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SlapSegII Analysis: Matching Segmented Fingerprint Images

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Abstract

This report is an extension of the SlapSegII[1] evaluation which measured the ability of slap segmentation algorithms to successfully segment four-finger slaps into individual fingerprint images. This study compared the matching accuracy of hand-marked segmentation and automated segmentation algorithm results to examine the effect of automated slap fingerprint segmentation errors on matching accuracy. A couple other issues this study examined are: 1) How detrimental was excluding fingerprint ridge structure (over-segmentation) to matching? 2) How much did fusion of multiple fingers compensate for segmentation errors? The only dataset from SlapSegII with mates available for matching was the dataset with 2-inch high slaps, so the study looked at matching accuracy for single finger, two index fingers and eight fingers (no thumbs).

1. Introduction

The SlapSegII evaluation was performed to measure the current capabilities of four-finger slap segmentation algorithms to correctly segment fingerprints within a certain geometric tolerance of hand-marked ground truth data. The tolerances were based on matching studies conducted on a data sample of the 2-inch tall slap fingerprint data. In those matcher studies various tolerance limits were studied and the SlapSegII tolerance limits were selected to have a minimal effect on the matching accuracy. This gave SlapSegII a more stringent success metric than SlapSeg04 which only required that the fingerprints be matchable using high quality matching algorithms. The advantage of SlapSegII was that it measured the segmentation algorithm’s ability to preserve the fingerprint ridge structure. While a good matcher may compensate for over-segmentation on some fingers it couldn’t match ridge detail that was missing, which would’ve been more significant to latent fingerprint matching.

This report evaluated the ability of fingerprint matching algorithms to match rolled images with both the hand-marked ground truth boxes and the results of the automated segmentation algorithms. Some caveats to this study were: 1) While this study used law enforcement operational quality data, results can vary from dataset to dataset. 2) The effect of fusing multiple fingers was examined but only for basic sum fusion by adding matcher scores. 3) The matching used 1-to-1 matching with mates and true non-mates (search probes with no mate in the gallery). It was beyond the scope of this study to measure the effect on a complete n-staged 1-to-many Automated Fingerprint Identification System (AFIS) taking into account all aspects of that system.

2. Dataset

The dataset used for this study was the 2-inch tall data from SlapSegII as it was the only dataset with mate data (rolled prints) available for matching. This data was operational law enforcement quality

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[1] www.nist.gov/itl/iad/ig/slapseg.cfm

that is used in AFIS systems today. Future work may include new data samples (ie., 3-inch live-scan data) as mates become available for studying matching accuracy. This 2-inch dataset contained right hand slaps for ~22,500 subjects and left hand slaps for ~20,000 subjects. There were ~12,500 subjects with both right and left hand slaps in the dataset that were used in the multiple finger fusion part of the study.

3. Testing Performed

The baseline matching results used the hand-marked ground-truth boxes to segment the individual fingerprint images that were then matched to the rolled fingerprint images. Then, the resulting images from each segmentation algorithm were matched against the rolled fingerprint images. Matcher threshold values were determined based on the baseline results (ie., threshold at False Match Rate (FMR) 10^{-4}) and then fixed when evaluating the results for each segmentation algorithm.

The three matching algorithms were high-end performers in the Proprietary Fingerprint Template (PFT)[2] evaluation but with different speed and template size characteristics. Matcher-I had the smallest feature template and was the fastest in both template extractions and matching. Matcher-II was two times slower than Matcher-I in template extractions, had larger templates, and was only slightly slower in matching speed. Matcher-III was 3-4 times slower than Matcher-I for template extraction, had the largest template size, and was 2-3 times as slow in matching speed.

The first set of tests compared baseline results with the segmentation algorithm results for single fingers, two fingers (combining left and right index fingers), and eight fingers. The fused matching scores were computed using the sum rule for left/right index fingers (2F) and all eight fingers (8F).

The second set of results looked at only the hand-marked segmentation boxes for three cases. The first case used the ground truth (GT) boxes. The second case used the hand-marked boxes moved to the minimum tolerance limit (GTL) used for SlapSegII (maximum ridge structure loss allowed). The third case used the hand-marked boxes moved 16 pixels[3] inside the minimum tolerance limit (GTL2). The minimum tolerance limit in SlapSegII was -32 pixels for the left and right sides and -64 pixels for the top and bottom edges.

The next test examined the change in the average matcher score for each segmentation algorithm compared to the GT results. The average matcher score was only computed for known mates in the dataset. The raw matcher score couldn’t be revealed so for this test the percentage change in the average score was recorded.

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[2] http://www.nist.gov/itl/iad/ig/pft.cfm

[3] All fingerprint images in this study were scanned at 500 pixels per inch (19.69 pixels per millimeter).

Finally, the actual number of False Non-Matches (FNM) and False Matches (FM) were recorded to compare the use of GT segmentation boxes to the use of segmentation algorithms boxes.

4. Results

Figures 1 and 2 show the detection error trade-off (DET) curves for Matcher-I using left and right index fingers. In both cases there was about a 2% increase in error rate from the hand-marked (GT) segmentation boxes to the highest error rate for the segmentation algorithms. Comparing this to the results from SlapSegII, the algorithms in SlapSegII that performed segmentation best based on the geometric limits produced matching results closest to the GT boxes. Appendix D has the complete set of DET curves for all fingers and matchers.

Figures 3 and 4 are DET curves that showed the variations of the hand-marked data. There was a significant increase in error going from GT to GTL to GTL2, which showed that allowing all sides to reach the minimum tolerance limits of SlapSegII was detrimental to matching. Based on these results, most of the segmentation algorithms in SlapSegII were not failing on all sides of the segmentation box. Also, looking at Figures 1 and 2 compared to Figures 3 and 4 the GTL results were about the same as the worst segmentation algorithm results. The GTL2 results were significantly worse than the segmentation algorithm results. Appendix E has the complete set of curves for all fingers and matching algorithms.

Figures 5 and 6 show the two-finger fusion matching results for each segmentation algorithm and variations of the hand-marked boxes. Note the scale change from the previous figures. Not surprisingly, two-finger fusion produced better matching results over single finger matching. Two-finger fusion also reduced the range in performance across the segmentation algorithms in Figure 5 as well as the hand-marked ground truth variations in Figure 6. Figures 7-8 show the same results for 8-finger fusion and again the scale was changed. More fingers further reduced the range but there remained a difference between the lower to better performing segmentation algorithms. The end of Appendix E has the full set of plots for all three matching algorithms.

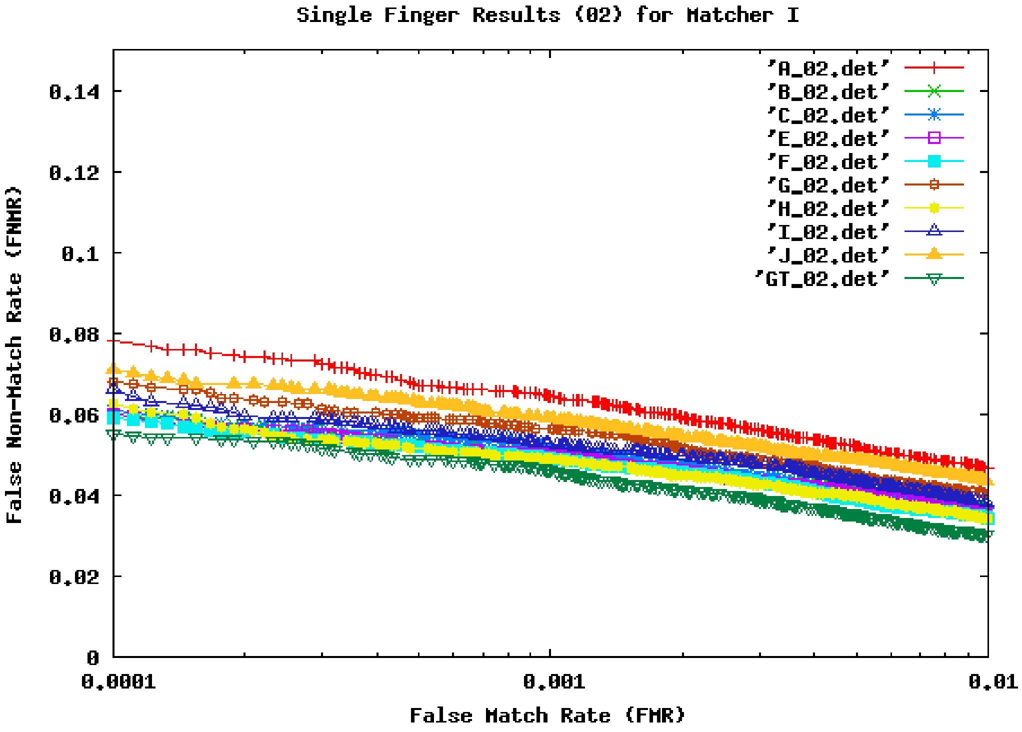

Figure 1: DET - Matcher-I – Finger 02 – Segmentation Algorithm Boxes.

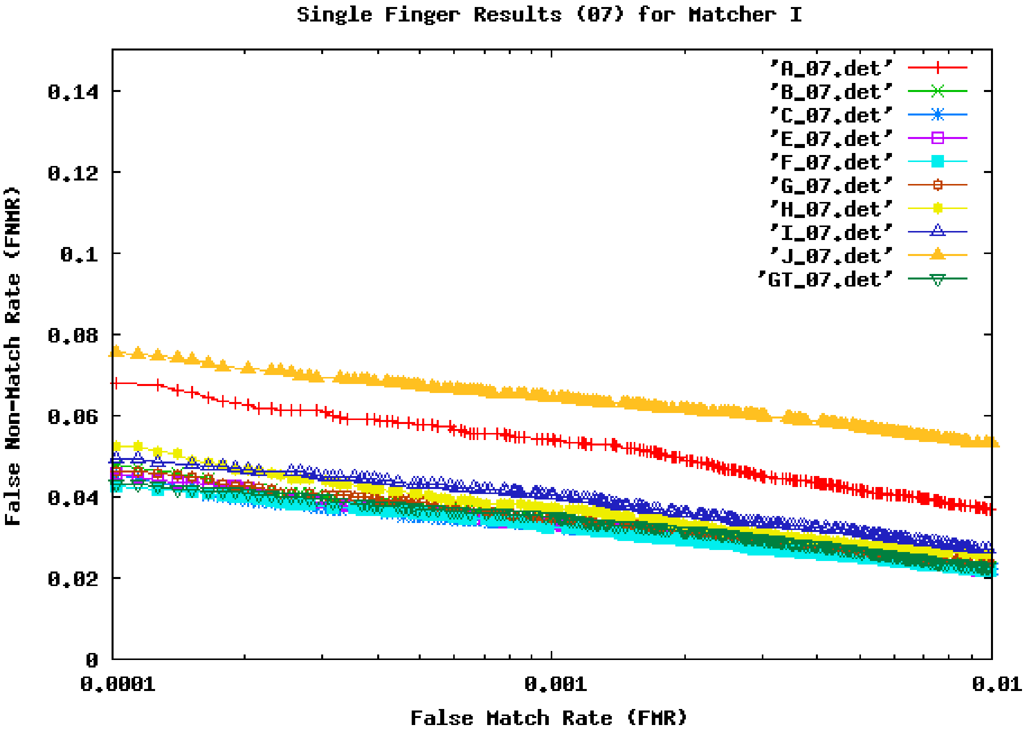

Figure 2: DET - Matcher-I – Finger 07 – Segmentation Algorithm Boxes.

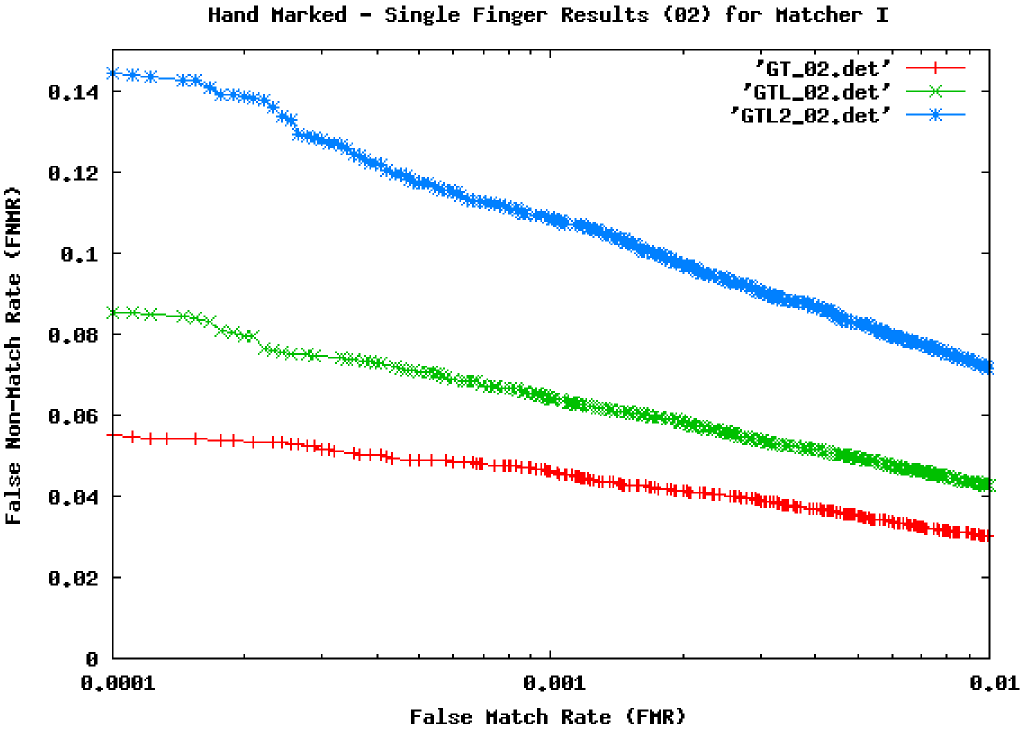

Figure 3: DET - Matcher-I – Finger 02 – GT Variation Boxes.

