`dermalog+0003`

DERMALOG Identification Systems GmbH

Friction Ridge Image and Features (FRIF) Technology Evaluation (TE): **Exemplar One-to-Many (E1N)**

Technical performance report of automated fingerprint feature extraction and search software.

Last Updated: 23 January 2026, 10:34:26 EST

Contents

Not Human Subjects Research
The National Institute of Standards and Technology's Research Protections Office reviewed the protocol for this project and determined it is "not human subjects research" as defined in 15 CFR 27, the Common Rule for the Protection of Human Subjects.

NIST
NATIONAL INSTITUTE OF STANDARDS AND TECHNOLOGY
U.S. DEPARTMENT OF COMMERCE

1 Participation Information

1.1 Names

Information in this section was provided ***by DERMALOG Identification Systems GmbH*** *and was* ***not*** *verified by NIST.*

- **Participant Name:** DERMALOG Identification Systems GmbH
- **FRIFTE E1N Identifier:** `dermalog+0003`
- **Country of Agreement Signatory:** Germany
- **Feature Extractor:**
  - **Marketing Name:** dermalog
  - **CBEFF Product Owner:** `0x000D`
- **Search:**
  - **Marketing Name:** dermalog
  - **CBEFF Product Owner:** `0x000D`

1.2 Dates

- **Participation Agreement Date:** 29 December 2025
- **First Submission Date:** 29 December 2025 (as version `0001`)
- **Final Submission Date:** 21 January 2026 (as version `0003`)
- **Final Validation Date:** 21 January 2026
- **Completion Date:** 23 January 2026
- **Report Last Updated Date:** 23 January 2026, 10:34:26 EST

1.3 Supplied Files

Testing was completed using *Ubuntu 24.04.3 LTS*. Libraries provided with `dermalog+0003` are listed in Table 1.

Table 1: Information regarding library files provided as part of `dermalog+0003`.

Filename	MD5 Checksum	Size (MB)
libfrifte_e1n_dermalog_0003.so	`c31086f9d705eecb418d3fa4a1025ffa`	172.3

2 Timing Sample

A fixed sample of images was randomly selected from FRIFTE E1N datasets. The sample was used to assess whether an implementation adheres to the computational speed requirements from the FRIFTE E1N Test Plan. These values are chosen in such a way that allows the implementation flexibility while allowing NIST to complete the evaluation in a reasonable amount of time. If an implementation exceeds the maximum allowable duration, the participant will be asked to reduce the processing time of their software prior to NIST completing the evaluation. As such, *all* published FRIFTE E1N submissions conform to the published speed requirements.

2.1 Processor Details

All measurements in this section were performed on a machine equipped with Intel Xeon Gold 6254 Central Processing Units (CPUs). Each CPU features a 3.10 GHz base frequency and 24.75 MB of cache. Timing tests are all **single threaded**—implementations are not permitted to use more than one CPU core during any function measured here. As such, these values can be used to understand expected scaled performance. NIST testing code embraces the single-threaded nature of implementations to `fork` processes during other non-timed portions of this evaluation, allowing participants to write thread-unsafe code while still using NIST resources to their maximum efficiency. This CPU supports executing several families of processor intrinsic functions, including AVX-512[1].

---

[1] The complete set of advertised CPU flags is `fpu, vme, de, pse, tsc, msr, pae, mce, cx8, apic, sep, mtrr, pge, mca, cmov, pat, pse36, clflush, dts, acpi, mmx, fxsr, sse, sse2, ss, ht, tm, pbe, syscall, nx, pdpe1gb, rdtscp, lm, constant_tsc, art, arch_perfmon, pebs, bts, rep_good, nopl, xtopology, nonstop_tsc, cpuid, aperfmperf, pni, pclmulqdq, dtes64, monitor, ds_cpl, vmx, smx, est, tm2, ssse3, sdbg, fma, cx16, xtpr, pdcm, pcid, dca, sse4_1, sse4_2, x2apic, movbe, popcnt, tsc_deadline_timer, aes, xsave, avx, f16c, rdrand, lahf_lm, abm, 3dnowprefetch, cpuid_fault, epb, cat_l3, cdp_l3, invpcid_single, intel_ppin, ssbd, mba, ibrs, ibpb, stibp, ibrs_enhanced, tpr_shadow, vnmi, flexpriority, ept, vpid, ept_ad, fsgsbase, tsc_adjust, bmi1, avx2, smep, bmi2, erms, invpcid, cqm, mpx, rdt_a, avx512f, avx512dq, rdseed, adx, smap, clflushopt, clwb, intel_pt, avx512cd, avx512bw, avx512vl, xsaveopt, xsavec, xgetbv1, xsaves, cqm_llc, cqm_occup_llc, cqm_mbm_total, cqm_mbm_local, dtherm, ida, arat, pln, pts, pku, ospke, avx512_vnni, md_clear, flush_l1d, arch_capabilities`

2.2 Composition

Table 2 shows the quantity of each type of fingerprint record comprising the Timing Sample, along with the maximum allowable feature extraction time permitted by FRIFTE E1N for that type of record.

Table 2: Number of records of each generalized finger position combinations comprising the Timing Sample, along with the maximum allowable feature extraction time for that type of record.

