# Finger-vein Recognition using Deep Fully Convolutional Neural Semantic Segmentation Networks

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# Outlines

## CNN based finger-vein exaction (problem statement)

- Finger-vein recognition is a process in which a person's finger vein patterns are captured using near-infrared (NIR) illumination and used as a basis for biometric recognition
- Extracting accurate vein patterns from NIR finger-vein images remains far from being trivial
- Poor quality of the acquired imagery, Poorly designed scanner devices, Close distance between finger and the camera , Poor NIR lighting, varying thickness of fingers,etc., Cause the images to contain low contrast areas and thus ambiguous regions between vein and non-vein areas.
- Deep learning techniques, and especially CNNs, are gaining increasing interest within the biometric community. And application of CNNs for vein extraction has received some research attentions in recent years.
- Large amounts of high-quality annotated samples, or ground-truth data, are typically required for CNN training, which very expensive and time consuming.
- This process even gets more tedious, and error-prone in case the annotators have to deal with ambiguous images (finger-vein images).

# Automated generation of CNN training data

## Automated label generation

- Given the difficulties of generating labeled data, it is not surprising that generating ground-truth labels automatically has been suggested for some CNN-based segmentation tasks in many field (in special medical imaging [?], [?], [?]

  **classical finger vein extraction methods**

  - "Maximum Curvature" MC [?]
  - "Repeated Line Tracking" RLT [?]
  - "Gabor Filter" GF [?]

# Linear Domain Adaptation

**Linear intensity transfer**

- Straight forward solution to weight the intensities of source data is using a linear normalization model:

$$b = (max(B) - min(B))\frac{a - min(A)}{max(A) - min(A)} + (min(B)). \tag{1}$$

- Extract the intensity ranges of iris, non-iris, pupil regions in the target database
- Using this model, adapt the intensities in source data to those of the target
- Train the network with the adapted data and test it on the targets

## Experimental framework

- Databases: Casia4i database[1], Iitd database[2], Casia5a database[3]
- Metrics: Segmentation error scores: nice1, nice2[4], and F1 score
- Network: Fully Convolutional Encoder-Decoder Network (FCN) [1]

| Method | Adapted-target | | | Baseline(Source-target) | | |
|---|---|---|---|---|---|---|
| Scores | nice1 | nice2 | f1 | nice1 | nice2 | f1 |
| Casia5a-casia4i | 0.186 | 0.220 | 0.610 | 0.292 | 0.640 | 0.003 |
| Casia5a-iitd | 0.148 | 0.172 | 0.781 | 0.229 | 0.221 | 0.473 |
| Casia4i-casia5a | 0.066 | 0.194 | 0.730 | 0.274 | 0.406 | 0.341 |
| Casia4i-iitd | 0.121 | 0.141 | 0.808 | 0.218 | 0.219 | 0.724 |
| Iitd-casia5a | 0.062 | 0.185 | 0.739 | 0.049 | 0.117 | 0.830 |
| Iitd-casia4i | 0.299 | 0.319 | 0.569 | 0.315 | 0.584 | 0.045 |

Table: Segmentation scores for the linear-based domain adaptation method against the baseline (source-target) results

1 http://biometrics.idealtest.org
2 http://www4.comp.polyu.edu.hk/ csajaykr/database.php
3 http://www.biometrics.idealtest.org
4 http://nice1.di.ubi.pt/dates.htm

# Linear Adaptation Experiment

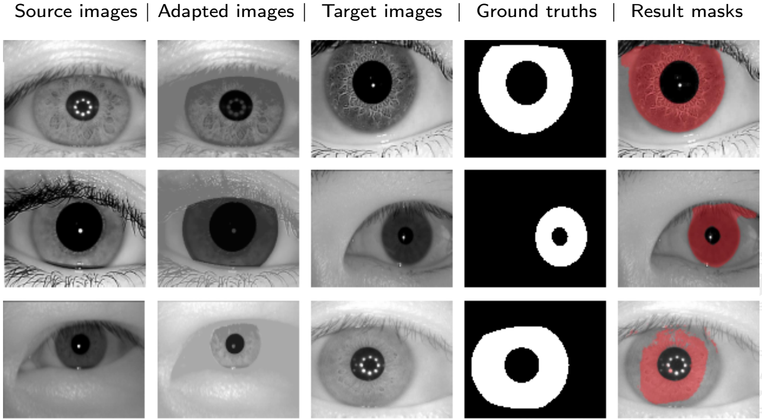


Figure: Sample adapted images and their corresponding segmentation results for Casia4i-Iitd (first row), Iitd-Casia5a (second row), and Casia5a-Casia4i (third row) database pairs (source-target) using the linear domain adaptation method