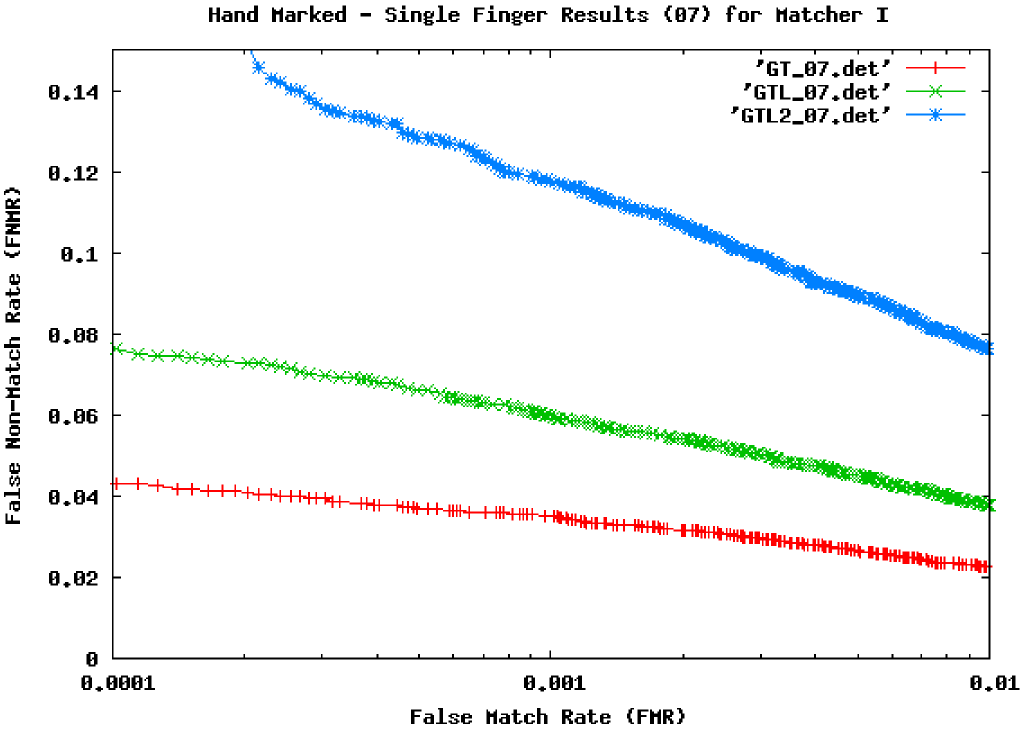

Figure 4: DET - Matcher-I – Finger 07 – GT Variation Boxes.

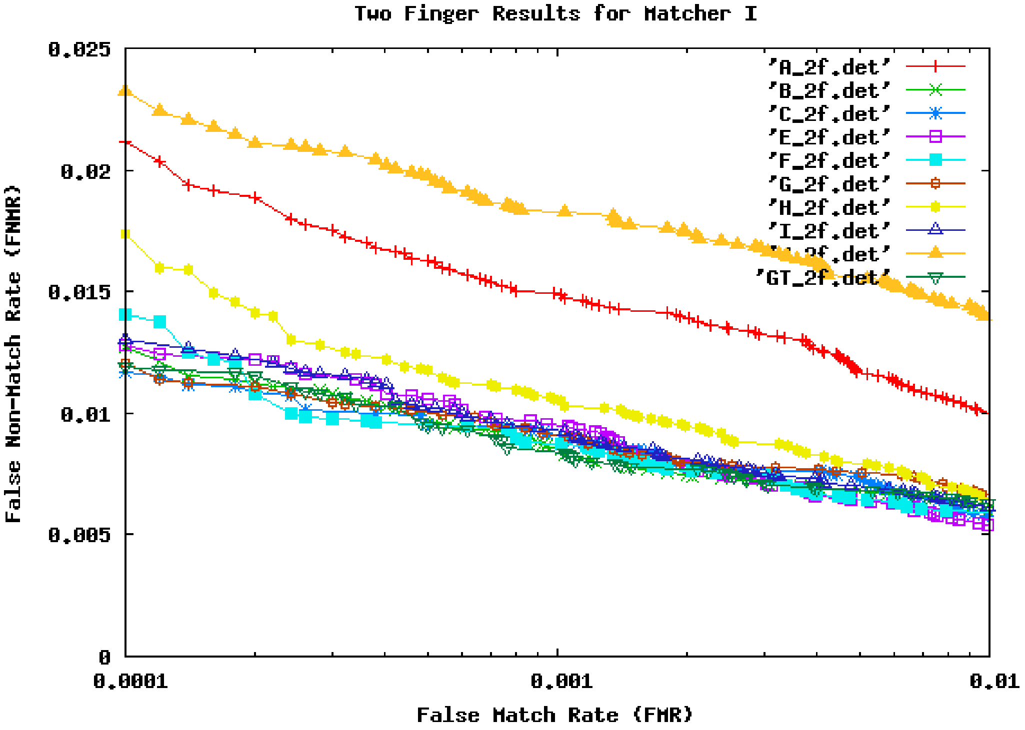

Figure 5: DET - Matcher-I – 2F Fusion – Segmentation Algorithm Boxes.

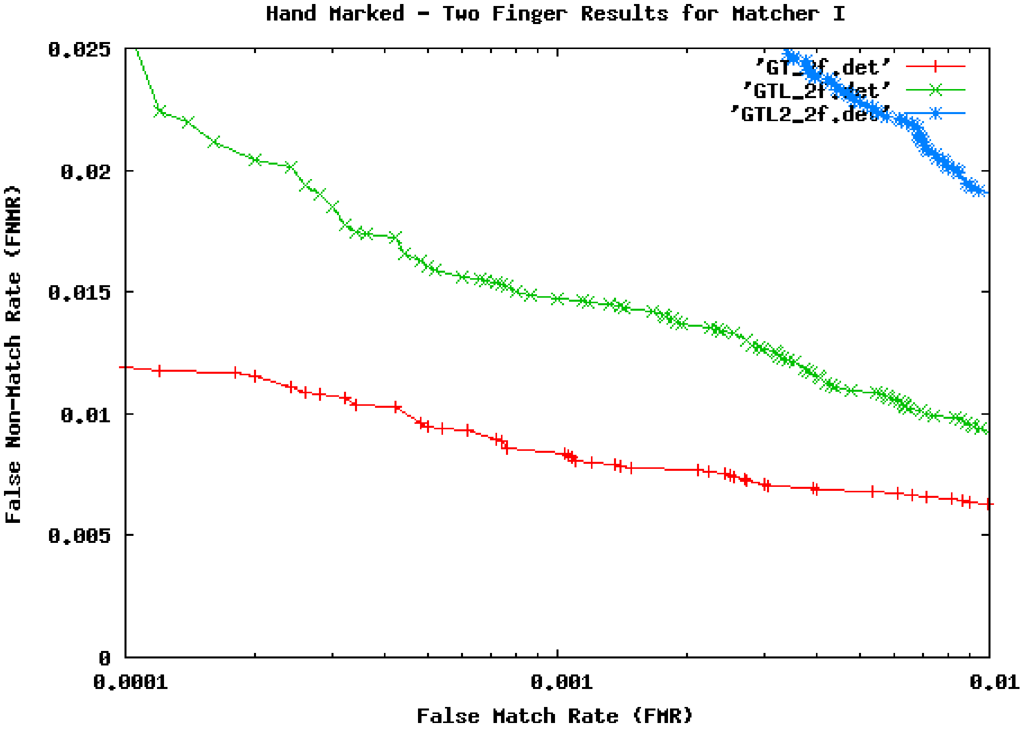

Figure 6: DET - Matcher-I – 2F Fusion – GT Variation Boxes.

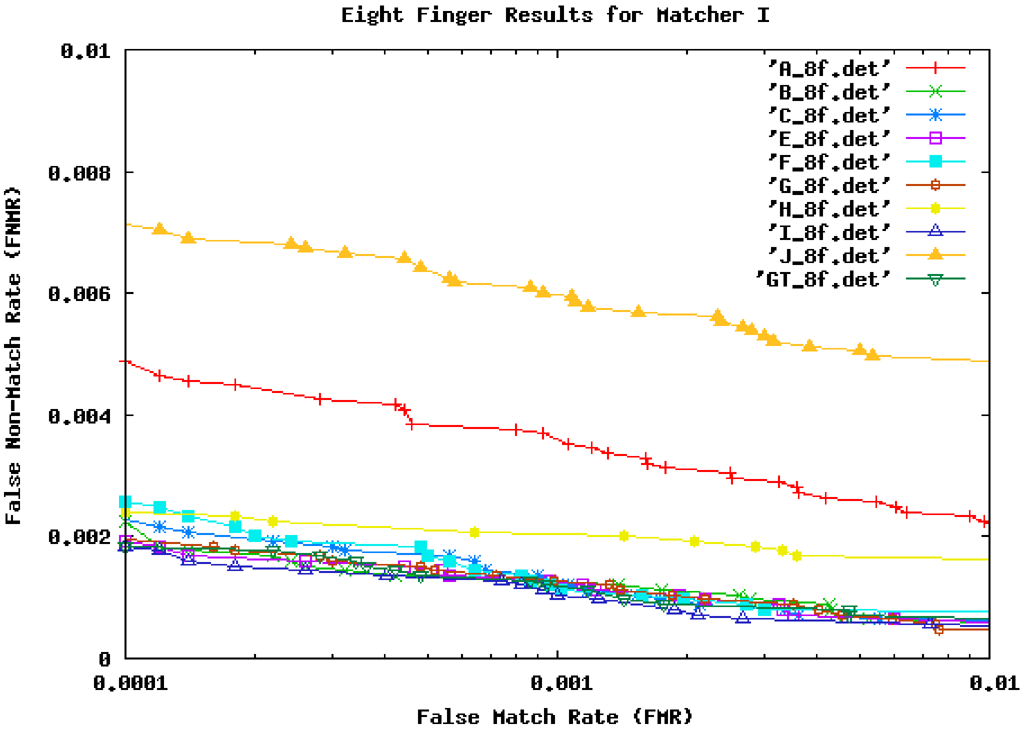

Figure 7: DET - Matcher-I – 8F Fusion – Segmentation Algorithm Boxes.

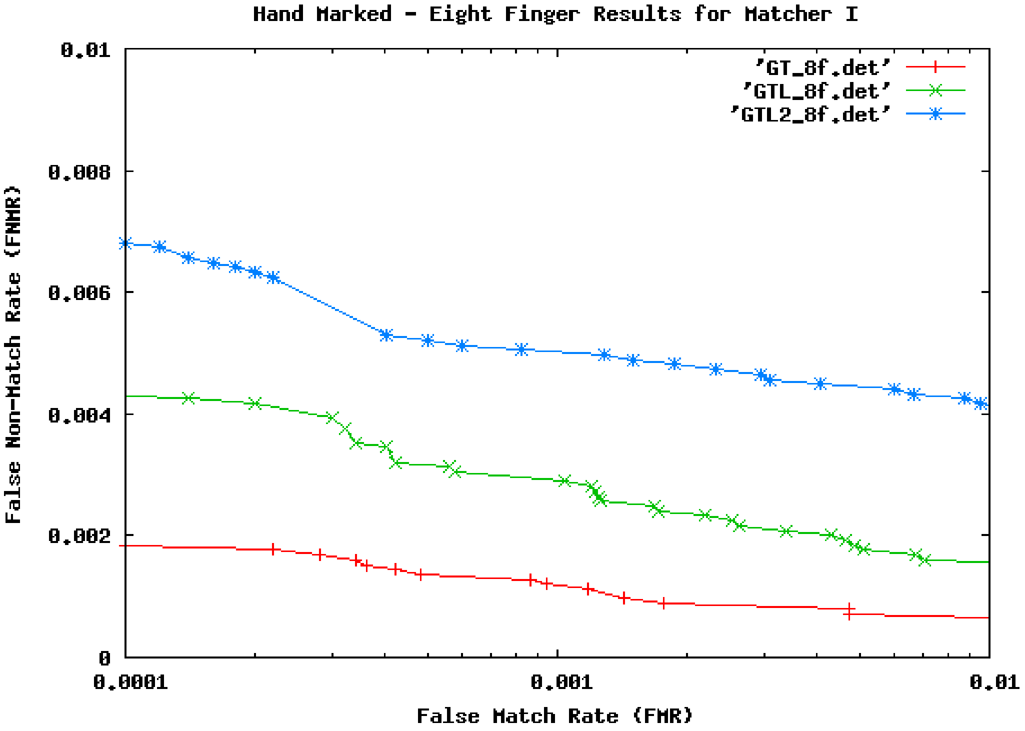

Figure 8: DET - Matcher-I – 8F Fusion – GT Variation Boxes.

Table 1 shows the complete set of FNMR points for single finger, two-finger and eight-finger combinations based on the thresholds that resulted in FMR of 10^{-4} for the hand-marked ground truth results (GT). All single finger matching results for the segmentation algorithms performed worse than the single finger matching results for the GT boxes. These results in table 1 also reinforce that two or more fingers can significantly compensate for reduced segmentation accuracy. In fact, the two-finger fusion matching results for the most accurate segmentation algorithms performed as well as the two-finger fusion GT matching results. Just as important, all the two-finger fusion matching for the segmentation algorithms performed better than the single finger matching results for GT boxes. Appendix A has the complete set of tables for the three matching algorithms used.

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	0.0549	0.0577	0.0560	0.1148	0.0431	0.0466	0.0748	0.1677	0.0119	0.0018
GTL	0.0802	0.0842	0.0839	0.1767	0.0735	0.0770	0.1175	0.2675	0.0203	0.0045
A	0.0753	0.0799	0.0808	0.1491	0.0629	0.0671	0.0983	0.2083	0.0191	0.0050
B	0.0598	0.0591	0.0559	0.1151	0.0416	0.0480	0.0742	0.1682	0.0119	0.0021
C	0.0605	0.0580	0.0538	0.1145	0.0412	0.0454	0.0729	0.1677	0.0120	0.0023
E	0.0590	0.0590	0.0557	0.1154	0.0423	0.0464	0.0730	0.1699	0.0122	0.0019
F	0.0584	0.0582	0.0555	0.1160	0.0414	0.0463	0.0710	0.1699	0.0113	0.0020
G	0.0654	0.0605	0.0551	0.1165	0.0434	0.0485	0.0769	0.1714	0.0123	0.0022
H	0.0587	0.0659	0.0576	0.1246	0.0460	0.0491	0.0765	0.1824	0.0134	0.0029
I	0.0624	0.0610	0.0597	0.1197	0.0477	0.0485	0.0778	0.1689	0.0125	0.0019
J	0.0688	0.0739	0.0708	0.1475	0.0737	0.0781	0.1021	0.2048	0.0226	0.0082

Table 1: FNMR for Matcher-I (Threshold from GT at FMR of 10^{-4})

Table 2 shows the percentage drop in the average confidence score compared to the hand-marked (GT) results for Matcher-I. Appendix B has the complete set of tables for all three matching algorithms.