Template Type	Description	Image Quantity	Maximum Duration (s)	Record Quantity
Probe	Left Index (Plain)	1	3	1 000
	Right Index (Plain)	1	3	1 000
	Left + Right Index (Plain)	2	6	1 000
	Left Slap	1	12	1 000
	Right Slap	1	12	1 000
	Left + Right Slap	2	24	1 000
	Identification Flats	3	30	1 000
	Ten Fingers (Plain)	4	30	1 000
	Ten Fingers (Roll)	10	30	1 000
Reference	Left + Right Index (Plain)	2	6	1 000
	Identification Flats	3	30	1 000
	Ten Fingers (Plain)	4	30	1 000
	Ten Fingers (Roll)	10	30	1 000

2.3 Feature Extraction

Features were extracted from all images depicted in Table 2 and stored in templates.

2.3.1 Template Creation Duration

Table 3 shows the distribution of template creation durations in seconds for templates created from the Timing Sample. Failures of any kind reported during template generation *are* included.

Table 3: Duration of template creation for the Timing Sample, in seconds.

Template Type	Description	Minimum	25%	Median	Mean	75%	Maximum	Failures	API Max
Probe	Left Index (Plain)	0.0	0.2	0.2	0.2	0.2	0.3	1	3
	Right Index (Plain)	0.1	0.2	0.2	0.2	0.2	0.3	2	3
	Left + Right Index (Plain)	0.2	0.4	0.4	0.4	0.4	0.7	0	6
	Left Slap	0.4	0.8	0.8	0.9	0.9	1.4	0	12
	Right Slap	0.3	0.8	0.8	0.9	0.9	1.3	0	12
	Left + Right Slap	1.0	1.6	1.7	1.7	1.8	2.7	0	24
	Identification Flats	1.6	2.1	2.3	2.3	2.5	3.6	0	30
	Ten Fingers (Plain)	1.1	2.4	2.6	2.6	2.8	3.5	0	30
	Ten Fingers (Roll)	2.1	4.6	5.1	5.1	5.7	8.3	0	30
Reference	Left + Right Index (Plain)	0.2	0.4	0.4	0.4	0.5	0.6	0	6
	Identification Flats	1.2	2.1	2.3	2.3	2.5	3.9	0	30
	Ten Fingers (Plain)	1.3	2.5	2.6	2.6	2.8	3.4	0	30
	Ten Fingers (Roll)	2.6	4.8	5.3	5.3	5.8	8.6	0	30

2.3.2 Template Size

Table 4 shows the distribution of sizes of templates, exclusive of when `dermalog+0003` indicated a failure.

Table 4: Template size summary statistics in kB for the Timing Sample.

Template Type	Description	Minimum	25%	Median	Mean	75%	Maximum	Failures
Probe	Left Index (Plain)	1.8	2.0	2.0	2.0	2.1	2.4	1
	Right Index (Plain)	1.8	2.0	2.0	2.0	2.1	2.3	2
	Left + Right Index (Plain)	1.8	3.9	4.0	4.0	4.1	4.7	0
	Left Slap	1.7	7.8	8.0	8.0	8.3	9.0	0
	Right Slap	1.8	7.8	8.0	8.0	8.2	9.4	0
	Left + Right Slap	5.3	15.6	16.0	16.0	16.4	18.4	0
	Identification Flats	9.1	20.0	20.5	20.4	21.0	24.4	0
	Ten Fingers (Plain)	10.0	20.4	21.0	20.9	21.6	23.6	0
	Ten Fingers (Roll)	16.3	23.5	24.8	24.8	26.1	30.9	0
Reference	Left + Right Index (Plain)	2.0	3.9	4.0	4.0	4.2	4.6	0
	Identification Flats	13.0	19.8	20.3	20.3	20.9	23.6	0
	Ten Fingers (Plain)	3.6	20.4	21.1	20.9	21.6	24.1	0
	Ten Fingers (Roll)	18.8	23.8	25.1	25.1	26.2	31.2	0

2.4 Enrollment Database

Reference templates are combined into a participant-defined database structure for optimal searching.

While the participant-defined enrollment database should contain information about all references, the space consumed by the enrollment database may be significantly different than the space consumed by concatenation of all individual reference templates. Additionally, the participant-defined database structure may be a structure unique for this evaluation and not necessarily similar to a structure deployed operationally. The sum of sizes for both types of reference storage are shown in Table 5 along with the difference between the two, for the various enrollment databases generated as part of the Timing Sample dataset.

The *Templates* column is computed by summing the buffer size returned by the `createTemplate()` API function. The *Database* column is computed by recursively summing the file sizes (as determined by the `stat()` syscall) of all files remaining in the database directory after returning from the `createEnrollmentDatabase()` API function.

Table 5: Sum of sizes of all reference templates in the Timing Sample dataset, the size needed when those templates are stored in a proprietary enrollment database, and the difference between the two, in GB.

Database Contents	Records	Templates	Database	Δ
Left + Right Index (Plain)	100 000	0.4	0.4	0.0
Left + Right Index (Plain)	1 600 000	6.6	6.3	-0.3
Identification Flats	3 000 000	62.7	61.3	-1.4
Ten Fingers (Plain)	5 000 000	106.5	108.4	1.9
Ten Fingers (Roll)	5 000 000	127.6	166.3	38.8

2.5 Search

The probe templates generated in Table 2 were searched against the enrollment databases described in Subsection 2.4. The results presented in Subsection 2.5 are based on the measurements made during those searches.

