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# Fingervein Sample Image Quality Assessment using Natural Scene Statistics

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**Abstract:** Natural Scene Statistics as used in non-reference image quality measures are proposed to be used as fingervein sample quality indicators. While NIQE and BRISQUE trained on common images with usual distortions do not work well in the fingervein quality context, their variants being trained on high and low quality fingervein sample data behave as expected from a biometric quality estimator. Experiments involve two publicly available fingervein datasets and two distinct template representations. The proposed (trained) quality measures are compared to a set of classical fingervein quality metrics which underlines their highly promising behaviour.

**Keywords:** Vascular biometrics, fingervein recognition, sample quality, natural scene statistics.

## 1 Introduction

The quality of acquired sample vein images has a significant impact on the recognition accuracy of vein-based identification systems (as it is the case with all biometric sample data, but even more critical for veins as the quality of NIR imagery is low in general). It is therefore fundamental to determine the level of quality for acquired sample data (for both enrolment and actual authentication) such that a re-capturing can be initiated in case the quality turns out to be insufficient. Furthermore, quality estimation is useful for selecting subsequent steps in the signal processing pipeline (algorithms / parameters) and in unsupervised scenarios for user guidance during capturing. The imaging principle implies that there will always be some low quality vein images due to light scattering from the skin and the finger tissue (in case of transillumination imaging), ambient temperature, user behaviour, and uneven illumination.

Although biometric image quality evaluation algorithms have increasingly been applied in fingerprint, face or iris biometric recognition procedures in recent years [GT07, BVS14], the ISO/IEC 29794:2016 Biometric Sample Quality standard does not yet include a unified quality evaluation criterion for vein sample images. Current literature in this field can be roughly divided into two groups: Techniques, which base their assessment on sample data directly, thus being independent from specific features used in recognition, e.g. the techniques used in experimental comparison later, i.e. three low-level image properties *Gradient*, *Contrast*, and *Entropy* [Ya13] and their fusion in the *Triangular* norm scheme [PLN14], a clarity and brightness uniformity measure [Wa17] originally proposed by *Wang* for palmvein data, and a *Radon* transform based approach [QCH18]. Second, there are

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techniques basing their assessment on extracted features used in recognition (e.g. looking at the number of vein pixels [Ng13]) or others that use an analysis of incorrect template comparisons in recognition experiments, typically done with more recent learning-based approaches (e.g. [QEY15, QEY19, Re22]). Alternatively, [ZCQ18] uses quality scores derived from traditional schemes to train their CNN. One major cause of poor matches in fingervein recognition is rotation of fingers in longitudinal direction [Pr19], rotation is thus a fingervein-specific quality factor. Rotation cannot be determined based on analysis of a single sample image but only in the context of an analysis of template comparison results.

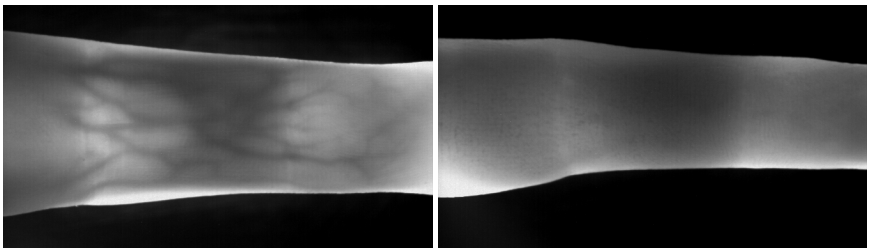
In this paper, we propose a learning-based fingervein sample quality assessment scheme which is based on training natural scene statistics (NSS) on fingervein sample data as used in general purpose image quality metrics (IQM) like NIQE [MSB12] and BRISQUE [MMB12]. In order to provide good generalisability (i.e. being independent from used recognition features), the IQM are trained on low and high quality sample data found by human judgement, respectively. So overall, we introduce (i) a learning based scheme, which uses (ii) NSS, a well established statistical model to capture image quality variations and we employ (iii) training-data based on human scoring to provide independence from specific features used in particular recognition schemes. The aim is to demonstrate a good generalisability among different datasets and fingervein recognition schemes, respectively.

In Section 2 we propose NSS-based image quality metrics for fingervein samples which are experimentally evaluated in Section 3 on two different public fingervein datasets, employing two different types of fingervein recognition techniques (i.e. a binarisation scheme exposing the vessel structure and a keypoint-based approach). Section 4 concludes the paper and provides an outlook to future work in this direction.