## Non-linear intensity transfer

- In the linear adaptation, all the source intensity ranges get normalized to "a single average intensity range of that region in the target database"
- The target intensity ranges follow a non-linear distribution
- To address this, calculate the mean of corresponding minimum values and apply kernel smoothing regression on the data to get a polynomial function $f(x)$:

$$f(x) = p_1 x^n + p_2 x^{n-1} + .... + p_n x + p_{n+1}. \qquad (2)$$

- Select a min for each sample, and estimated the max using the polynomial

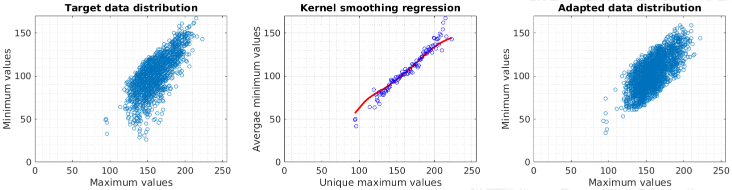


Figure: Sample non-linear data adaptation steps

# Non-linear Damion Adaptation

| Method | Adapted-target (NB) | | | Baseline(Source-target) | | |
|---|---|---|---|---|---|---|
| Scores | nice1 | nice2 | f1 | nice1 | nice2 | f1 |
| Casia5a-casia4i | 0.274 | 0.353 | 0.098 | 0.292 | 0.640 | 0.003 |
| Casia5a-iitd | 0.266 | 0.305 | 0.498 | 0.229 | 0.221 | 0.473 |
| Casia4i-casia5a | 0.027 | 0.074 | 0.859 | 0.274 | 0.406 | 0.341 |
| Casia4i-iitd | 0.102 | 0.095 | 0.812 | 0.218 | 0.219 | 0.724 |
| Iitd-casia5a | 0.034 | 0.088 | 0.813 | 0.049 | 0.117 | 0.830 |
| Iitd-casia4i | 0.208 | 0.174 | 0.374 | 0.315 | 0.584 | 0.045 |

Table: Segmentation scores for the non-linear-based domain adaptation method against the baseline (source-target) results

# Non-linear Damion Adaptation

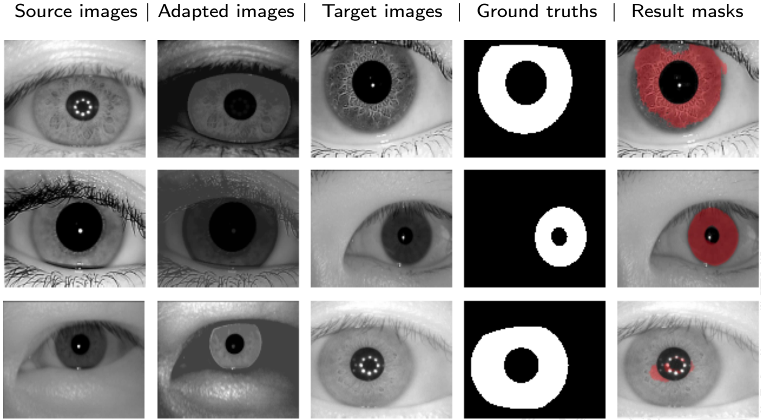


Figure: Sample adapted images and their corresponding segmentation results for Casia4i-Iitd (first row), Iitd-Casia5a (second row), and Casia5a-Casia4i (third row) database pairs (source-target) using the non-linear domain adaptation method

# Alternative Approach

## Training with minimum labeled data

- With the aim of minimizing the number of labeled data required to train the FCN, and maintaining optimal segmentation scores
- Decreased the number of labeled samples required to train the FCN stepwise
- Tested the FCN on the corresponding databases

| Database | | Casia5a | | | Casia4i | | | Iiitd | |
|---|---|---|---|---|---|---|---|---|---|
| Score | nice1 | nice2 | f1 | nice1 | nice2 | f1 | nice1 | nice2 | f1 |
| 15 pcs | 0.075 | 0.082 | 0.875 | 0.205 | 0.263 | 0.502 | 0.089 | 0.097 | 0.856 |
| 25 pcs | 0.064 | 0.077 | 0.896 | 0.099 | 0.115 | 0.814 | 0.077 | 0.083 | 0.879 |
| 50 pcs | 0.050 | 0.070 | 0.909 | 0.078 | 0.068 | 0.841 | 0.063 | 0.070 | 0.889 |
| 100 pcs | 0.021 | 0.040 | 0.921 | 0.038 | 0.039 | 0.926 | 0.035 | 0.037 | 0.941 |

| Method | | target -target | |
|---|---|---|---|
| Scores | nice1 | nice2 | f1 |
| Casia5a-casia5a | 0.019 | 0.038 | 0.925 |
| Casia4i-casia4i | 0.033 | 0.038 | 0.937 |
| Iiitd-iitd | 0.027 | 0.032 | 0.951 |

- Optimal segmentation scores can be achieved using (ap) 100 training samples
- Slightly lower, but very close scores can be achieved with 50 to 25 samples

# Conclusion and Future Work

## Conclusion

- We proposed two domain adaptation methods for CNN based iris segmentation
- Feature representations affecting the weights during training process are not limited to tonal distributions, and further features such as geometric properties of iris, non-iris, and pupil are definitely affecting this process
- Tonal distribution (intensity ranges of iris, non-iris, and pupil) plays a key role in generalization of FCNs on new iris data that differs from the training data

- **Future work**
  - We will investigate the relations between the two proposed methods and the reasons for the different results
  - We also explore more feature representations which encourage further distinctions between two domains, hoping to be able to develop a more comprehensive domain adaptation method

Thank you, Remarks?

# References


Vijay Badrinarayanan, Alex Kendall, and Roberto Cipolla.
Segnet: A deep convolutional encoder-decoder architecture for image segmentation.
*arXiv preprint arXiv:1511.00561*, 2015.