2.5.1 Search Duration

Table 6 shows the amount of time elapsed during searches of the probe sets when searching against the enrollment databases described in Subsection 2.4. While unsuccessful searches expend operator time, they are not included in this metric, because search failures typically occur instantaneously (e.g., a template indicates that a probe was of too poor quality to search), which can artificially lower the average search time.

FRIFTE E1N defines maximum average search durations for participants based on the number of subjects in the enrollment database. Due to the potential for extended runtimes, NIST may choose to allow some discretion in the enforcement of maximum search durations during times of high demand for compute resources. For example, if a maximum average search duration was 200 seconds, but after completing all searches, the average search duration was 210 seconds, it may be prudent to continue the evaluation, since a resubmission may require regeneration of millions of templates and several thousand repeated searches.

Table 6: Search durations from the Timing Sample dataset, in seconds.

Probes	Mated?	Enrollment Database	≈ Database Size	Min	25%	Median	Mean	75%	Maximum	API Max	Failures	Searches
Left Index (Plain)	False	Left + Right Index (Plain)	100 000	0.1	0.1	0.1	0.1	0.1	0.2	4.0	1	1 000
	True			0.1	0.1	0.1	0.1	0.1	0.4		1	
Right Index (Plain)	False			0.1	0.1	0.1	0.1	0.1	0.1		2	
	True			0.1	0.1	0.1	0.1	0.1	0.2		2	
Left + Right Index (Plain)	False		1 600 000	1.0	1.0	1.0	1.0	1.0	1.8	64.3	0	
	True			1.0	1.0	1.0	1.0	1.0	1.6		0	
Left Slap	False	Identification Flats	3 000 000	2.6	3.1	3.1	3.1	3.1	3.2	120.6	0	
	True			2.5	3.1	3.1	3.1	3.1	5.2		0	
Right Slap	False			2.4	3.0	3.0	3.0	3.1	3.2		0	
	True			2.6	3.1	3.1	3.1	3.1	5.1		0	
Left + Right Slap	False			3.4	4.7	4.7	4.7	4.8	5.0		0	
	True			4.0	4.8	4.8	4.8	4.8	7.7		0	
Identification Flats	False			3.5	4.9	4.9	4.9	4.9	5.0		0	
	True			4.2	4.9	5.0	5.0	5.0	7.8		0	
Ten Fingers (Plain)	False	Ten Fingers (Plain)	5 000 000	5.8	8.3	8.3	8.3	8.4	12.0	201.0	0	
	True			7.9	8.4	8.5	8.5	8.5	13.6		0	
	False	Ten Fingers (Roll)		6.8	9.9	9.9	9.9	10.0	22.7		0	
	True			9.5	10.0	10.0	10.1	10.1	18.7		0	
Ten Fingers (Roll)	False			9.3	9.5	9.5	9.6	9.6	18.0		0	
	True			9.5	9.6	9.7	9.7	9.7	16.2		0	

3 Metrics

3.1 Location

The FRIF TE E1N application programming interface (API) can require that implementations include the finger position for a candidate on the candidate list. This is particularly useful when the probe template does not include a finger position. When the implementation is invoked in this way, search accuracy metrics are reported in terms of a *location*—**region** or **subject**.

- **Region**: The correct region of the correct subject was returned.
  - For probes sourced from a distal phalanx, the correct position 1–10 shall be returned.
  - For probes sourced from a palm or a non-distal phalanx, the most localized region shall be returned. Some palm regions may be interchangeable based on the exemplars provided (e.g., a palm probe's source could reasonably be seen in a lower palm, hypothenar, and writer's palm exemplar). Credit is given for **Region** in this case.
- **Subject**: Any position from the correct subject is returned. This is designed to reward the situation where an implementation cannot ascertain the most localized region from the set of exemplars enrolled and may indicate segmentation error.

3.1.1 Notes

- Multi-position probes are never requested to return a finger position.

3.2 Detection Error Tradeoff (DET)

The Detection Error Tradeoff (DET) plots in this document show the tradeoff between the False Positive Identification Rate (FPIR) and False Negative Identification Rate (FNIR) when searching probes against an enrollment database. For mated searches (used to compute FNIR), a single mated identity for each probe was present in the enrollment database. For non-mated searches (used to compute FPIR), there was no mate for the probe in the enrollment database.

3.2.1 Notes

- The requested size of the candidate list was always 100 subjects.
- The set of non-mated similarity scores come from the highest score when searching probes without a mate present in the enrollment database.
- The set of mated similarity scores comes from searches of probes where the mate is present in the enrollment database and the algorithm successfully found the mate. The mate may appear at *any* rank in the candidate list.
- Due to the quantity of searches, a sample of scores across the entire range of mated and non-mated scores were used to produce DET values.

3.3 Cumulative Match Characteristic (CMC)

The Cumulative Match Characteristic (CMC) plots in this document show the FNIR without respect for similarity score when searching probes against an enrollment database where a single mated identity for each probe was present. A description of the non-mated subject records represented in an enrollment database is documented in subsequent sections.

3.3.1 Notes

- The metric *hit rate* is equivalent to 1 − miss rate, or 1 − FNIR. For example, an FNIR of 0.1 indicates a hit rate of 0.9 (i.e., 90%).