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GTL	-7.57	-7.73	-7.49	-11.81	-8.58	-7.50	-9.95	-15.89	-16.33	-9.68
A	-4.12	-4.36	-5.24	-6.07	-4.66	-3.76	-4.44	-6.32	-8.90	-4.92
B	-0.29	0.00	0.07	0.20	0.12	-0.16	0.23	0.01	-0.20	-0.01
C	-0.33	-0.01	0.12	0.34	0.05	-0.05	0.29	0.20	-0.39	0.03
E	-0.22	-0.00	-0.09	0.09	0.11	-0.01	0.30	0.02	-0.28	-0.02
F	-0.23	0.09	0.06	-0.01	0.13	-0.03	0.29	0.05	-0.27	-0.00
G	-1.21	-0.58	-0.28	-0.17	-0.15	-0.41	-0.14	-0.13	-1.35	-0.42
H	-0.54	-1.20	-0.38	-0.89	-0.40	-0.53	-0.07	-1.72	-1.08	-0.76
I	-0.52	-0.29	-0.58	-0.48	-0.49	-0.39	-0.37	-0.25	-1.05	-0.44
J	-1.95	-2.67	-2.37	-4.07	-3.35	-3.69	-3.58	-5.27	-5.77	-3.47

Table 2: Percent Change in Average Confidence Score Compared to GT for Matcher-I

Tables 3-4 show the actual number of False Non Matches (FNM) and False Matches (FM) for each segmentation algorithm. Again the threshold was fixed based on the hand-marked results (GT) at FMR of 10^{-4}. In some cases there were several hundred matches made with the hand-marked segmentation boxes that were missed with the segmentation algorithms. The sample size should be increased to make any significant analysis of the false matches but there was a small increase in the number of false matches when comparing GT to the segmentation algorithms. Appendix C has the complete set of tables for all three matching algorithms.

	02	03	04	05	07	08	09	10	2f	8f
GT	1239	1303	1264	2592	849	919	1476	3311	149	23
GTL	1813	1899	1898	3989	1448	1520	2322	5272	252	57
A	1699	1803	1826	3375	1239	1318	1938	4097	239	63
B	1350	1337	1261	2600	819	943	1462	3317	147	27
C	1365	1308	1212	2589	812	892	1434	3315	152	30
E	1330	1329	1257	2603	834	911	1438	3349	153	24
F	1321	1314	1255	2613	815	912	1398	3348	139	26
G	1480	1359	1248	2644	858	955	1515	3364	154	28
H	1331	1486	1310	2812	906	967	1507	3597	168	37
I	1407	1375	1347	2701	939	959	1530	3326	157	25
J	1555	1663	1597	3336	1451	1537	2016	4046	282	103

Table 3: Number of FNM for Matcher-I (Threshold from GT at FMR of 10^{-4})

	02	03	04	05	07	08	09	10	2f	8f
GT	9	9	9	9	8	8	8	8	5	5
GTL	17	10	13	12	14	10	7	5	12	4
A	15	7	11	12	16	9	7	8	8	2
B	10	9	6	11	18	7	5	6	7	6
C	10	6	4	6	13	6	8	1	4	6
E	11	7	7	7	15	5	6	6	8	5
F	10	9	7	3	12	4	7	6	10	10
G	15	11	4	8	14	5	7	2	5	2
H	15	10	5	7	17	13	8	4	12	0
I	13	6	4	5	13	6	8	6	9	3
J	12	5	6	14	12	7	4	7	6	2

Table 4: Number of FM for Matcher-I (Threshold from GT at FMR of 10^{-4})

5. Summary

The results show there was a drop off in matching accuracy performance as segmentation boxes deviated from the hand-marked segmentation boxes. At an FMR of 10^{-4} the FNMR for single finger, two fingers (right and left index) and eight fingers increased approximately 2%, 1% and 0.5% respectively compared to results from the hand-marked segmentation boxes. The use of multiple fingers definitely improved matching performance, but for the least accurate segmentation algorithms the score returned by the matcher was about 5% lower than hand-marked segmentation boxes. Two other observations also showed that using multiple fingers improved matching of segmented fingerprint data. First, two finger matching accuracies for all the segmentation algorithms were better than the single finger results for the hand-marked ground truth. Second, two finger and eight finger matching rates for the most accurate segmentation algorithms were equal to matching rates for the hand-marked segmentation boxes.

Finally, analysis of the tolerance limits used in the SlapSegII evaluation showed that placing the segmentation boxes at twice the inner tolerance limit increased the FNMR rate (FMR 10^{-4}) by a factor of 3.

There were three issues not addressed in this report. First, what would the effect of these segmentation errors be on an “end-to-end” AFIS? Second, how will segmentation boxes that are larger than the hand marked segmentation boxes affect matching? Finally, how would the loss of fingerprint information due to over segmentation affect matching against latent fingerprints? Certainly, the later issue alone would be a good enough reason to preserve as much of the fingerprint information as possible during slap fingerprint segmentation.

Appendix A

These tables show the False Non-Match Rates (FNMR) at a False Match Rate of 10^{-4} for the hand marked segmentation (GT) boxes using three different matching algorithms. The threshold from the GT results remained fixed for the other rows in the table. GTL was the hand marked segmentation (GT) adjusted to the minimum tolerance allowed in SlapSegII which was -32 for the left and right sides and -64 for the top and bottom.

The three matching algorithms were high-end performers in the Proprietary Fingerprint Template (PFT)[1] evaluation but with different speed and template size characteristics. Matcher-I had the smallest feature template and was the fastest in both template extractions and matching. Matcher-II was two times slower than Matcher-I in template extractions, had larger templates, and was only slightly slower in matching speed. Matcher-III was 3-4 times slower than Matcher-I for template extraction, had the largest template size, and was 2-3 times as slow in matching speed.

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[1] http://www.nist.gov/itl/iad/ig/pft.cfm

	02	03	04	05	07	08	09	10	2f	8f
GT	0.0549	0.0577	0.0560	0.1148	0.0431	0.0466	0.0748	0.1677	0.0119	0.0018
GTL	0.0802	0.0842	0.0839	0.1767	0.0735	0.0770	0.1175	0.2675	0.0203	0.0045
A	0.0753	0.0799	0.0808	0.1491	0.0629	0.0671	0.0983	0.2083	0.0191	0.0050
B	0.0598	0.0591	0.0559	0.1151	0.0416	0.0480	0.0742	0.1682	0.0119	0.0021
C	0.0605	0.0580	0.0538	0.1145	0.0412	0.0454	0.0729	0.1677	0.0120	0.0023
E	0.0590	0.0590	0.0557	0.1154	0.0423	0.0464	0.0730	0.1699	0.0122	0.0019
F	0.0584	0.0582	0.0555	0.1160	0.0414	0.0463	0.0710	0.1699	0.0113	0.0020
G	0.0654	0.0605	0.0551	0.1165	0.0434	0.0485	0.0769	0.1714	0.0123	0.0022
H	0.0587	0.0659	0.0576	0.1246	0.0460	0.0491	0.0765	0.1824	0.0134	0.0029
I	0.0624	0.0610	0.0597	0.1197	0.0477	0.0485	0.0778	0.1689	0.0125	0.0019
J	0.0688	0.0739	0.0708	0.1475	0.0737	0.0781	0.1021	0.2048	0.0226	0.0082

Table A.1: FNMR for Matcher I (Threshold from GT at FMR of 10^{-4})

	02	03	04	05	07	08	09	10	2f	8f
GT	0.0148	0.0118	0.0135	0.0294	0.0099	0.0124	0.0183	0.0388	0.0021	0.0005
GTL	0.0198	0.0159	0.0163	0.0407	0.0143	0.0180	0.0256	0.0648	0.0025	0.0005
A	0.0275	0.0226	0.0262	0.0451	0.0219	0.0265	0.0326	0.0646	0.0030	0.0007
B	0.0203	0.0133	0.0148	0.0319	0.0110	0.0149	0.0200	0.0439	0.0017	0.0005
C	0.0200	0.0128	0.0140	0.0299	0.0104	0.0143	0.0183	0.0414	0.0017	0.0006
E	0.0197	0.0125	0.0142	0.0298	0.0096	0.0137	0.0190	0.0425	0.0018	0.0005
F	0.0202	0.0125	0.0144	0.0307	0.0094	0.0136	0.0191	0.0421	0.0017	0.0006
G	0.0256	0.0139	0.0149	0.0295	0.0127	0.0171	0.0214	0.0434	0.0031	0.0006
H	0.0184	0.0202	0.0158	0.0409	0.0144	0.0184	0.0234	0.0593	0.0027	0.0009
I	0.0229	0.0147	0.0188	0.0350	0.0168	0.0166	0.0239	0.0443	0.0026	0.0006
J	0.0293	0.0282	0.0305	0.0614	0.0435	0.0479	0.0520	0.0725	0.0089	0.0039

Table A.2: FNMR for Matcher II (Threshold from GT at FMR of 10^{-4})

	02	03	04	05	07	08	09	10	2f	8f
GT	0.0233	0.0180	0.0172	0.0420	0.0191	0.0225	0.0289	0.0602	0.0063	0.0020
GTL	0.0319	0.0245	0.0239	0.0618	0.0284	0.0316	0.0414	0.0972	0.0088	0.0026
A	0.0379	0.0311	0.0320	0.0628	0.0338	0.0363	0.0457	0.0876	0.0105	0.0028
B	0.0286	0.0185	0.0181	0.0449	0.0201	0.0221	0.0305	0.0642	0.0062	0.0014
C	0.0297	0.0191	0.0169	0.0425	0.0196	0.0226	0.0311	0.0616	0.0062	0.0016
E	0.0282	0.0187	0.0176	0.0436	0.0192	0.0223	0.0300	0.0607	0.0063	0.0017
F	0.0278	0.0194	0.0172	0.0430	0.0186	0.0230	0.0304	0.0616	0.0062	0.0014
G	0.0334	0.0190	0.0182	0.0443	0.0206	0.0000	0.0326	0.0613	0.0067	0.0013
H	0.0266	0.0250	0.0192	0.0511	0.0230	0.0256	0.0317	0.0743	0.0070	0.0014
I	0.0310	0.0199	0.0219	0.0466	0.0253	0.0250	0.0344	0.0623	0.0071	0.0014
J	0.0328	0.0269	0.0289	0.0713	0.0487	0.0485	0.0559	0.0890	0.0119	0.0048

Table A.3: FNMR for Matcher III (Threshold from GT at FMR of 10^{-4})

Appendix B

These tables show the percent change in the matcher confidence score compared to the hand marked segmentation boxes (GT) for single finger, two finger and eight finger combinations and three different matchers. GTL was the hand marked segmentation (GT) adjusted to the minimum tolerance allowed in SlapSegII which was -32 for the left and right sides and -64 for the top and bottom. The threshold was chosen based on the GT data at False Match Rate (FMR) 10^{-4} and fixed for all other rows in the table.

The three matching algorithms were high-end performers in the Proprietary Fingerprint Template (PFT)[1] evaluation but with different speed and template size characteristics. Matcher-I had the smallest feature template and was the fastest in both template extractions and matching. Matcher-II was two times slower than Matcher-I in template extractions, had larger templates, and was only slightly slower in matching speed. Matcher-III was 3-4 times slower than Matcher-I for template extraction, had the largest template size, and was 2-3 times as slow in matching speed.

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A	-4.12	-4.36	-5.24	-6.07	-4.66	-3.76	-4.44	-6.32	-8.90	-4.92
B	-0.29	0.00	0.07	0.20	0.12	-0.16	0.23	0.01	-0.20	-0.01
C	-0.33	-0.01	0.12	0.34	0.05	-0.05	0.29	0.20	-0.39	0.03
E	-0.22	-0.00	-0.09	0.09	0.11	-0.01	0.30	0.02	-0.28	-0.02
F	-0.23	0.09	0.06	-0.01	0.13	-0.03	0.29	0.05	-0.27	-0.00
G	-1.21	-0.58	-0.28	-0.17	-0.15	-0.41	-0.14	-0.13	-1.35	-0.42
H	-0.54	-1.20	-0.38	-0.89	-0.40	-0.53	-0.07	-1.72	-1.08	-0.76
I	-0.52	-0.29	-0.58	-0.48	-0.49	-0.39	-0.37	-0.25	-1.05	-0.44
J	-1.95	-2.67	-2.37	-4.07	-3.35	-3.69	-3.58	-5.27	-5.77	-3.47

Table B.1: Percent Change in Average Matcher Score Compared to GT for Matcher I

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GTL	-11.34	-10.69	-11.03	-15.51	-13.97	-12.54	-13.51	-20.35	-26.45	-13.24
A	-5.95	-6.16	-7.96	-8.25	-7.99	-6.24	-6.46	-7.84	-14.68	-7.00
B	-1.13	-0.57	-0.48	-0.50	-0.79	-0.85	-0.56	-0.29	-1.92	-0.65
C	-1.08	-0.69	-0.32	-0.21	-0.68	-0.71	-0.49	-0.10	-1.82	-0.53
E	-0.47	-0.28	-0.33	-0.41	-0.22	-0.40	-0.20	-0.21	-0.81	-0.31
F	-0.54	-0.25	-0.21	-0.44	-0.26	-0.43	-0.12	-0.11	-0.90	-0.28
G	-1.40	-0.30	-0.15	0.02	-0.48	-0.55	-0.25	0.07	-1.86	-0.42
H	-0.56	-1.25	-0.44	-1.21	-0.89	-1.00	-0.47	-1.58	-1.44	-0.90
I	-0.93	-0.66	-1.18	-1.24	-1.09	-0.93	-0.93	-0.82	-2.16	-0.95
J	-2.14	-3.09	-2.05	-4.18	-3.39	-3.89	-2.88	-6.09	-5.94	-3.39

Table B.2: Percent Change in Average Matcher Score Compared to GT for Matcher II

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GTL	-18.11	-17.37	-19.34	-22.84	-23.87	-20.86	-21.16	-28.01	-46.88	-21.13
A	-9.73	-9.22	-12.48	-12.25	-12.61	-9.50	-9.49	-11.39	-25.15	-10.72
B	-0.95	-0.67	0.00	0.26	-0.73	-0.81	-0.12	-0.16	-1.92	-0.45
C	-1.18	-0.62	-0.12	0.64	-0.60	-0.69	-0.19	0.04	-2.20	-0.46
E	-0.01	-0.19	-0.07	0.23	0.19	-0.17	0.29	0.30	0.06	-0.01
F	-0.12	-0.05	-0.05	-0.21	0.06	-0.16	0.14	0.09	-0.44	-0.10
G	-1.77	-0.75	-0.21	0.01	-1.31	-1.00	0.05	-0.39	-3.63	-0.79
H	-0.38	-1.64	-0.48	-0.89	-0.06	-0.98	-0.32	-1.66	-0.81	-0.80
I	-0.53	-0.54	-1.19	-0.79	-0.73	-0.89	-0.85	-1.08	-1.71	-0.86
J	0.08	1.19	1.54	-3.39	-0.14	0.43	0.45	-7.32	0.16	-0.48

Table B.3: Percent Change in Average Matcher Score Compared to GT for Matcher III

Appendix C

The six tables in this appendix show the actual number of False Non-Matches (FNM) and False Matches (FM) for single finger, two-finger, and eight finger combinations and three different matching algorithms. GT was the results for the hand marked segmentation boxes, GTL was the results for GT adjusted to the minimum tolerance allowed in SlapSegII, which was -32 for left and right sides, -64 for the top and bottom. The matcher threshold was chosen based on the GT data (first row in the table) at FMR of 10^{-4} and fixed for all other rows in each table.