## 2 Natural Scene Statistics in Fingervein Image Quality

NIQE [MSB12] uses only measurable deviations from statistical regularities in natural images, without training on (human-rated) any distorted images. The NSS features used in the NIQE index are similar to those used in BRISQUE [MMB12], however, NIQE only uses the NSS features of natural images and is not - as BRISQUE - trained on features obtained from both natural and distorted images (and the corresponding human judgments of the quality of the latter). As a consequence, the NIQE index is not tied to any specific distortion type, while BRISQUE is limited to the types of distortions it has been tuned to.

Both original versions of BRISQUE and NIQE use a trained model that has been derived from natural images. Obviously, fingervein sample images are quite different from common natural images and therefore, we might expect limited value in applying those IQM from scratch. In contrast, we substitute fingervein samples as training data to generate a custom model for this type of data. The first step we conducted is to manually select 50 obviously high quality and 50 obviously low quality fingervein sample images from the considered test datasets (see Fig. 1 for examples). For the NIQE training only the high quality images are used to train the model, while for BRISQUE we set the opinion score for the high quality images to 0, and for low quality images to 100, respectively (the opinion score refers to the human perceptual differential mean opinion score (DMOS)).



(a) High quality (b) Low quality

Fig. 1: UTFVP fingervein samples

Thus, for each of the two IQM we employ three different models:

1. Pre-trained IQM (BRISQUE, NIQE)
2. IQM trained on a single fingervein dataset (BRISQUE Train, NIQE Train)
3. IQM trained on all considered fingervein datasets (BRISQUE Full, NIQE Full)

## 3 Experiments

### 3.1 Experimental Settings

For the experiments, two publicly available fingervein databases were used. The data sets under investigation are:

- The *University of Twente Finger Vascular Pattern Database* (**UTFVP**) [TV13] contains six fingers (ring, middle and index finger from both hands) from 60 volunteers in two sessions. At each session two samples per finger were captured (resulting in 4 samples per finger). The samples have an original resolution of $672 \times 380$ pixels, while their region of interest (RoI) is $672 \times 285$ pixels.
- The *Shandong University Machine Learning and Applications - Homologous Multimodal Traits Database* (**SDUMLA-HMT**) [YLS11] fingervein dataset is composed of 3816 images in total, with each of 6 fingers (index, middle and ring finger of both hands) captured for 6 times from 106 subjects. The images are recorded as 8-bit greyscale, and stored in a resolution of $320 \times 240$ pixels.

The finger detection, finger alignment and RoI extraction for UTFVP and SDUMLA (the fingervein part is denoted like this for brevity) is done as described in [Lu13]. After preprocessing, the resulting features are used to perform the baseline experiments. We conducted these experiments by applying the PLUS OpenVein Finger- and Hand-Vein Toolkit (`http://www.wavelab.at/sources/OpenVein-Toolkit/` [KU19]). We selected two very distinct recognition techniques: The feature extraction schemes used are (i)

binary vessel structure based *Maximum Curvature (MC)* [MNM07] and (ii) keypoint based *SIFT* [KRU14]. The MC feature templates are subsequently compared using a correlation-based approach proposed in [MNM07], the so called Miura matcher, while SIFT-based recognition is applied as described in [KRU14].

As for the training of NIQE and BRISQUE 100 samples of each dataset were used, these images have been removed from the datasets for the following experiments. For the SDUMLA database even the entire subject's data was removed if one of its samples was used for training. Thus, overall, 1340 out of 1440 images of the UTFVP dataset and 1512 of the 3816 images of the SDUMLA dataset were used.

Table 1 shows the corresponding recognition performance as obtained using the software in "FVC verification mode" [KU19]. To enable a subsequent analysis of sample images leading to incorrect template comparison results, the table also shows the number of false-positives (FP) and false-negatives (FN) template comparisons.

| Dataset | Algorithm | EER | FP | FN |
|---|---|---|---|---|
| UTFVP | MC | 0.42% | 3743 | 8 |
| | SIFT | 1.59% | 14511 | 29 |
| SDUMLA | MC | 9.51% | 108124 | 360 |
| | SIFT | 8.68% | 97440 | 333 |

Tab. 1: Overview on EER, count of FP and FN with the employed template comparison method.

It is clearly visible, that SDUMLA is the more difficult dataset. It is further interesting to note, that the number of FP is higher then the number of FN (while one would eventually expect the opposite). This observation suggests that the entropy of fingervein template data might not be as high as expected.