4 FpVTE 2012—Class A

Results in this section involve plain impression index fingers. Probes containing left index, right index, and both index fingers were searched against an enrollment database consisting of both index fingers. Individual index finger probes were searched against an enrollment database of 100 000 subjects, while probes containing both index fingers are searched against an enrollment database of 1 600 000 subjects.

The datasets in this section are equivalent to those used in NIST FpVTE 2012 (Class A). Detailed information about FpVTE 2012 can be found in NIST IR 8034.

Notes:

- No examiner extended feature set data was provided with the images.

4.1 Template Generation

The approximate total number of index finger records that underwent template generation along with a tally of records that failed to process are shown in Table 7.

Table 7: Summary of template generation for FpVTE 2012—Class A.

Image Contents	Template Type	Failure to Extract	≈Total
Left Index (Plain)	Probe	65	30 000
Right Index (Plain)		70	30 000
Left + Right Index (Plain)		14	30 000
	Reference	12	100 000
		129	1 600 000

4.2 Both Index Fingers

Probe templates with features extracted from 30 000 pairs of index fingers were searched against an enrollment database of 1 600 000 subjects. Each probe template was generated by a single function call providing `dermalog+0003` two separate images (i.e., left index and right index). Likewise, each subject template incorporated into the database was generated by a single function call providing `dermalog+0003` two separate images (i.e., left index and right index). Approximately one-third of the probes had a corresponding mate in the enrollment database. Each subject in the enrollment database had only left and right index fingers represented.

4.2.1 DET

The DET plots in Figure 1 show the tradeoff of errors of `dermalog+0003` when searching pairs of index fingers from FpVTE 2012—Class A against enrollment database of 1 600 000 subjects where, for approximately one-third of the probes, a single mated identity consisting of left and right index fingers was present. Tabular versions of FNIR at select FPIR can be viewed in Table 8.

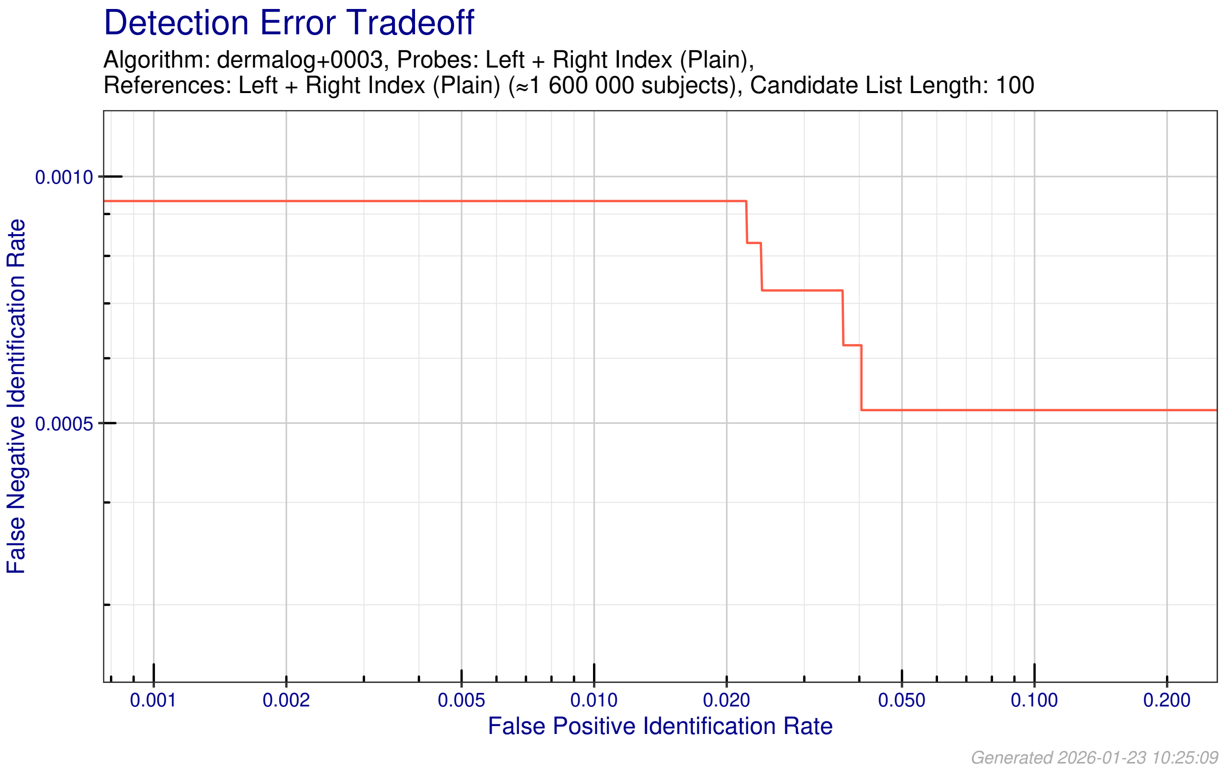

Figure 1: DET when searching both index fingers against an enrollment database of both index fingers.

Table 8: FNIR values from the DET plotted in Figure 1.

Probe Content	FPIR ≤ 0.001	FPIR ≤ 0.005	FPIR ≤ 0.01
Left + Right Index (Plain)	0.0009	0.0009	0.0009

Table 9: Similarity score thresholds from the DET plotted in Figure 1.