The three matching algorithms were high-end performers in the Proprietary Fingerprint Template (PFT)[1] evaluation but with different speed and template size characteristics. Matcher-I had the smallest feature template and was the fastest in both template extractions and matching. Matcher-II was two times slower than Matcher-I in template extractions, had larger templates, and was only slightly slower in matching speed. Matcher-III was 3-4 times slower than Matcher-I for template extraction, had the largest template size, and was 2-3 times as slow in matching speed.

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[1] http://www.nist.gov/itl/iad/ig/pft.cfm

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	1239	1303	1264	2592	849	919	1476	3311	149	23
GTL	1813	1899	1898	3989	1448	1520	2322	5272	252	57
A	1699	1803	1826	3375	1239	1318	1938	4097	239	63
B	1350	1337	1261	2600	819	943	1462	3317	147	27
C	1365	1308	1212	2589	812	892	1434	3315	152	30
E	1330	1329	1257	2603	834	911	1438	3349	153	24
F	1321	1314	1255	2613	815	912	1398	3348	139	26
G	1480	1359	1248	2644	858	955	1515	3364	154	28
H	1331	1486	1310	2812	906	967	1507	3597	168	37
I	1407	1375	1347	2701	939	959	1530	3326	157	25
J	1555	1663	1597	3336	1451	1537	2016	4046	282	103

Table C.1: Number of FNM for Matcher I (Threshold from GT at FMR of 10-4)

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	9	9	9	9	8	8	8	8	5	5
GTL	17	10	13	12	14	10	7	5	12	4
A	15	7	11	12	16	9	7	8	8	2
B	10	9	6	11	18	7	5	6	7	6
C	10	6	4	6	13	6	8	1	4	6
E	11	7	7	7	15	5	6	6	8	5
F	10	9	7	3	12	4	7	6	10	10
G	15	11	4	8	14	5	7	2	5	2
H	15	10	5	7	17	13	8	4	12	0
I	13	6	4	5	13	6	8	6	9	3
J	12	5	6	14	12	7	4	7	6	2

Table C.2: Number of FM for Matcher I (Threshold from GT at FMR of 10-4)

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	334	267	304	664	197	245	363	767	26	7
GTL	448	357	369	919	285	354	505	1279	32	7
A	621	511	592	1018	436	522	646	1276	37	9
B	458	298	335	720	219	293	394	869	22	6
C	452	288	317	673	206	281	361	819	21	7
E	446	281	322	670	188	271	374	837	23	6
F	458	284	325	699	185	269	377	832	22	7
G	578	315	335	665	250	337	421	856	39	7
H	413	454	355	924	285	363	462	1167	34	12
I	516	331	424	787	331	326	472	877	34	8
J	663	636	691	1387	857	941	1023	1426	112	50

Table C.3: Number of FNM for Matcher II (Threshold from GT at FMR of 10-4)

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	9	8	8	9	7	8	9	9	5	4
GTL	24	34	24	57	29	25	40	87	24	22
A	11	14	6	27	19	11	24	25	10	5
B	6	8	8	12	5	6	11	8	5	5
C	9	6	6	13	5	5	9	13	4	5
E	7	5	7	13	6	7	12	16	6	2
F	5	6	4	14	3	6	13	16	4	2
G	6	9	9	9	12	7	8	15	4	1
H	4	10	11	12	8	6	8	11	6	6
I	5	10	8	8	7	8	7	14	4	4
J	11	15	8	16	11	9	14	18	6	6

Table C.4: Number of FM for Matcher II (Threshold from GT at FMR of 10-4)

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	530	408	389	948	375	444	571	1185	79	26
GTL	720	554	540	1396	561	621	815	1912	111	33
A	859	705	724	1416	665	715	899	1723	129	35
B	648	420	410	1016	393	473	600	1265	79	19
C	670	431	384	957	387	448	613	1212	78	20
E	639	421	399	985	380	461	596	1196	79	22
F	631	437	390	972	363	456	603	1211	78	17
G	754	429	411	999	405	474	641	1208	85	16
H	603	567	434	1153	453	503	634	1462	88	18
I	700	451	494	1054	501	494	675	1228	90	18
J	741	608	652	1613	957	952	1098	1754	150	60

Table C.5: Number of FNM for Matcher III (Threshold from GT at FMR of 10-4)

	02	**03**	**04**	**05**	**07**	**08**	**09**	**10**	**2f**	**8f**
GT	10	10	10	9	8	8	8	8	5	7
GTL	30	18	25	15	9	11	12	20	3	11
A	19	9	15	11	7	6	8	8	2	3
B	9	8	12	5	3	1	11	6	3	6
C	11	7	11	11	7	3	11	11	3	11
E	13	8	18	6	4	1	4	4	6	9
F	9	14	26	7	7	3	8	6	3	4
G	12	11	20	6	6	0	6	5	1	6
H	18	12	13	7	9	4	4	4	2	4
I	16	9	13	10	7	4	9	9	0	7
J	25	12	21	8	5	2	2	12	1	2

Table C.6: Number of FM for Matcher III (Threshold from GT at FMR of 10-4)

Appendix D

This appendix has plots of False Non-Match Rate (FNMR) vs False Match Rate (FMR) for single finger, two finger, and eight finger combinations using three different matching algorithms. The segmentation boxes used were from the segmentation algorithms in SlapSegII. Note that the y-axis (FNMR) scale changes between the single finger, two finger and eight finger plots.

The three matching algorithms were high-end performers in the Proprietary Fingerprint Template (PFT)[1] evaluation but with different speed and template size characteristics. Matcher-I had the smallest feature template and was the fastest in both template extractions and matching. Matcher-II was two times slower than Matcher-I in template extractions, had larger templates, and was only slightly slower in matching speed. Matcher-III was 3-4 times slower than Matcher-I for template extraction, had the largest template size, and was 2-3 times as slow in matching speed.

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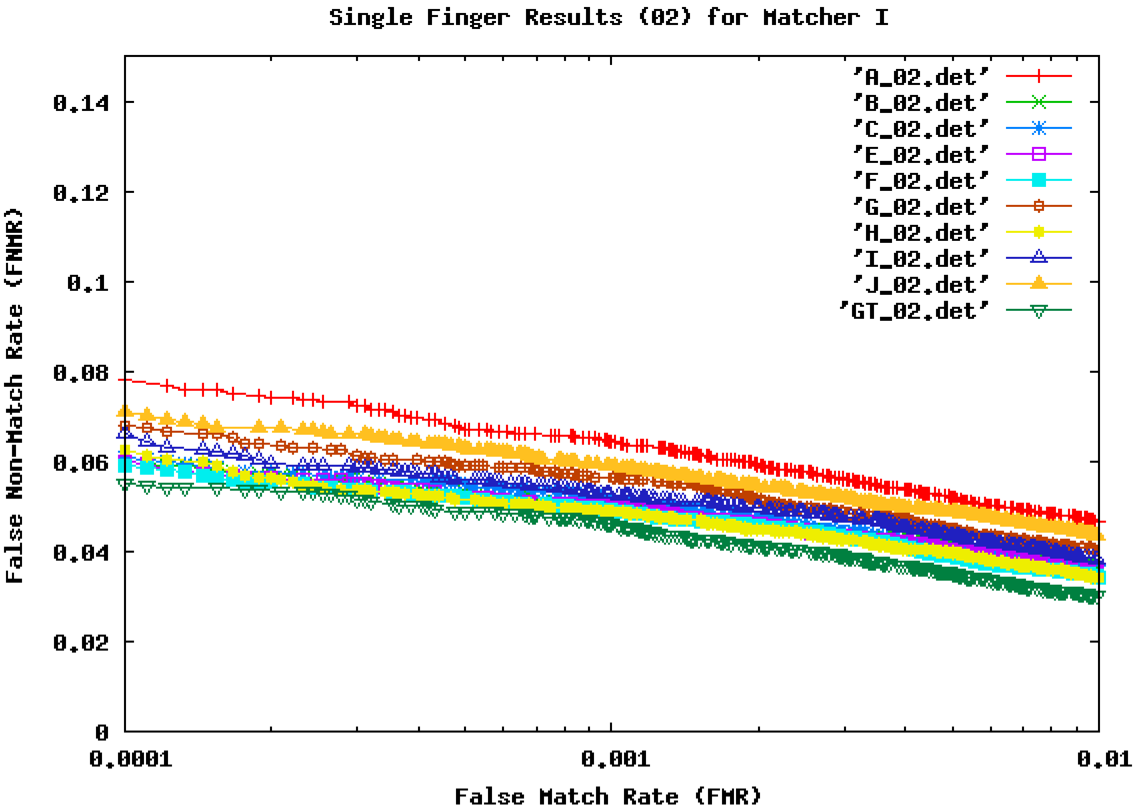
[1] http://www.nist.gov/itl/iad/ig/pft.cfm


Single Finger Results (02) for Matcher I
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0.08
0.06
0.04
0.02
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0.0001
0.001
0.01
False Match Rate (FMR)
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'C_02.det'
'E_02.det'
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'J_02.det'
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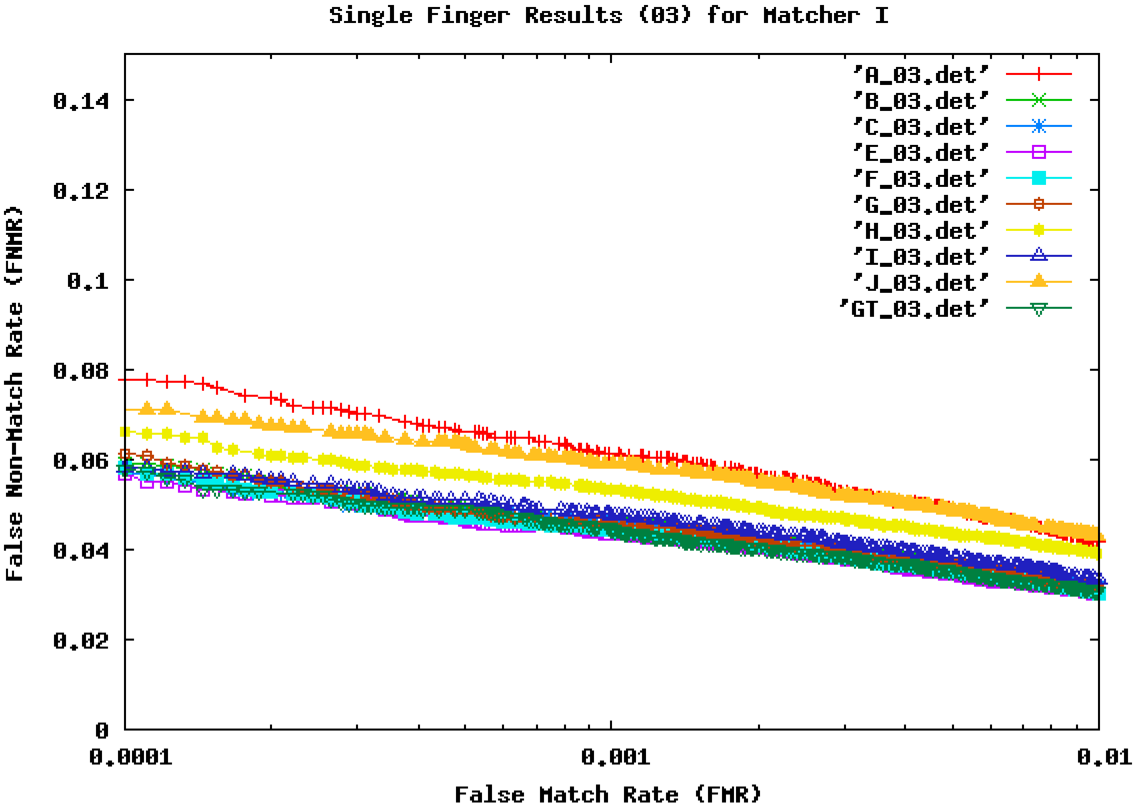
Single Finger Results (03) for Matcher I
False Non-Match Rate (FNMR)
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0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
'A_03.det'
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'J_03.det'
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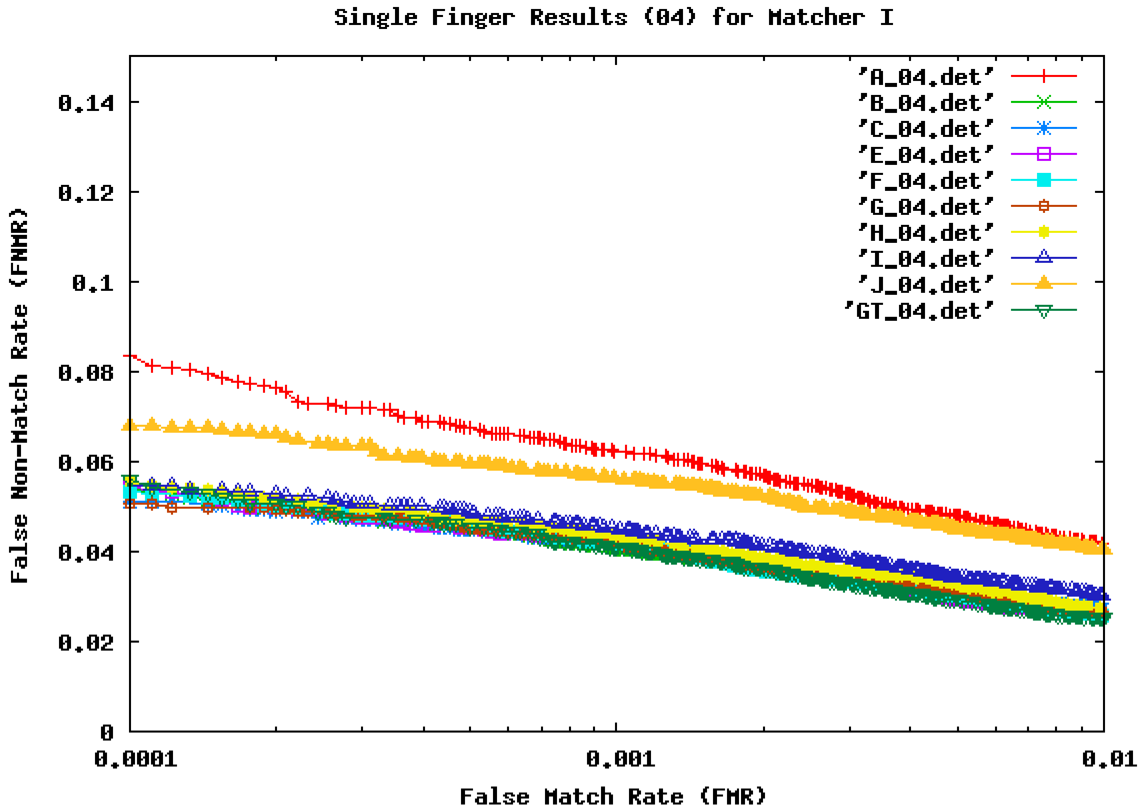
Single Finger Results (04) for Matcher I
False Non-Match Rate (FNMR)
False Match Rate (FMR)
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0.04
0.06
0.08
0.1
0.12
0.14
0.0001
0.001
0.01
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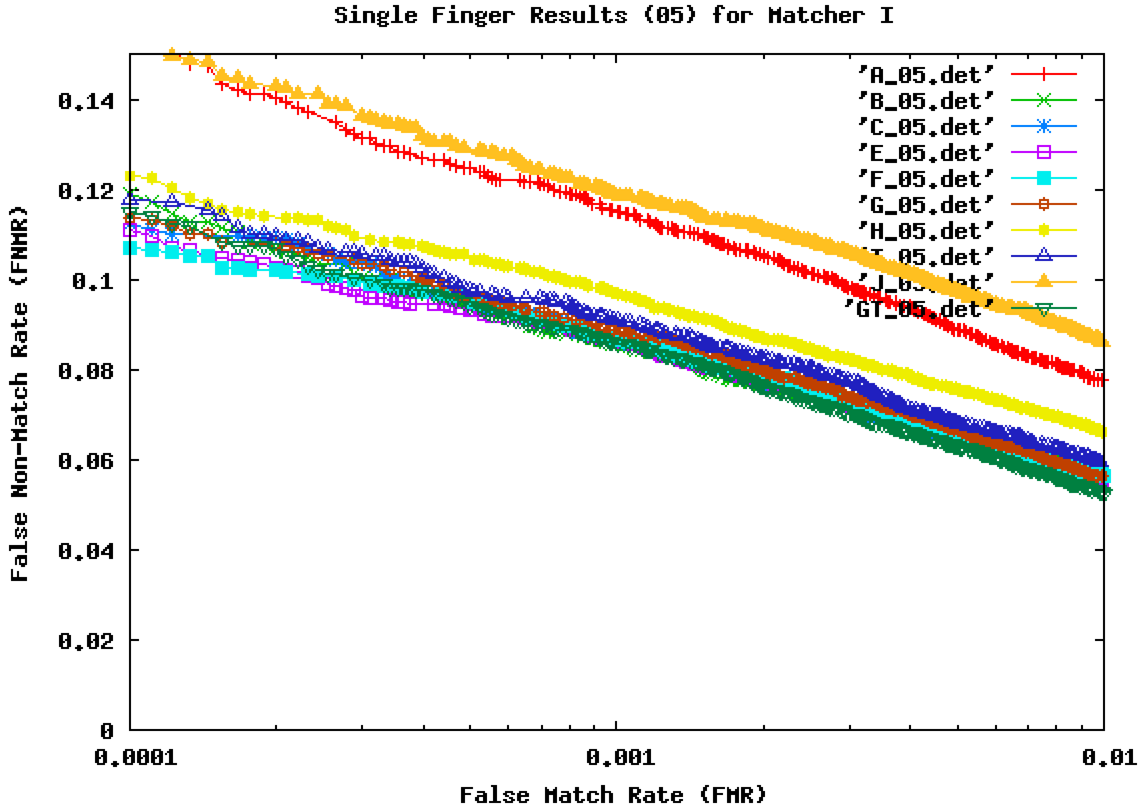
'J_04.det'
'GT_04.det'


