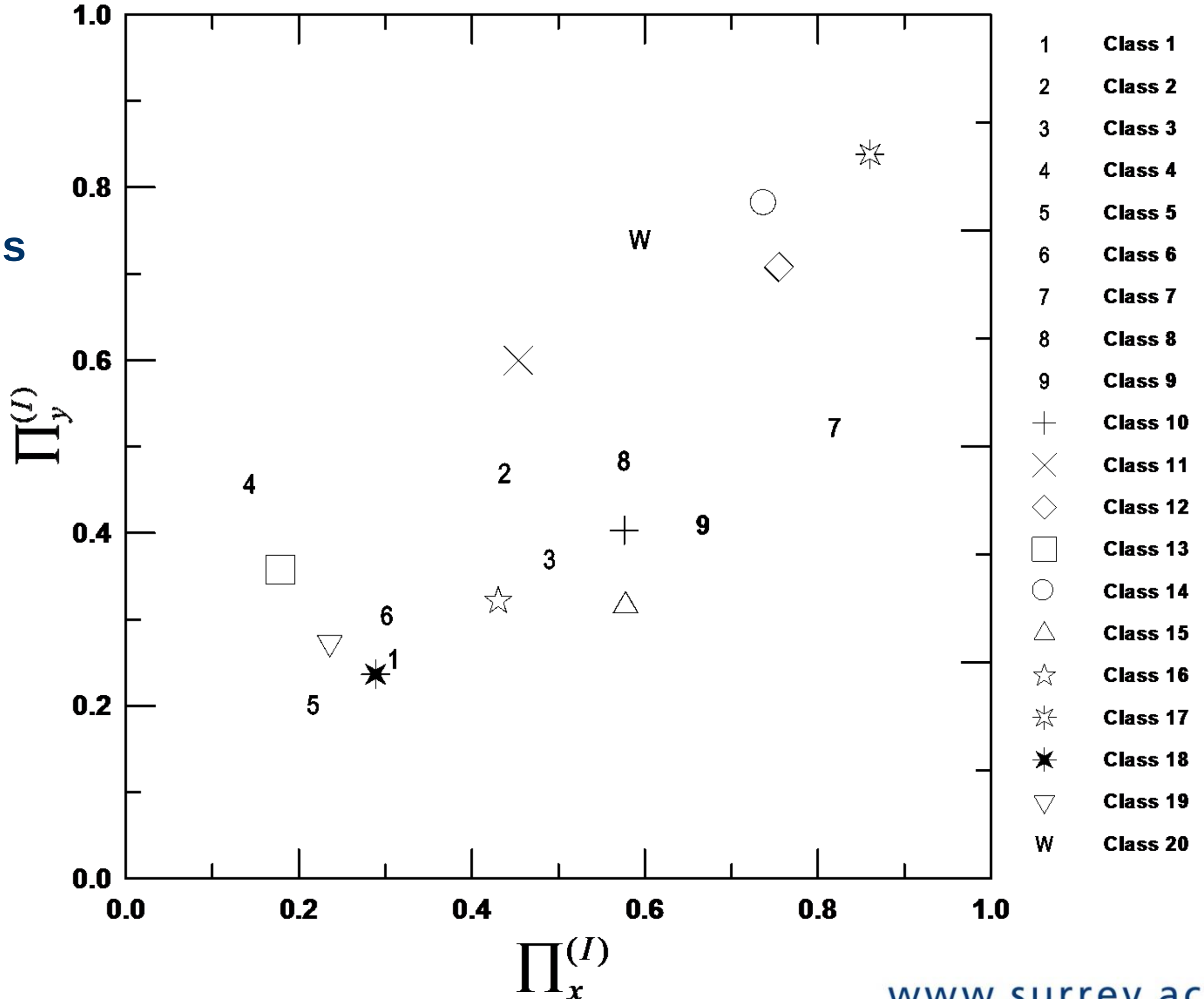
1.6E-4
1.2E-4
8.0E-5
4.0E-5
0.0E+0
S_w/S_b
Method I
Method II
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36
Solution Number