Probe Content	FPIR ≤ 0.001	FPIR ≤ 0.005	FPIR ≤ 0.01
Left + Right Index (Plain)	38.2995	33.5576	31.5425

4.2.2 CMC

The CMC plots in Figure 2 show the FNIR of `dermalog+0003` when searching pairs of index fingers from FpVTE 2012—Class A against enrollment database of 1 600 000 subjects where, for approximately one-third of the probes, a single mated identity consisting of left and right index fingers was present. Tabular versions of FNIR at select ranks can be viewed in Table 10.

Figure 2: CMC when searching both index fingers against an enrollment database of both index fingers.

Table 10: FNIR values from CMC plotted in Figure 2.

Probe Content	Rank 1	Rank ≤ 2	Rank ≤ 5	Rank ≤ 10	Rank ≤ 50	Rank ≤ 100
Left + Right Index (Plain)	0.0008	0.0006	0.0005	0.0005	0.0005	0.0005

5 FpVTE 2012—Class B

Results in this section involve variations of *Identification Flat* captures (i.e., right slap, left slap, and thumb slaps, otherwise known as finger positions 13–15 or a *4-4-2* configuration). Probes of right slap, left slap, right *and* left slap, and a complete Identification Flat were searched against an enrollment database of 3 000 000 subjects containing all ten fingers in an Identification Flat configuration.

The datasets in this section are equivalent to those used in NIST FpVTE 2012 (Class B). Detailed information about FpVTE 2012 can be found in NIST IR 8034.

Notes:

- No examiner extended feature set data was provided with the images.
- Slap segmentation, if required, was performed by `dermalog+0003`.

5.1 Template Generation

The approximate total number of records that underwent template generation along with a tally of records that failed to process are shown in Table 11. Each template was generated by a single function call providing `dermalog+0003` all of the listed image types.

Table 11: Summary of template generation for FpVTE 2012—Class B.

Image Contents	Template Type	Failure to Extract	≈Total
Left Slap	Probe	1	30 000
Right Slap		4	30 000
Left + Right Slap		0	30 000
Identification Flats		0	30 000
	Reference	1	3 000 000

5.2 Search

The probe templates from Table 11 were searched against an enrollment database of 3 000 000 subjects containing images as specified in the reference template row of Table 11. Approximately one-third of the probes had a corresponding mate in the enrollment database.

5.2.1 DET

The DET plot in Figure 3 show the tradeoff of errors of `dermalog+0003` when searching each probe set from FpVTE 2012—Class B against enrollment database of 3 000 000 subjects where, for approximately one-third of the probes, a single mated identity consisting of all ten fingers in an Identification Flat configuration was present. Tabular versions of FNIR at select FPIR can be viewed in Table 12.

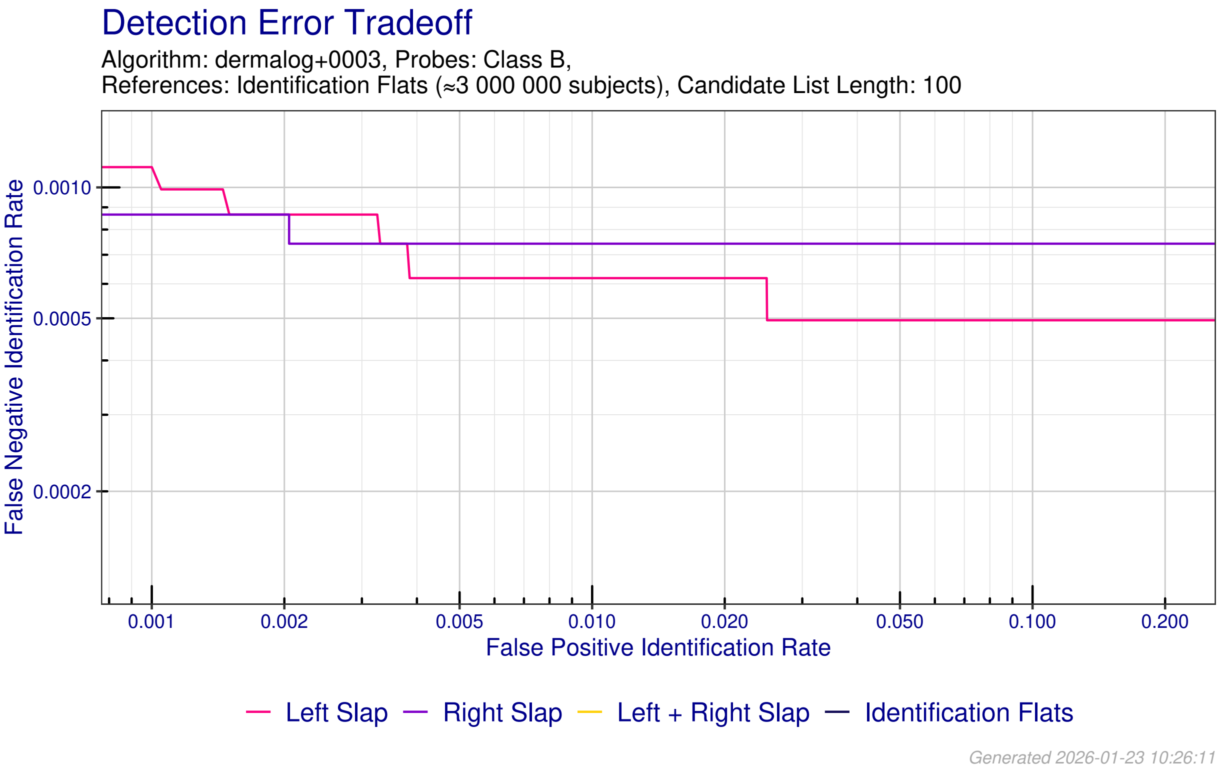

Figure 3: DET when searching probe templates from FpVTE 2012—Class B against an enrollment database of Identification Flats.