Single Finger Results (05) for Matcher I
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False Match Rate (FMR)
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0.06
0.08
0.1
0.12
0.14
0.0001
0.001
0.01
'A_05.det'
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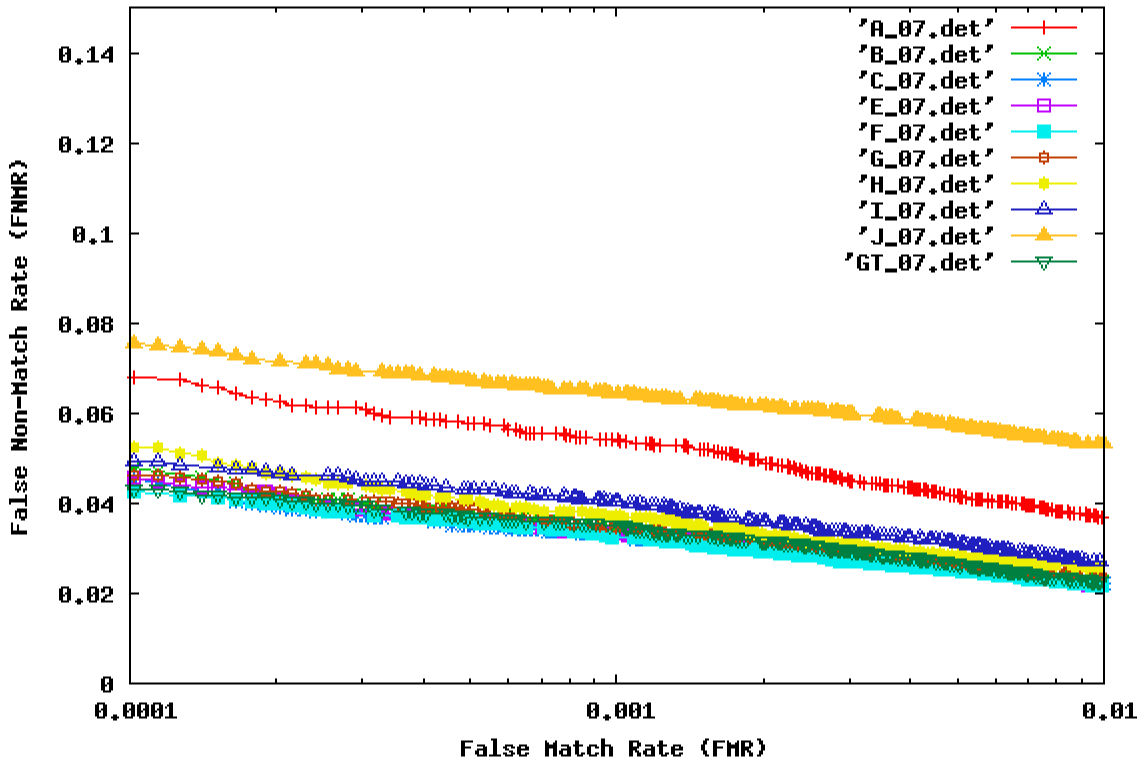
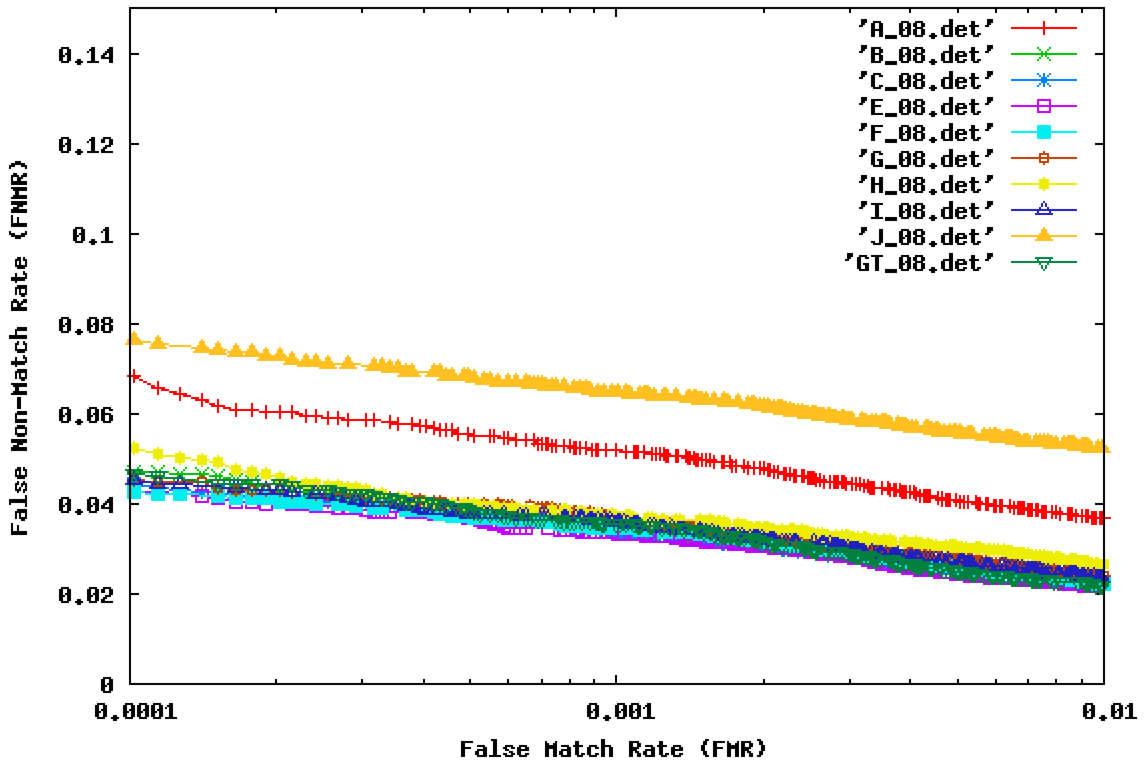
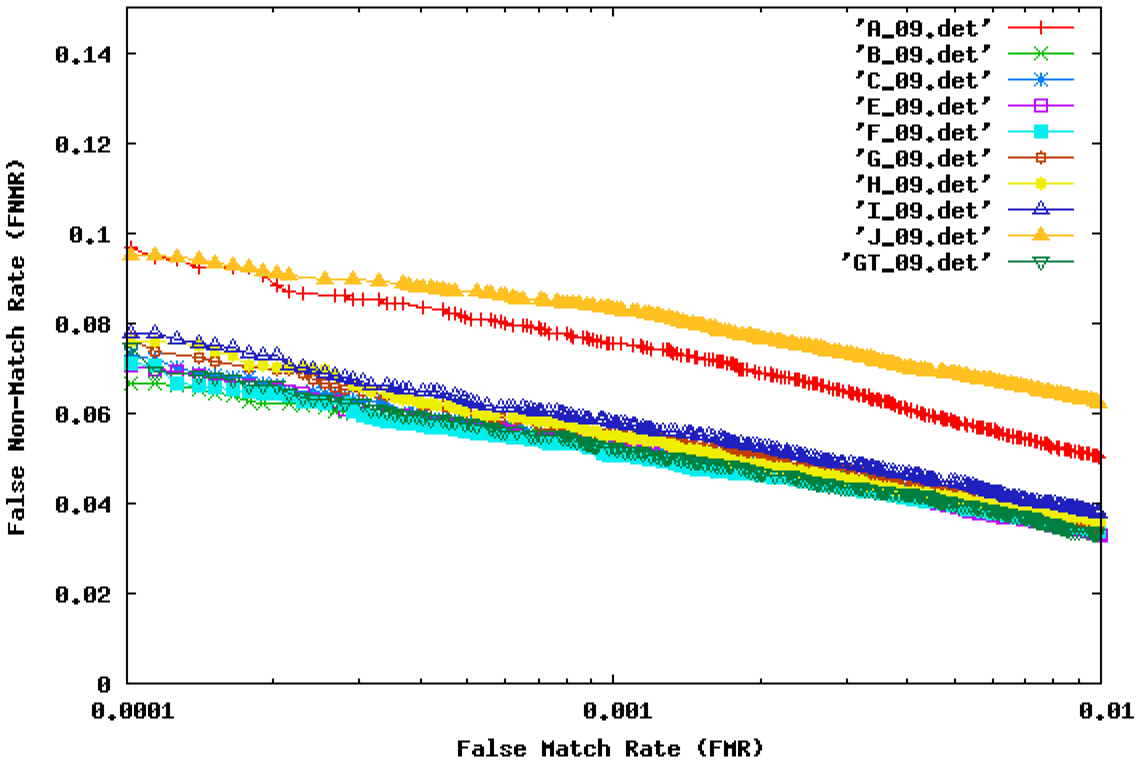
'C_05.det'
'E_05.det'
'F_05.det'
'G_05.det'
'H_05.det'
'I_05.det'
'J_05.det'
'GT_05.det'