Fish Images database

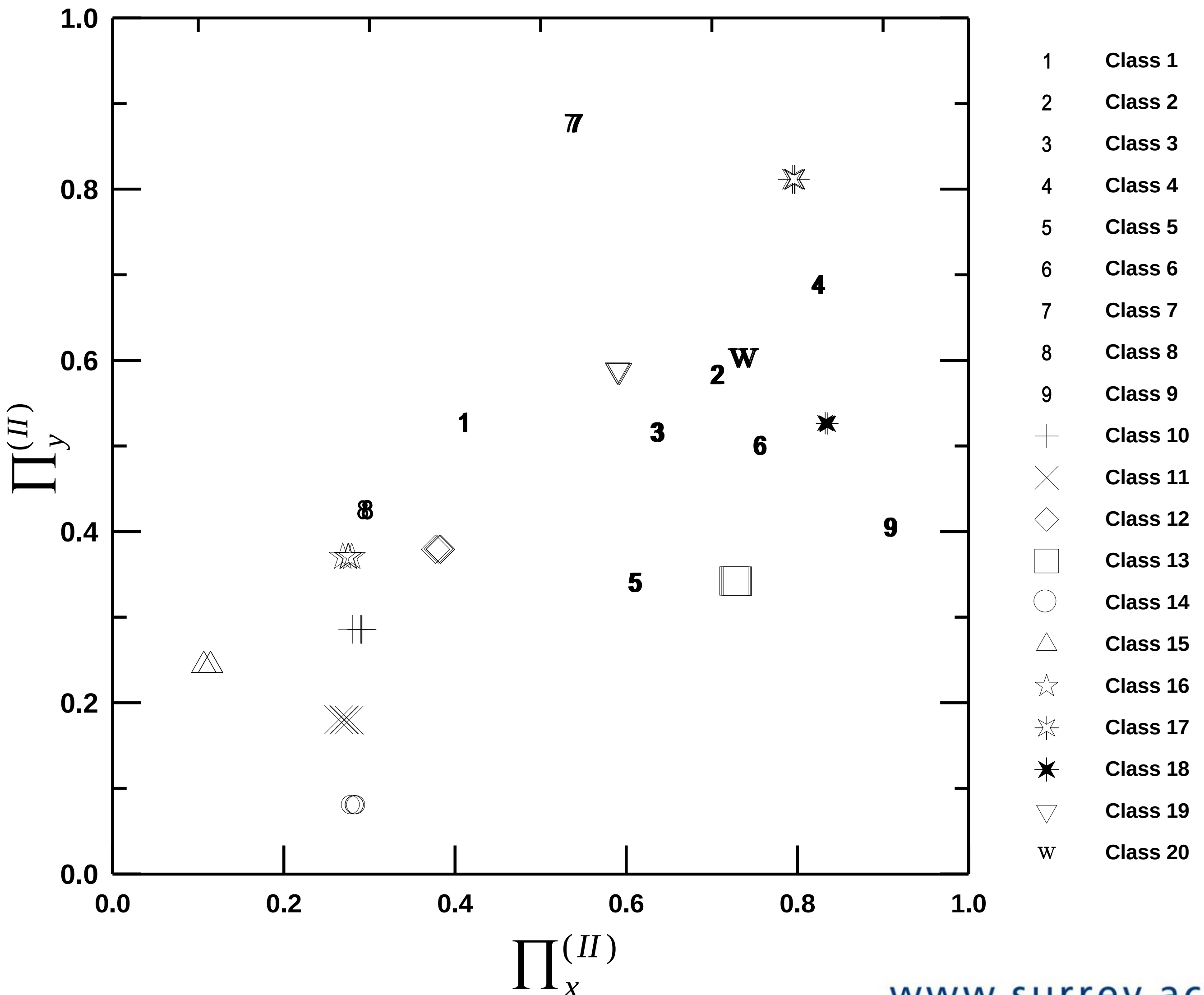
- 20 class of 256x256 images
- 4 samples per class



• **Method I, 2D feature space using 2 solutions**



- **Method II, 2D feature space using one solution**



Conclusion

- **Two methods of Evolutionary Trace transform are developed for robust image feature extraction: Method I and Method II.**
- **Features from Method I represent a 1D feature space and can be combined with another solution to form a pair of features in 2D space. Whereas features from Method II can form a 2D space directly. Therefore, Method II take longer time to build non dominated solutions.**
  - While both methods evolved by using a few resolution (64x64) images, both methods show a comparative results in higher resolution and different images.
  - Few solutions from both methods were explored and evaluated on a relatively large image database of **8554** images. While, Method I appears to provide better classification accuracy and take less time to evolve, Method II shows slightly less accuracy percentage. A fair comparison would be good if an average of more solutions are considered from both methods.

Future Work:

- **Multiple solutions can be used with separate classifiers to build Heterogeneous Ensembles that could enhance performance further.**
- **Combined deformations (such as rotation + scale) and noise on test images would be practical to evaluate the two methods further. Complexity analysis on each solution should also be considered for fine tuning the algorithm.**

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Thank you for your attention!

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