Table 12: FNIR values from the DET plotted in Figure 3.

Probe Content	FPIR ≤ 0.001	FPIR ≤ 0.005	FPIR ≤ 0.01
Left Slap	0.0011	0.0006	0.0006
Right Slap	0.0009	0.0007	0.0007
Left + Right Slap	0.0000	0.0000	0.0000
Identification Flats	0.0000	0.0000	0.0000

5.2.2 CMC

The CMC plot in Figure 4 show the FNIR of `dermalog+0003` when searching each probe set from FpVTE 2012—Class B against enrollment database of 3 000 000 subjects where, for approximately one-third of the

Table 13: Similarity score thresholds from the DET plotted in Figure 3.

Probe Content	FPIR ≤ 0.001	FPIR ≤ 0.005	FPIR ≤ 0.01
Left Slap	46.5150	37.7699	34.1431
Right Slap	49.3068	36.8211	33.5424
Left + Right Slap	52.6720	38.7531	33.1579
Identification Flats	54.2406	36.8767	30.3745

probes, a single mated identity consisting of all ten fingers in an Identification Flat configuration was present. Tabular versions of FNIR at select ranks can be viewed in Table 14.

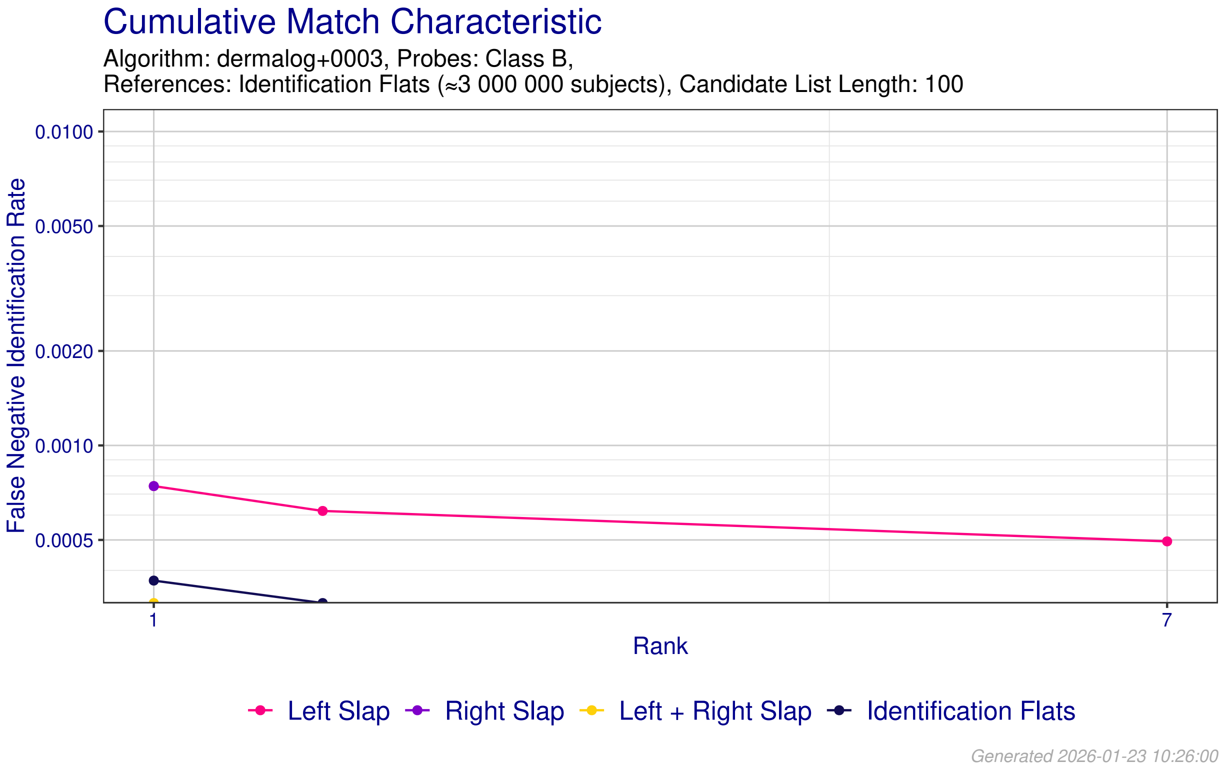

Figure 4: CMC when searching probe templates from FpVTE 2012—Class B against an enrollment database of Identification Flats.

Table 14: FNIR values from CMC plotted in Figure 4.