Single Finger Results (07) for Matcher I



Single Finger Results (08) for Matcher I





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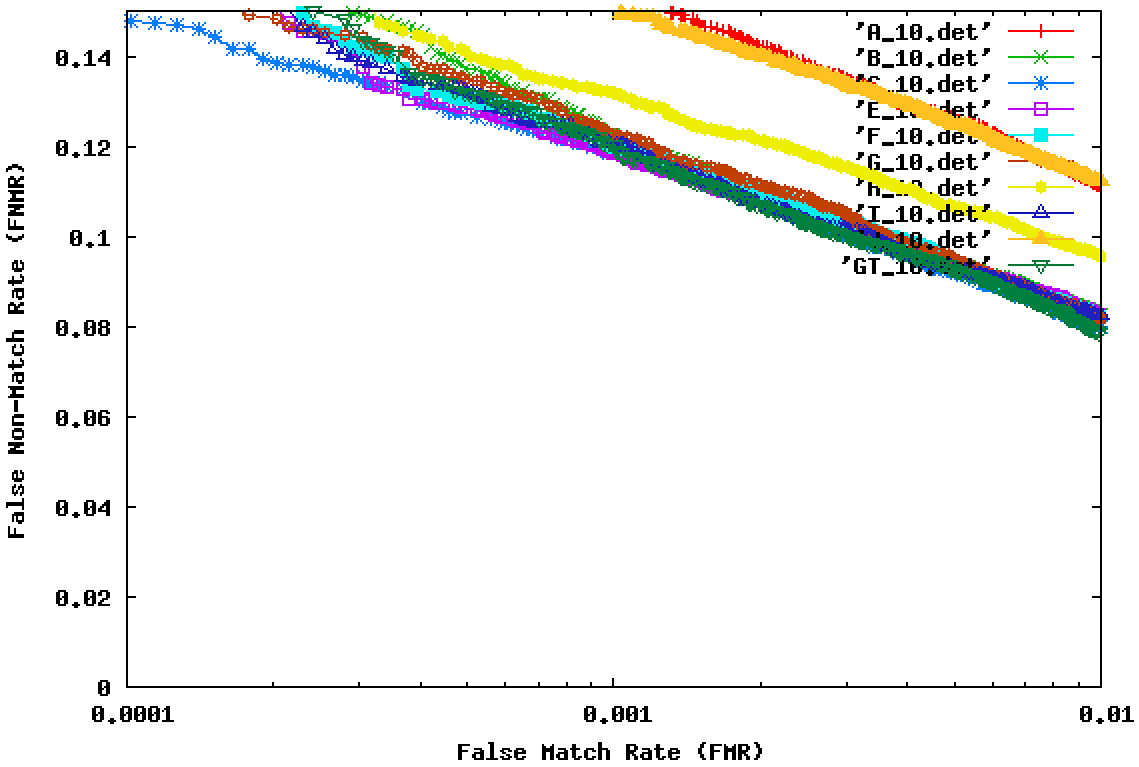
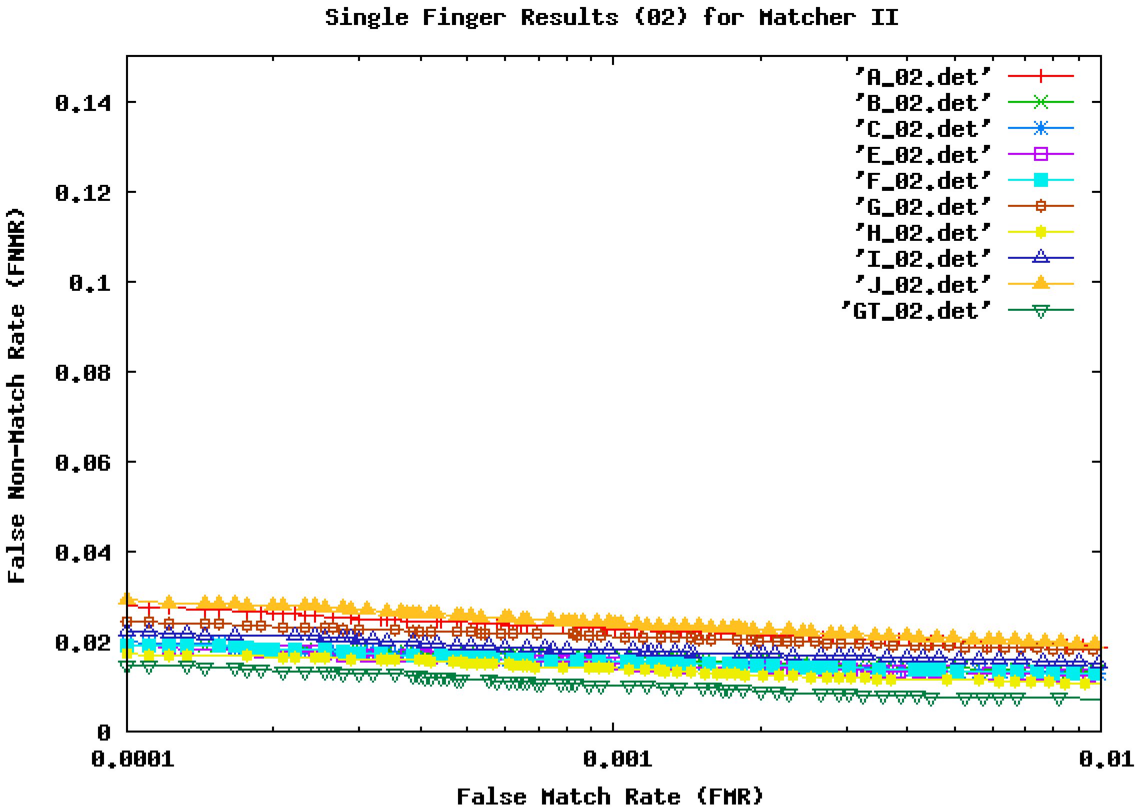


Single Finger Results (10) for Matcher I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0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
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'C_02.det'
'E_02.det'
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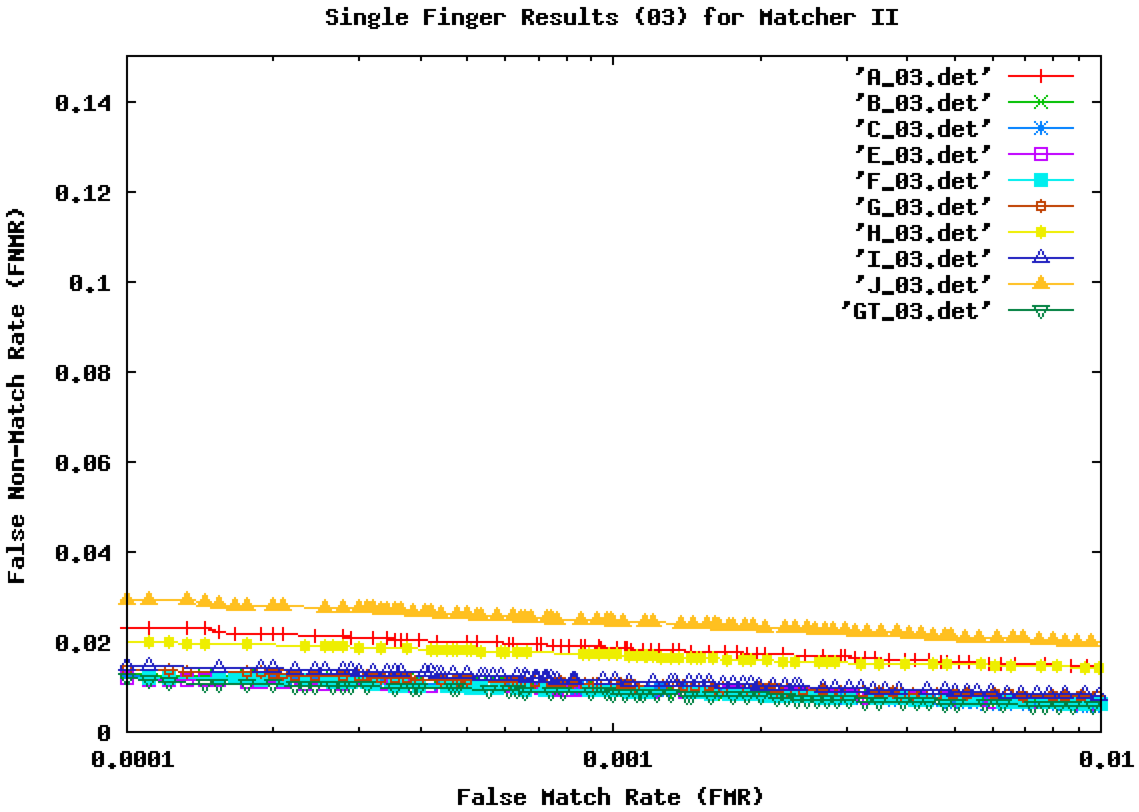
'J_02.det'
'GT_02.det'


Single Finger Results (03) for Matcher II
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0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
'A_03.det'
'B_03.det'
'C_03.det'
'E_03.det'
'F_03.det'
'G_03.det'
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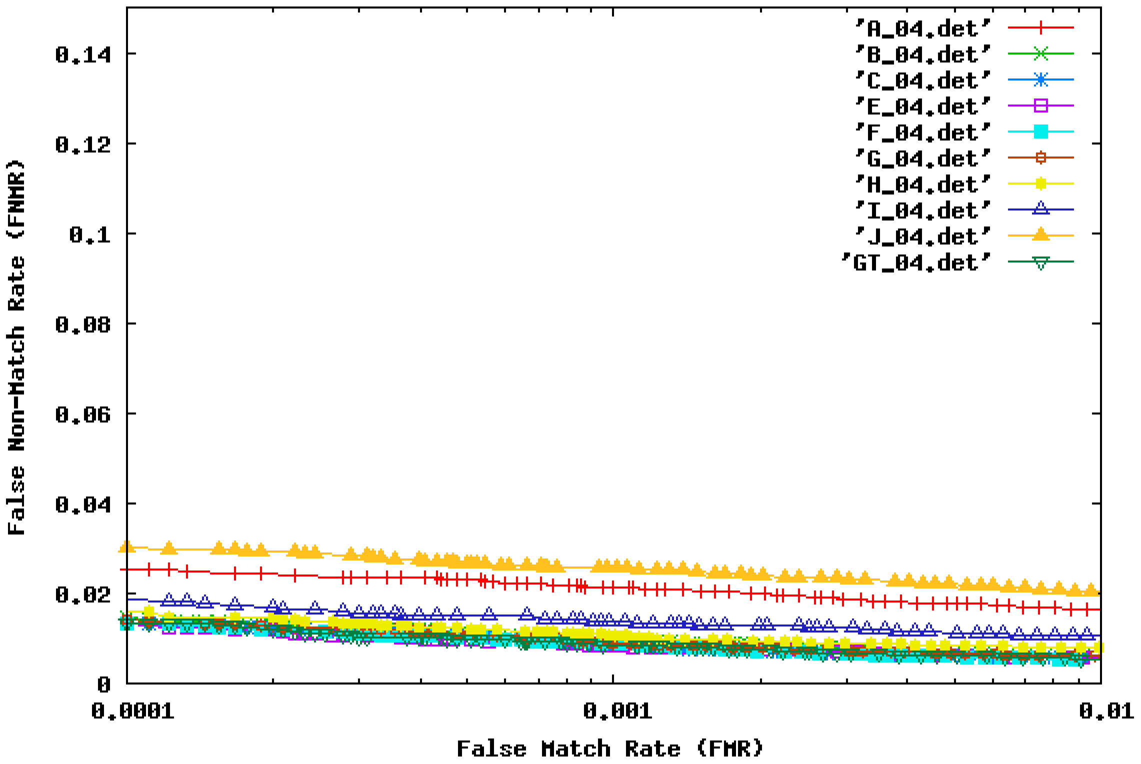
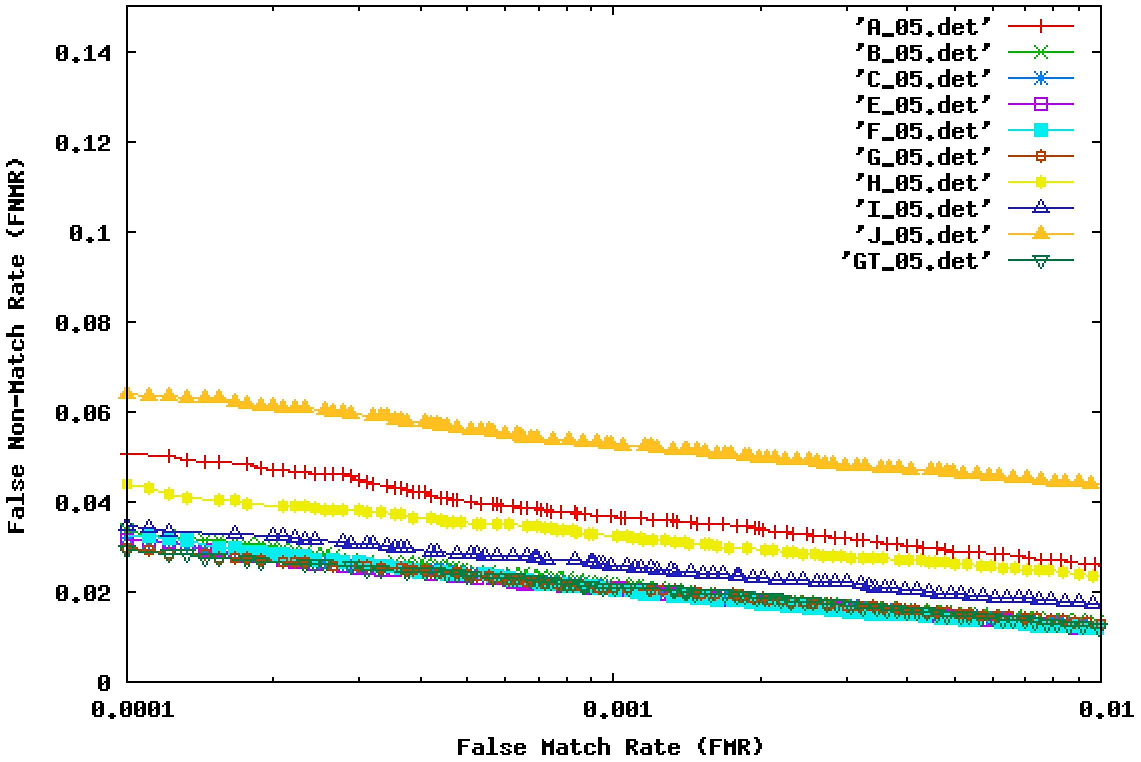
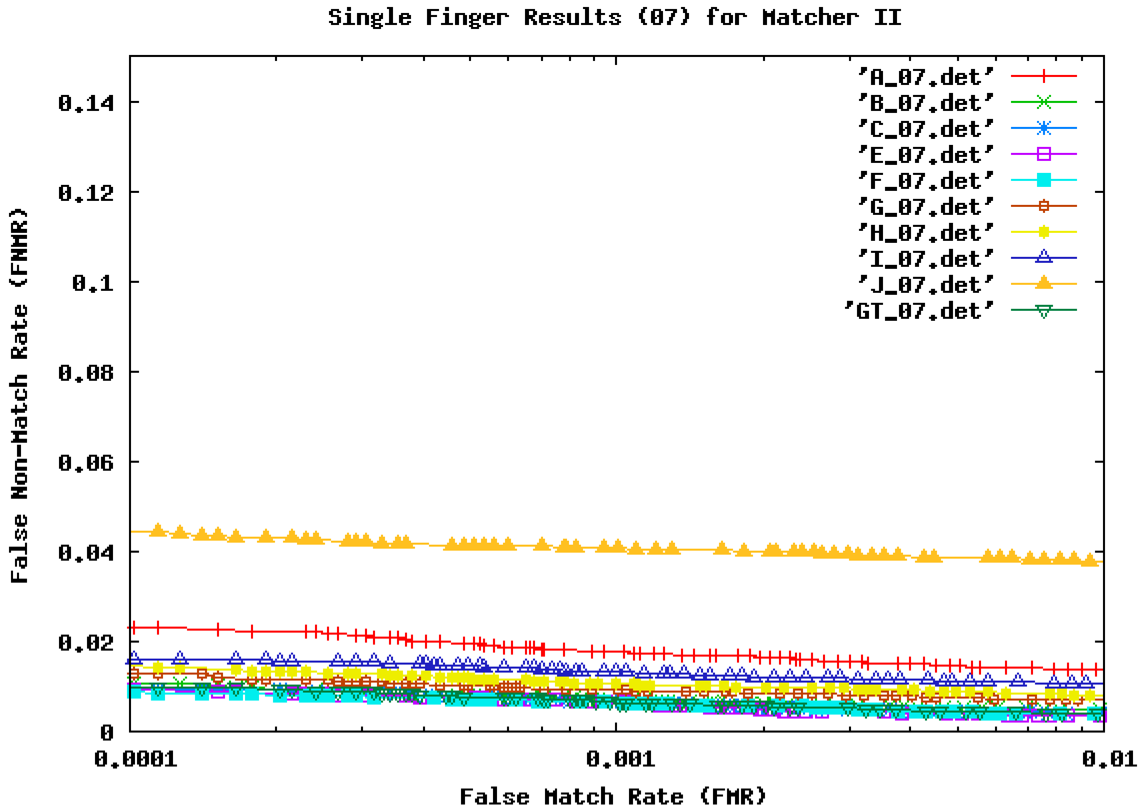
'J_03.det'
'GT_03.det'