For calculating quality scores, we use the IQM described in Section 2, in particular the MATLAB implementations from the developers of NIQE and BRISQUE[3]. In all cases, we used (i) the default settings and (ii) trained with the fingervein data as described, for these IQM lower values are meant to indicate better quality. Additionally, we have re-implemented the vein quality measures as described in the Introduction: *Gradient*, *Contrast*, *Entropy* [Ya13] and their fusion in the *Triangular* norm scheme, the *Wang* metric, and a *Radon* transform based approach. For the latter schemes, higher values are meant to indicate better quality, while for the BRISQUE/NIQE based metrics lower values indicate better quality.

The following three experiments have been conducted:

1. The first experiment evaluates, if additional manually selected 50 low quality and 50 high quality samples, respectively, can be separated by an SVM-based classification process using vein quality employing 80% of the data for training and 20% for evaluation, repeated 1000 times, measuring classification accuracy in mean EER.

[3] All available from `http://live.ece.utexas.edu/research/quality/`

2. In the second experiment, we conduct a verification experiment using two different template and template comparison types, respectively, and record the false positive and false negative template comparisons at the EER setting. From the sample pairs involved in those false template comparisons, we compute the average quality and the average quality difference and compare these values to the quality values (mean, standard deviation $\sigma$) computed from the entire dataset.
3. The third experiment successively discards an increasing number of low quality sample images from the datasets (sorted according to quality, lowest quality discarded first) and compares the verification EER of these datasets exhibiting increasingly higher quality with the EER of the original ones.

The first experiment investigates if the considered quality measures are consistent in their assessment with respect to different manually selected high and low quality sample subsets, respectively. In the second experiment we test the hypothesis if sample images involved in false positive or false negative template comparisons exhibit a lower quality as compared to the average sample quality. The third experiment assesses if the quality measures actually serve their purpose: When filtering out poor quality samples, does the recognition accuracy improve ?

### 3.2 Experimental Results

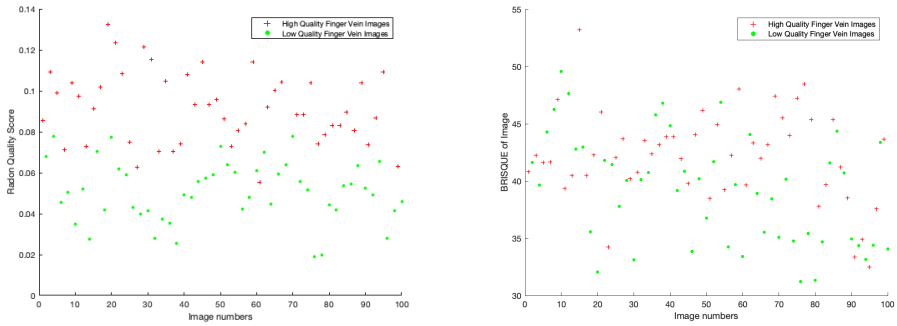
Table 2 displays the result of the first experiment, i.e. the classification of fingervein sample images according to the quality measures' values applied to two database subsets selected to be of high and low quality, respectively. At first sight it gets immediately clear that for the SDUMLA dataset not only biometric recognition is more difficult, but obviously also the discrimination of high and low quality sample images based on quality measures.

| | Gradient | Contrast | Entropy | Triangular | Radon | Wang |
|---|---|---|---|---|---|---|
| UTFVP | 4% | 12% | 44% | 10% | 8% | 10% |
| SDUMLA | 26% | 18% | 34% | 24% | 22% | 40% |
| | NIQE | Brisque | NIQE Train | Brisque Train | NIQE Full | Brisque Full |
| UTFVP | 16% | 60% | 21 % | 19% | 18% | 21% |
| SDUMLA | 20% | 64% | 9% | 3% | 19% | 5% |

Tab. 2: EER of classification using the quality measures as features on the selections of poor and high quality images of the two datasets (UTFVP, SDUMLA).

A further obvious observation is that the original BRISQUE measure (trained on natural images and classical distortions) is not at all able to separate high from low quality samples (50% EER is random guessing), also supported by Fig. 2.b which reveals a chaotic mixture of high and low quality data (green dots are manually selected low quality samples and red dots high quality ones). We also notice Entropy performing very poorly.

On the other hand, we observe the two trained BRISQUE variants to achieve the best result on SDUMLA data, but not performing too well on UTFVP. NIQE is clearly better than




(a) Radon metric on the UTFVP data (b) BRISQUE metric on the SDUMLA data

Fig. 2: Scatter plots of separation capabilities.