Probe Content	Rank 1	Rank ≤ 2	Rank ≤ 5	Rank ≤ 10	Rank ≤ 50	Rank ≤ 100
Left Slap	0.0007	0.0006	0.0006	0.0005	0.0005	0.0005
Right Slap	0.0007	0.0007	0.0007	0.0007	0.0007	0.0007
Left + Right Slap	0.0000	0.0000	0.0000	0.0000	0.0000	0.0000
Identification Flats	0.0004	0.0000	0.0000	0.0000	0.0000	0.0000

6 FpVTE 2012—Class C

Results in this section involve different impression types with all ten fingers. When plain impression fingerprints were used, the configuration contained left slap, right slap, and left and right thumbs (i.e., finger positions 11–14, or a *4-4-1-1* configuration[2].), as both probes and references. Probes were searched against enrollment databases of 5 000 000 subjects containing all ten fingers.

The datasets in this section are equivalent to those used in NIST FpVTE 2012 (Class C). Detailed information about FpVTE 2012 can be found in NIST IR 8034.

Notes:

- No examiner extended feature set data was provided with the images.
- Slap segmentation, if required for the plain impressions, was performed by `dermalog+0003`.

6.1 Template Generation

The approximate total number of records that underwent template generation along with a tally of records that failed to process are shown in Table 15. Each template was generated by a single function call providing `dermalog+0003` all of the listed image types.

Table 15: Summary of template generation for FpVTE 2012—Class C.

Image Contents	Template Type	Failure to Extract	≈Total
Ten Fingers (Plain)	Probe	0	30 000
Ten Fingers (Roll)		0	30 000
Ten Fingers (Plain)	Reference	630	5 000 000
Ten Fingers (Roll)		109	5 000 000

---

[2] The FRIF TE API remaps finger positions 11 and 12 to 1 and 6, respectively

6.2 Search

The probe templates from Table 15 were searched against two enrollment databases of 5 000 000 subjects containing images as specified in the reference template rows of Table 15. Approximately one-third of the probes had a corresponding mate in the enrollment database.

6.2.1 DET

The DET plot in Figure 5 shows the tradeoff of errors of `dermalog+0003` when searching probe templates from FpVTE 2012—Class C against enrollment databases of 5 000 000 subjects created from the reference templates from FpVTE 2012—Class C where, for approximately one-third of the probes, a single mated identity was present. Tabular versions of FNIR at select FPIR can be viewed in Table 16.

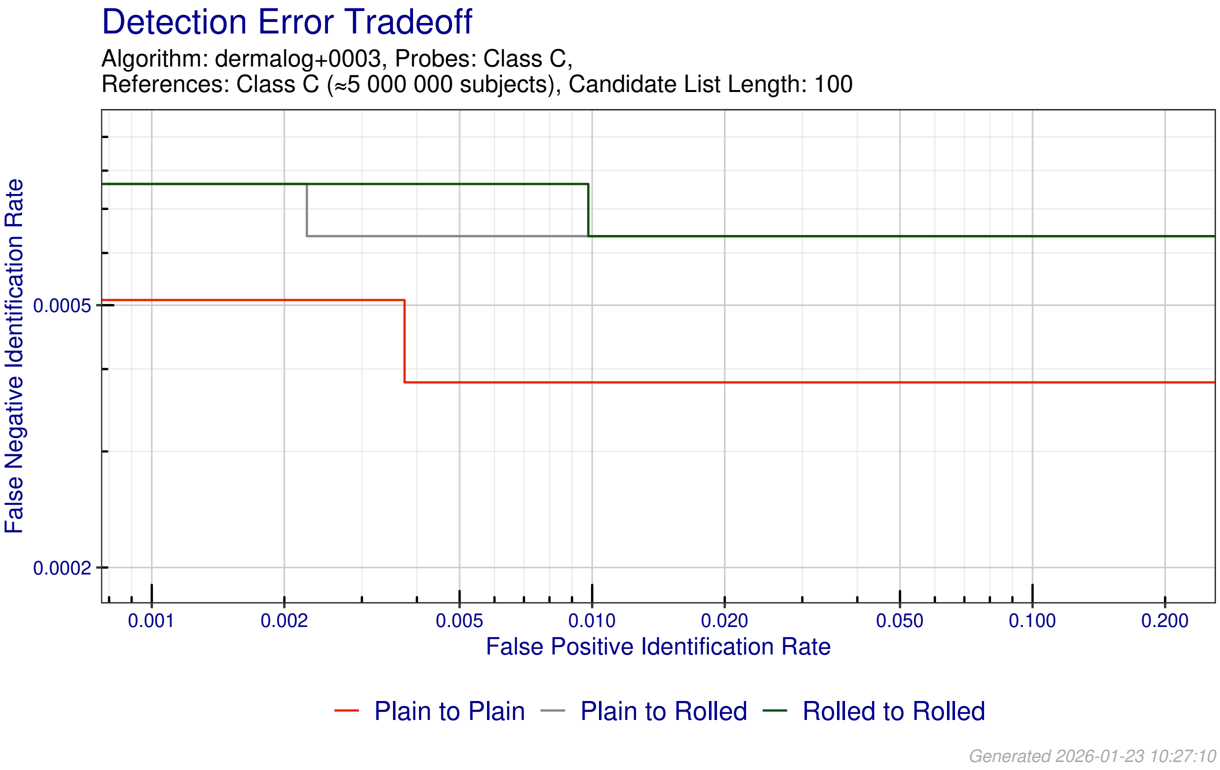

Figure 5: DET when searching probe templates from FpVTE 2012—Class C against a enrollment databases generated from reference templates from FpVTE 2012—Class C.