Single Finger Results (04) for Matcher II



Single Finger Results (05) for Matcher II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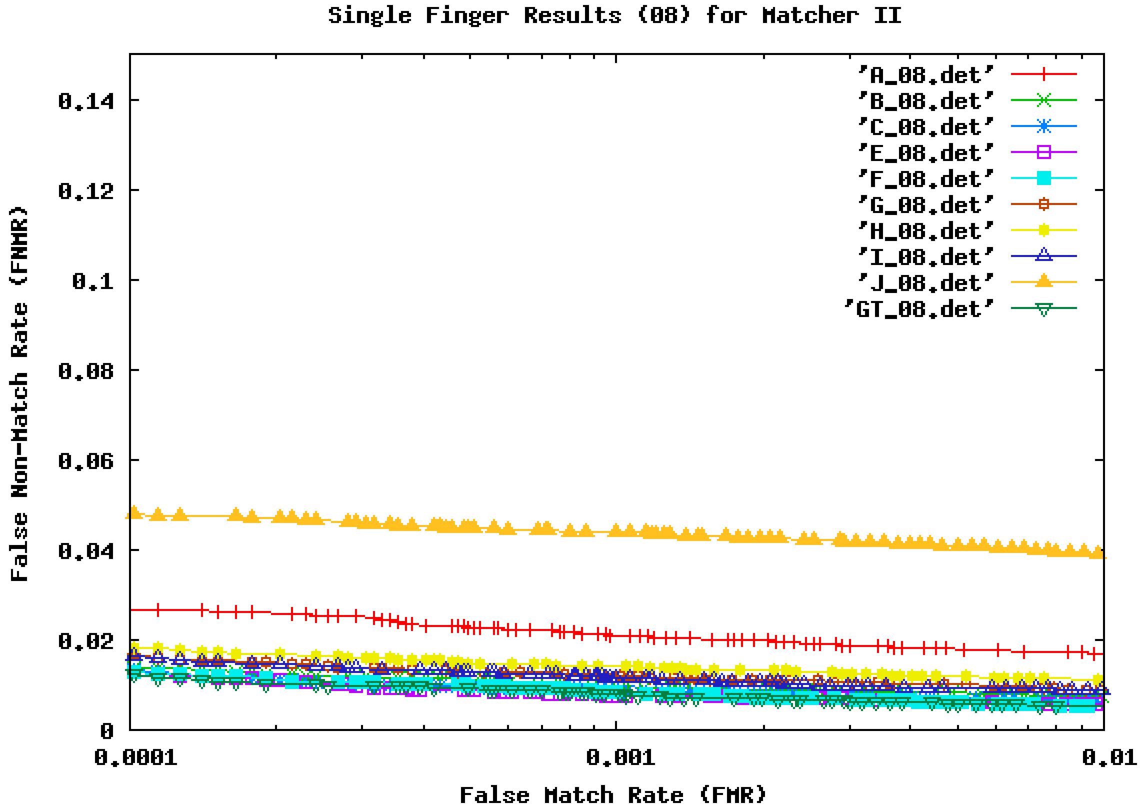
'H_07.det'
'I_07.det'
'J_07.det'
'GT_07.det'
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)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False Non-Match Rate (FNMR)
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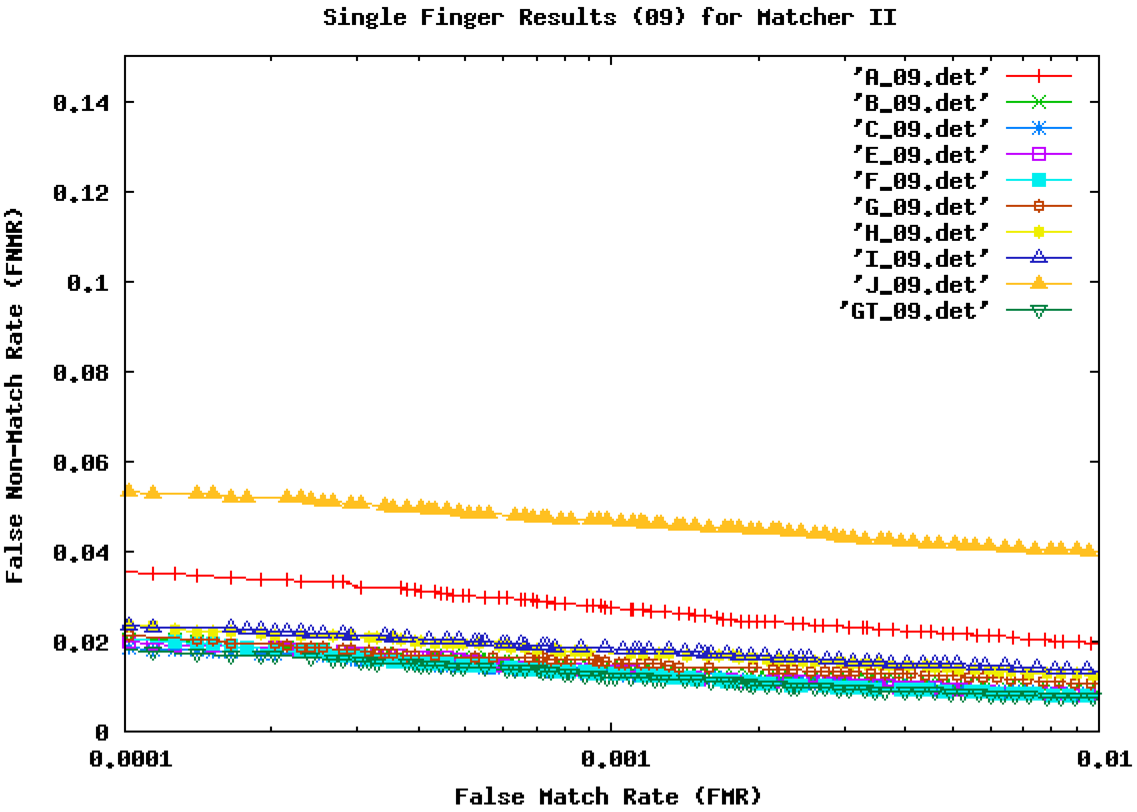
False Match Rate (FMR)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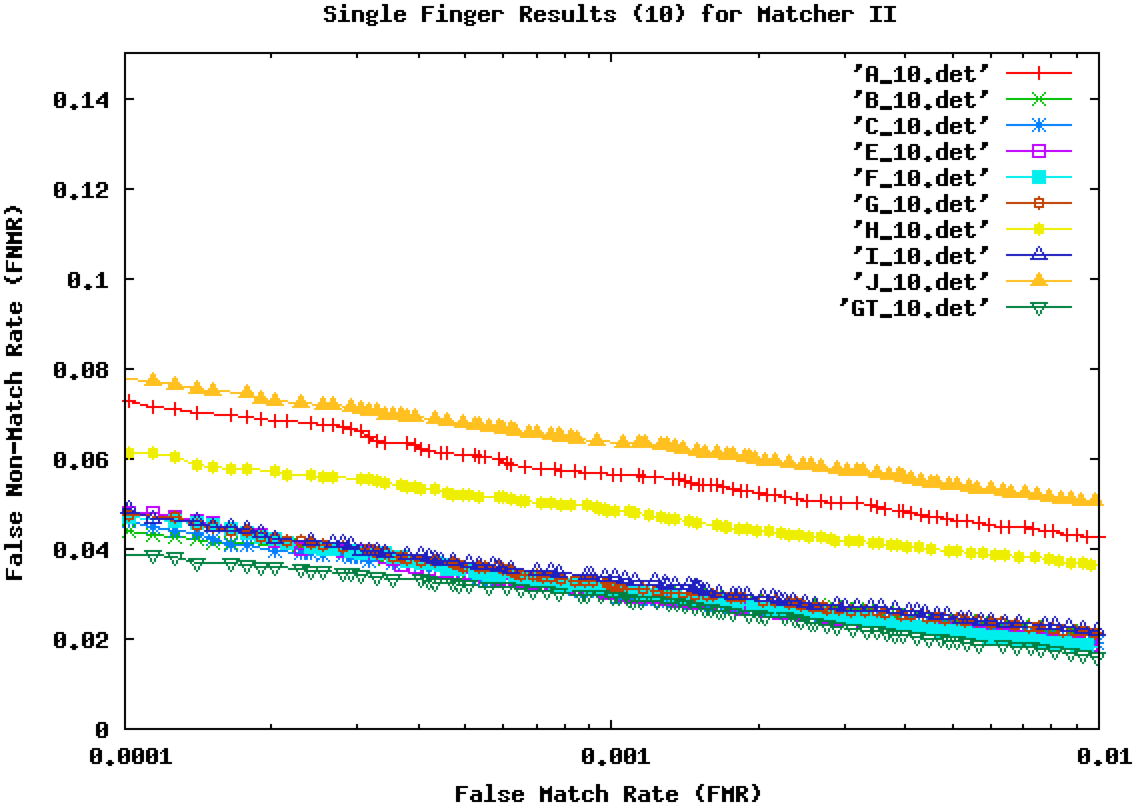
Single Finger Results (10) for Matcher II
False Non-Match Rate (FNMR)
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0.06
0.04
0.02
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0.0001
0.001
0.01
False Match Rate (FMR)
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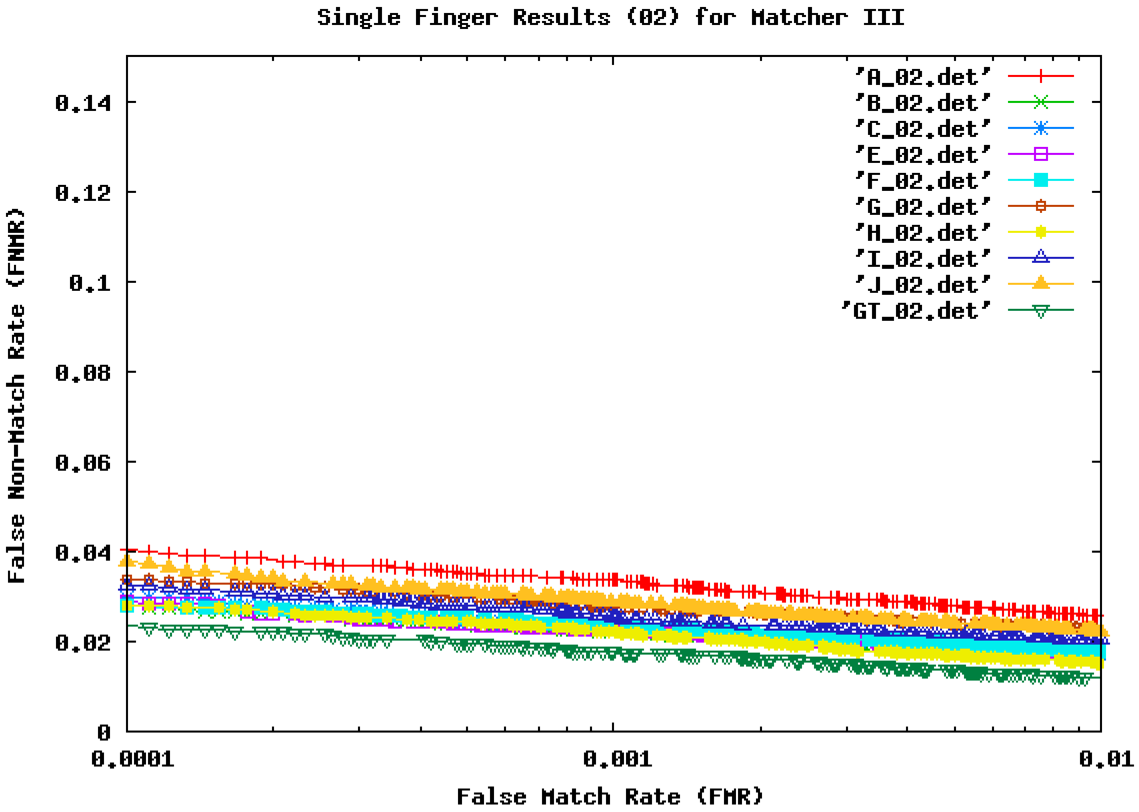
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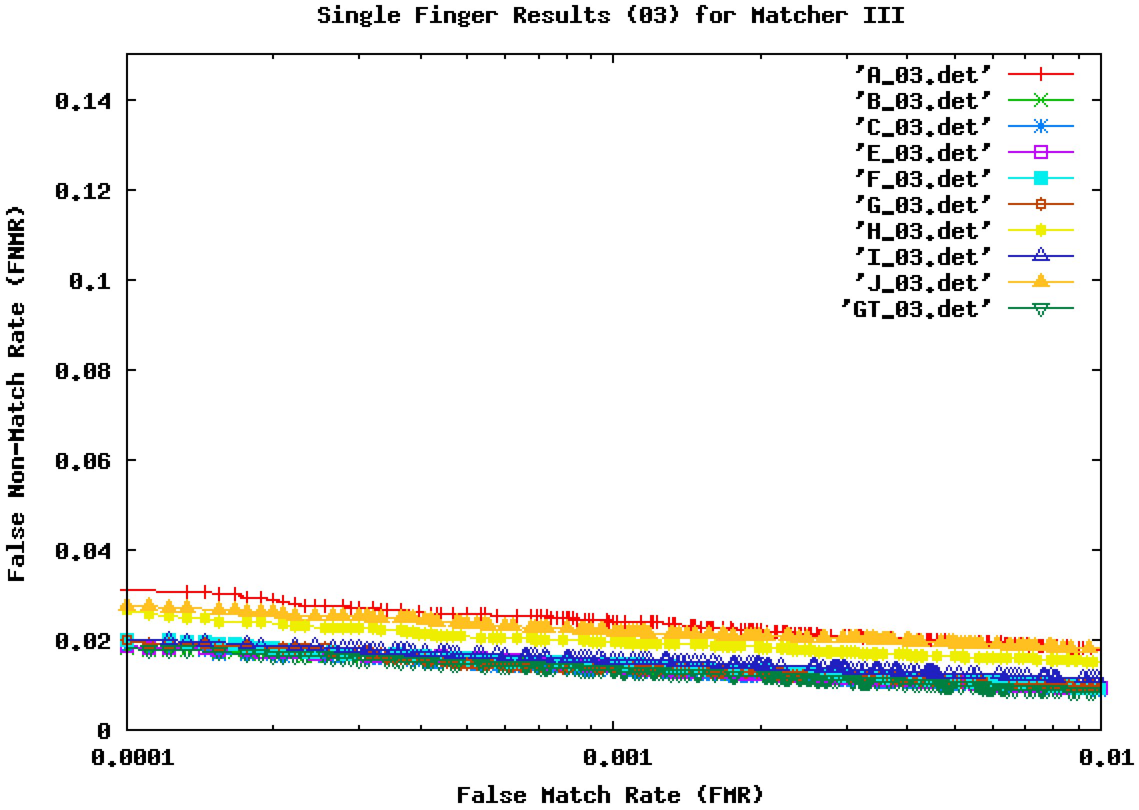
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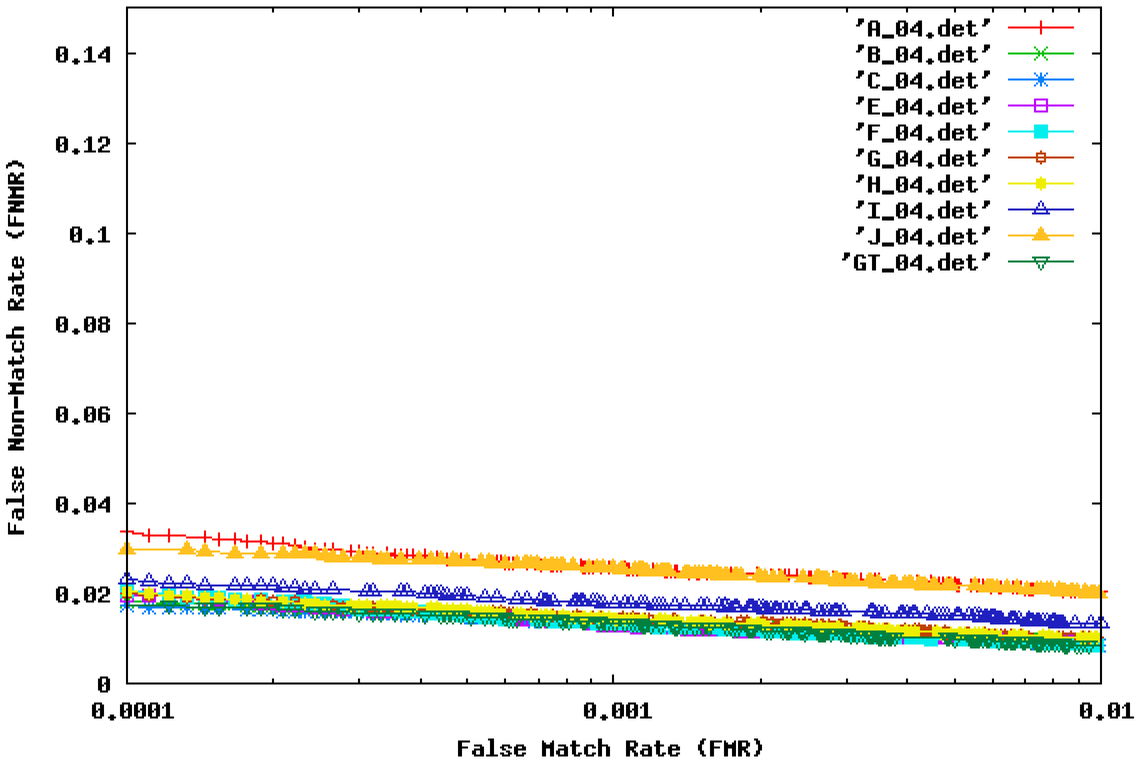
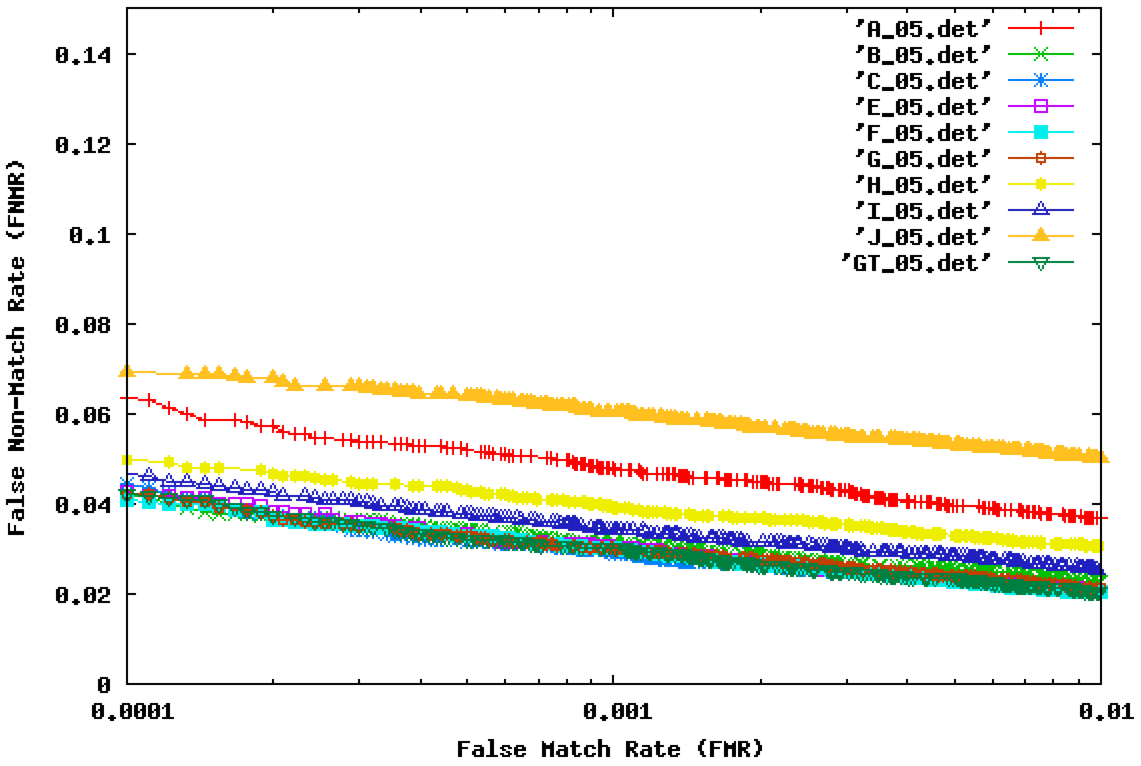
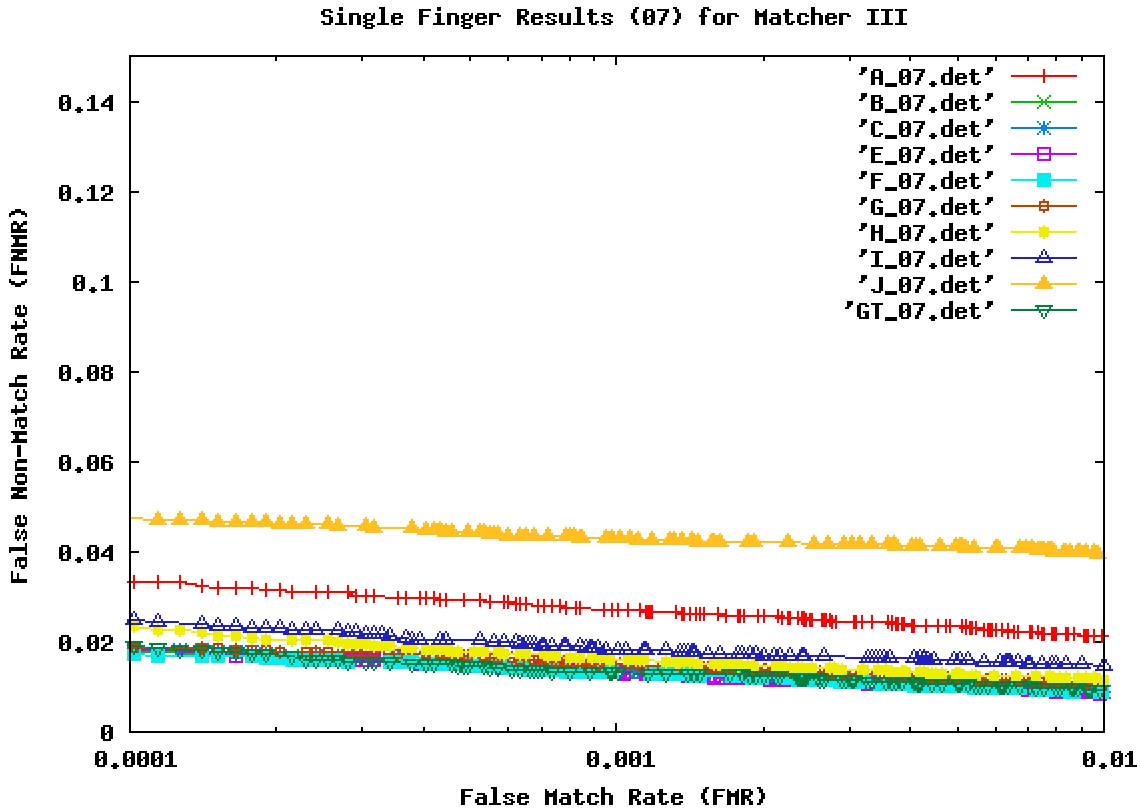