BRISQUE in its original version (indicating that original BRISQUE mainly suffers for the poor modelling of the low quality class), but does not improve at all under training with fingervein data for UTFVP and only for SDUMLA in case training is done with (separated) SDUMLA data. We also notice well performing earlier techniques in particular on UTFVP data, e.g. Gradient and Radon measures, which is again supported by the good separation of the two classes shown in Fig. 2.a for the Radon case.

Tables 3 - 6 display the results of the second experiment, i.e. the quality analysis of fingervein samples involved in false positive or false negative template comparison. Results are shown for both datasets and two template generation / comparison techniques, i.e. MC and SIFT. The aim of this investigation is to verify, if sample images involved in false comparison results exhibit worse quality as compared to average samples. The only quality measure where this is the case for all 4 settings is NIQE Full. For three settings (Tables 3 - 5) the following quality measures deliver this desired result: Gradient, NIQE, NIQE Train, and BRISQUE Full. Only Entropy exhibits this property for other three settings (Tables 4 - 6).

When looking at the difference figures for UTFVP data, most differences found are larger than the standard deviation across the entire data, but not always, and hardly significant so. So for these data, it cannot be clearly stated that the poor quality candidate pairs (as these are involved in incorrect comparisons) actually exhibit a higher quality difference than random pairs drawn from the data. There is no clear difference with respect to this behaviour among traditional and NSS-based quality measures, respectively.

For the SDUMLA results (Tables 5 and 6), we observe that the quality difference between sample pairs causing false negative comparisons is always smaller than the the quality difference between sample pairs causing false positive comparisons. For these data, this difference is also lower than the standard deviation of the entire data for most quality measures, but never larger. Thus, for SDUMLA, the expectations formulated (at least for

| | false positive | | false negative | | all samples | |
|---|---|---|---|---|---|---|
| | mean | diff. | mean | diff. | mean | $\sigma$ |
| Gradient | 0.49 | 0.2 | 0.53 | 0.17 | 0.6 | 0.18 |
| Contrast | 0.66 | 0.15 | 0.75 | 0.09 | 0.72 | 0.13 |
| Entropy | 0.63 | 0.16 | 0.76 | 0.09 | 0.7 | 0.14 |
| Triangular | 0.27 | 0.16 | 0.35 | 0.17 | 0.35 | 0.16 |
| Radon | 0.06 | 0.02 | 0.07 | 0.03 | 0.07 | 0.02 |
| Wang | 0.20 | 0.03 | 0.21 | 0.02 | 0.21 | 0.03 |
| NIQE | 5.9 | 0.88 | 6.4 | 0.92 | 5.83 | 0.79 |
| NIQE Train | 10.9 | 5.32 | 14.8 | 8.6 | 10.4 | 5.58 |
| NIQE Full | 7.5 | 3.6 | 9.47 | 4.12 | 6.5 | 3.53 |
| Brisque | 39.2 | 6.4 | 39.9 | 9.23 | 41.4 | 5.3 |
| Brisque Train | 40.2 | 19.7 | 49.3 | 20.2 | 36.5 | 17.6 |
| Brisque Full | 53.9 | 33.1 | 53.6 | 25.4 | 39.6 | 29.5 |

Tab. 3: Analysis False Positives/False Negatives of UTFVP with MC template comparison.

| | false positive | | false negative | | all samples | |
|---|---|---|---|---|---|---|
| | mean | diff. | mean | diff. | mean | $\sigma$ |
| Gradient | 0.57 | 0.21 | 0.41 | 0.14 | 0.6 | 0.18 |
| Contrast | 0.69 | 0.14 | 0.63 | 0.09 | 0.72 | 0.13 |
| Entropy | 0.67 | 0.15 | 0.68 | 0.07 | 0.7 | 0.14 |
| Triangular | 0.33 | 0.18 | 0.24 | 0.09 | 0.35 | 0.16 |
| Radon | 0.07 | 0.02 | 0.07 | 0.02 | 0.07 | 0.02 |
| Wang | 0.21 | 0.03 | 0.20 | 0.03 | 0.21 | 0.03 |
| NIQE | 5.98 | 0.88 | 6.17 | 0.90 | 5.83 | 0.79 |
| NIQE Train | 11.3 | 6.05 | 14.9 | 8.9 | 10.4 | 5.58 |
| NIQE Full | 7.32 | 3.95 | 10.3 | 5.3 | 6.5 | 3.53 |
| Brisque | 40.8 | 6.4 | 37.4 | 8.8 | 41.4 | 5.3 |
| Brisque Train | 39.5 | 20.2 | 48.3 | 15.3 | 36.5 | 17.6 |
| Brisque Full | 46.9 | 34.1 | 60.6 | 22.7 | 39.6 | 29.5 |

Tab. 4: Analysis False Positives/False Negatives of UTFVP with SIFT template comparison.

one type of difference) do not turn out to be correct. There is no clear difference with respect to this behaviour among traditional and NSS-based quality measure, respectively.