Table 16: FNIR values from the DET plotted in Figure 5.

Probe Content	Reference Content	FPIR ≤ 0.001	FPIR ≤ 0.005	FPIR ≤ 0.01
Ten Fingers (Plain)	Ten Fingers (Plain)	0.0005	0.0004	0.0004
Ten Fingers (Plain)	Ten Fingers (Roll)	0.0008	0.0006	0.0006
Ten Fingers (Roll)	Ten Fingers (Roll)	0.0008	0.0008	0.0006

6.2.2 CMC

The CMC plot in Figure 6 show the FNIR of `dermalog+0003` when searching probe templates from FpVTE 2012—Class C against enrollment databases of 5 000 000 subjects created from the reference templates from

Table 17: Similarity score thresholds from the DET plotted in Figure 5.

Probe Content	Reference Content	FPIR ≤ 0.001	FPIR ≤ 0.005	FPIR ≤ 0.01
Ten Fingers (Plain)	Ten Fingers (Plain)	61.5418	48.8169	43.9494
Ten Fingers (Plain)	Ten Fingers (Roll)	55.7303	43.1531	38.6720
Ten Fingers (Roll)	Ten Fingers (Roll)	57.4722	43.2584	39.2191

FpVTE 2012—Class C where, for approximately one-third of the probes, a single mated identity was present. Tabular versions of FNIR at select ranks can be viewed in Table 18.

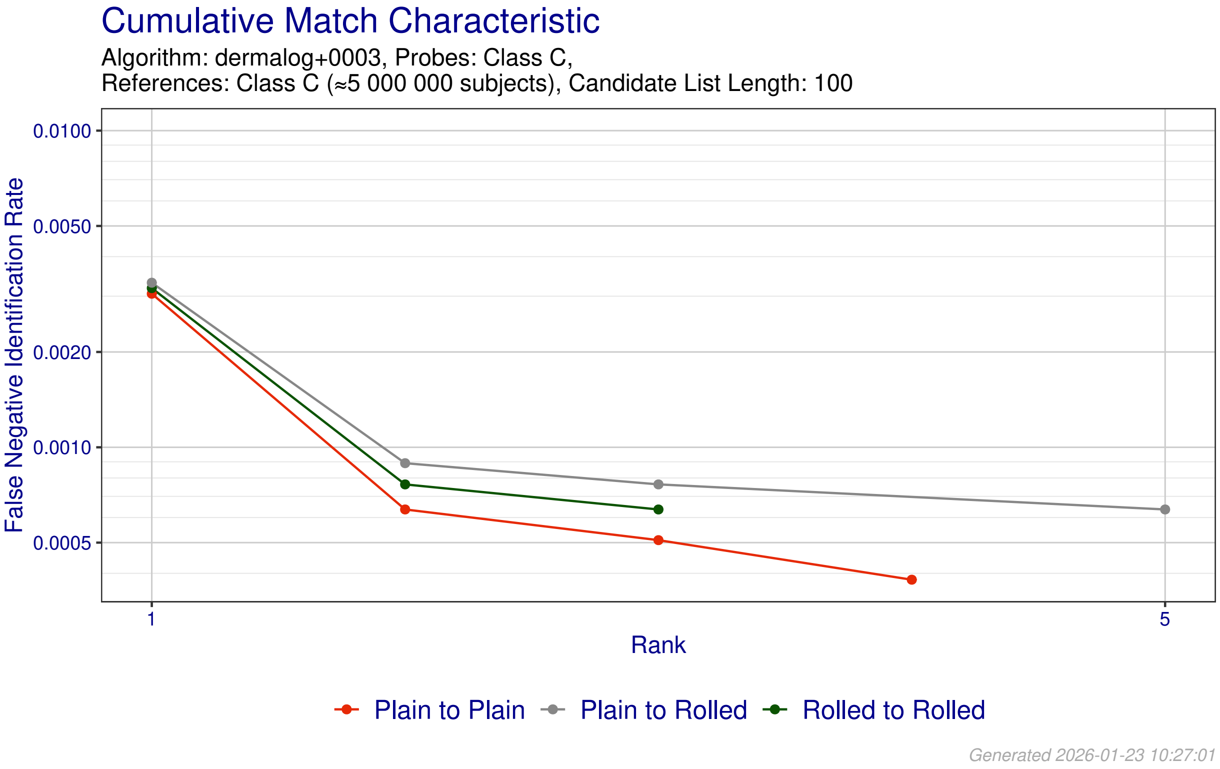

Figure 6: CMC when searching probe templates from FpVTE 2012—Class C against enrollment databases generated from reference templates from FpVTE 2012—Class C.

Table 18: FNIR values from CMC plotted in Figure 6.

Probe Content	Reference Content	Rank 1	Rank ≤ 2	Rank ≤ 5	Rank ≤ 10	Rank ≤ 50	Rank ≤ 100
Ten Fingers (Plain)	Ten Fingers (Plain)	0.0031	0.0006	0.0004	0.0004	0.0004	0.0004
Ten Fingers (Plain)	Ten Fingers (Roll)	0.0033	0.0009	0.0006	0.0006	0.0006	0.0006
Ten Fingers (Roll)	Ten Fingers (Roll)	0.0032	0.0008	0.0006	0.0006	0.0006	0.0006