Summarising the results of Experiment 2, we have found that the NSS-based quality measures do a good job in assigning a lower quality to sample pairs involved in incorrect comparison results (thus correspond to the expectations one has for a sensible quality measure), but concerning the difference in quality observed between the sample images of such pairs, no quality measure indicates that a large quality difference is the reason for the incorrect results.

| | false positive | | false negative | | all samples | |
|---|---|---|---|---|---|---|
| | mean | diff. | mean | diff. | mean | $\sigma$ |
| Gradient | 0.55 | 0.12 | 0.57 | 0.07 | 0.58 | 0.14 |
| Contrast | 0.78 | 0.07 | 0.78 | 0.04 | 0.80 | 0.09 |
| Entropy | 0.78 | 0.07 | 0.79 | 0.04 | 0.81 | 0.08 |
| Triangular | 0.37 | 0.12 | 0.40 | 0.06 | 0.42 | 0.14 |
| Radon | 0.02 | 0.02 | 0.02 | 0.02 | 0.03 | 0.02 |
| Wang | 0.24 | 0.04 | 0.22 | 0.02 | 0.23 | 0.04 |
| NIQE | 6.40 | 0.95 | 6.4 | 0.76 | 6.3 | 0.86 |
| NIQE Train | 11.4 | 4.13 | 11.5 | 3.06 | 10.8 | 3.8 |
| NIQE Full | 6.51 | 1.78 | 7.24 | 1.72 | 6.3 | 2.22 |
| Brisque | 39.6 | 5.59 | 41.2 | 3.8 | 40.6 | 4.9 |
| Brisque Train | 70.7 | 20.6 | 68.2 | 17.1 | 68.7 | 18.7 |
| Brisque Full | 63.4 | 29.3 | 62.7 | 25.0 | 60.3 | 25.9 |

Tab. 5: Analysis False Positives/False Negatives of SDUMLA with MC template comparison.

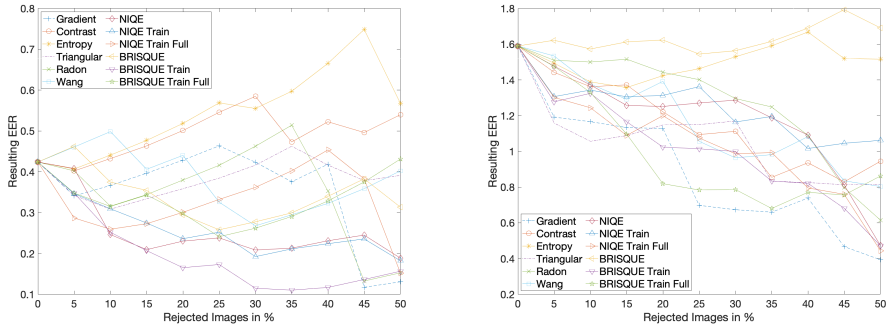
| | false positive | | false negative | | all samples | |
|---|---|---|---|---|---|---|
| | mean | diff. | mean | diff. | mean | $\sigma$ |
| Gradient | 0.58 | 0.14 | 0.54 | 0.07 | 0.58 | 0.14 |
| Contrast | 0.80 | 0.09 | 0.76 | 0.05 | 0.80 | 0.09 |
| Entropy | 0.78 | 0.08 | 0.78 | 0.05 | 0.81 | 0.08 |
| Triangular | 0.41 | 0.14 | 0.37 | 0.07 | 0.42 | 0.14 |
| Radon | 0.02 | 0.02 | 0.02 | 0.02 | 0.03 | 0.02 |
| Wang | 0.23 | 0.04 | 0.22 | 0.02 | 0.23 | 0.04 |
| NIQE | 6.27 | 0.96 | 6.4 | 0.77 | 6.3 | 0.86 |
| NIQE Train | 10.7 | 4.22 | 12.2 | 3.18 | 10.8 | 3.8 |
| NIQE Full | 6.4 | 2.18 | 7.4 | 1.76 | 6.3 | 2.22 |
| Brisque | 40.8 | 5.5 | 40.0 | 4.32 | 40.6 | 4.9 |
| Brisque Train | 68.3 | 21.4 | 66.0 | 17.5 | 68.7 | 18.7 |
| Brisque Full | 59.3 | 29.4 | 63.5 | 22.0 | 60.3 | 25.9 |

Tab. 6: Analysis False Positives/False Negatives of SDUMLA with SIFT template comparison.

The results of Experiment 1 and Experiment 2 already indicate, that the introduced NSS-based quality metrics do a reasonably good job in predicting the actual quality of fingervein quality samples. However, so far we have not provided proof that rejecting low quality samples actually improves recognition performance, which is the most important application setting for biometric quality measures. Experiment 3 directly looks at the corresponding behaviour: After sorting the sample images according to their respective quality, we successively remove a share of the samples (lowest quality first) from the datasets and conduct verification experiments on the remaining dataset.

Figs. 3 and 4 report the main results of this work. We plot the achieved verification EER against the share of low quality rejected sample images. In this setup, we expect monoton-

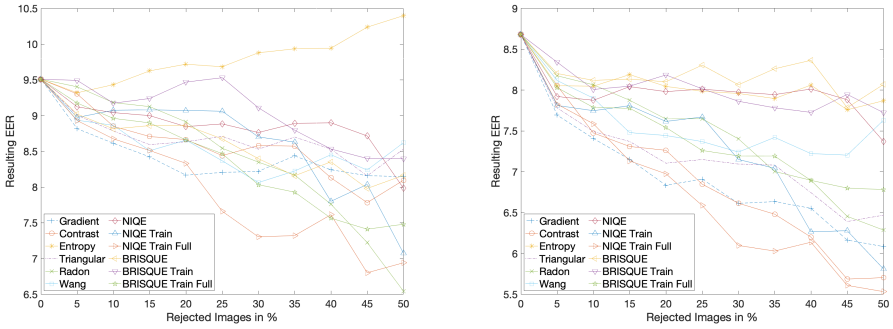
ically decreasing EER for an increasing share of rejected low-quality samples in case the considered quality measure serves its purpose well.




(a) MC (b) SIFT

Fig. 3: EER trend with increasing rate of rejected images on UTFVP dataset.

Fig. 3 shows the results of the UTFVP data. Two things get immediately clear: Some quality measures do not work as expected, and the obtained results do depend on the template representation used. Entropy turns out to perform very poor overall (i.e. the EER is actually increasing), and the same is true for BRISQUE considering SIFT (Fig. 3.b). For MC templates, the three best suited quality measures are BRISQUE Train, NIQE Train, and NIQE, while for SIFT templates the top measures are BRISQUE Train, Gradient, and NIQE Full / Radon (when considering monotonicity of EER decrease).




(a) MC (b) SIFT

Fig. 4: EER trend with increasing rate of rejected images on SDUMLA dataset.

Fig. 4 displays the SDUMLA results. We notice a significant difference to the UTFVP results, in particular for MC templates. For SDUMLA data, almost all quality measures exhibit a more or less monotonic EER decrease, while for UTFVP data several quality measures showed a partially increasing EER result. Again, Entropy and BRISQUE do not behave as expected, and again we find a template representation dependent result which quality measures turn out to be best. For MC templates (Fig. 4.a), the three best suited

quality measures are Radon, BRISQUE Full, and NIQE Full, while for SIFT templates (Fig. 4.b), the top three are NIQE Full, Contrast, and NIQE Train / Gradient.

One might argue, that a decrease in overall dataset size will cause a non-constant EER in any case - however, we conduct a relative comparison among different quality measures, and some clearly outperform others in terms of what we expect from a decent quality measure, and further, results in [Fr20] indicate that the EER computed from verification scores does not change significantly for varying dataset sizes.

## 4 Conclusion and Future Work

We have found BRISQUE and NIQE not to be suited as fingervein quality measures when used pretrained on common images and classical distortions. On the other hand, when trained on high and low quality fingervein sample data, both approaches exhibit the desired properties and provide better results as compared to classical fingervein sample quality measures in most settings. However, we have found that the optimal quality measure depends on the considered dataset (with its distinct "distortion" types) and the applied template representation scheme (as e.g. obviously a poor quality sample for MC does not have to be low quality for SIFT and vice versa in some cases).

In future work we aim to train BRISQUE and NIQE with high / low quality samples as identified in verification experiments (as opposed to the employed approach based on human assessment) and we will compare the results to other learning-based fingervein quality measures.

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