Single Finger Results (04) for Matcher III



Single Finger Results (05) for Matcher III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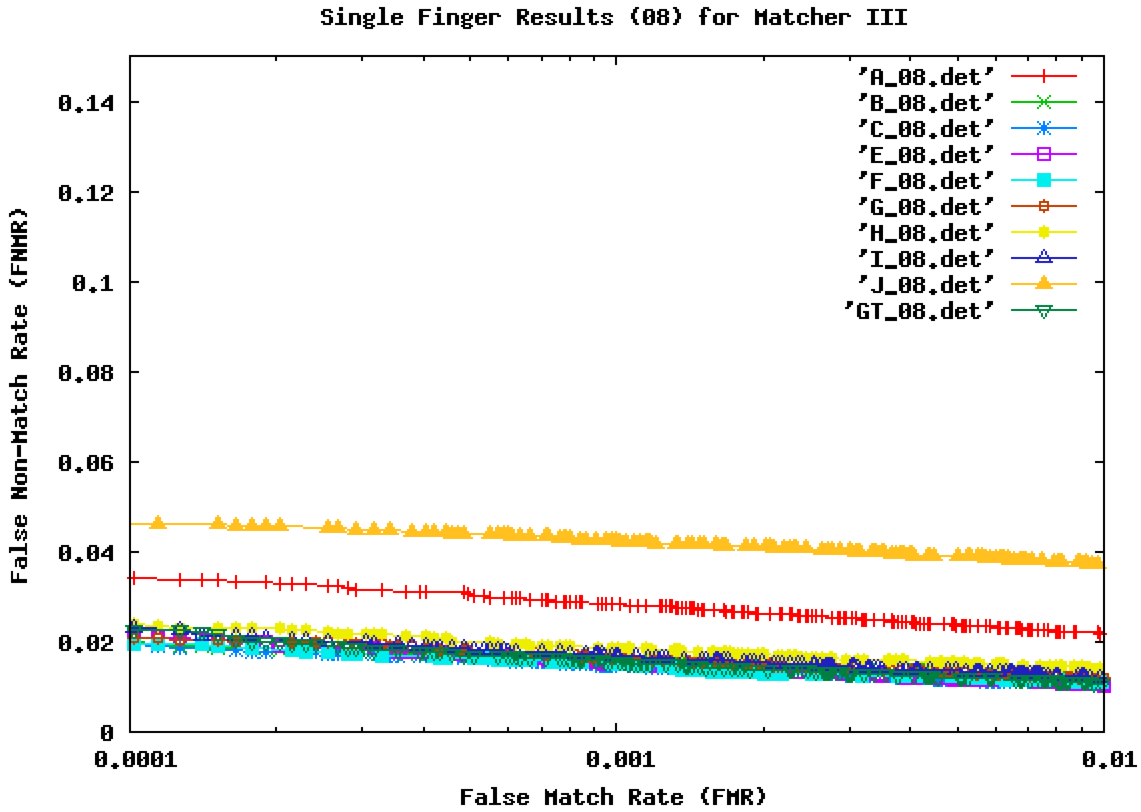
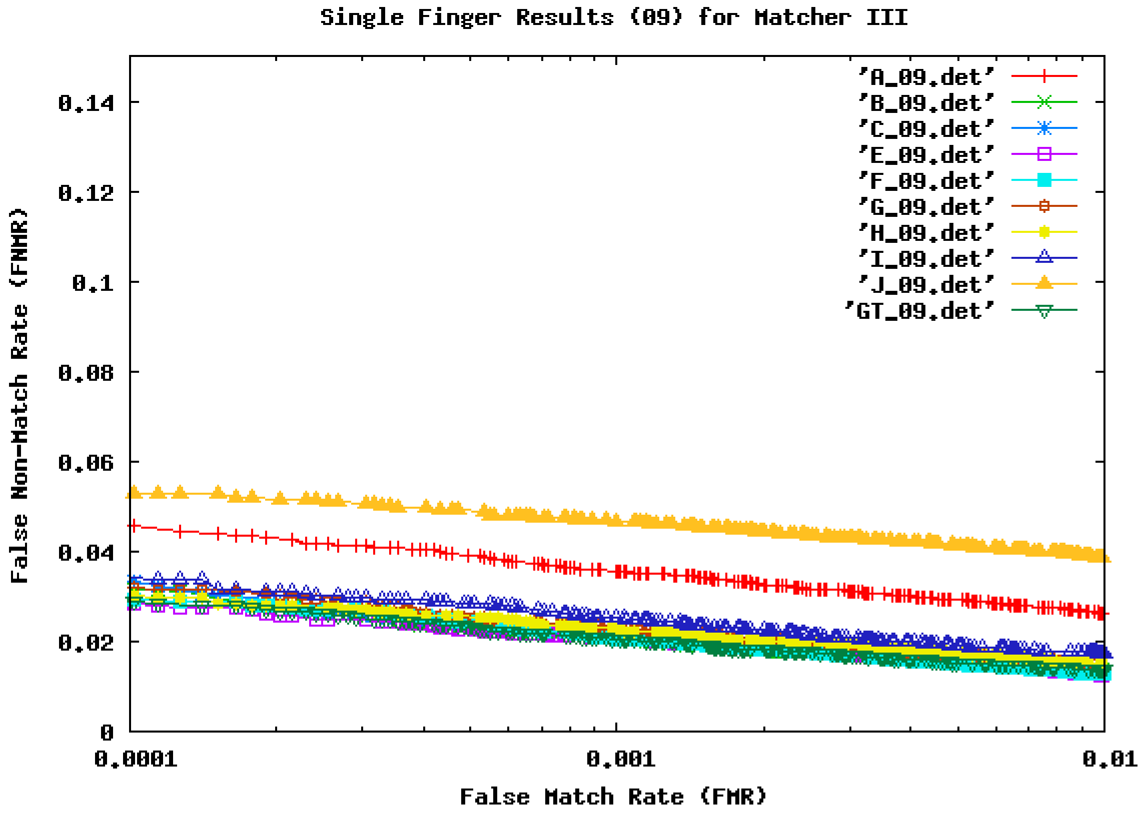
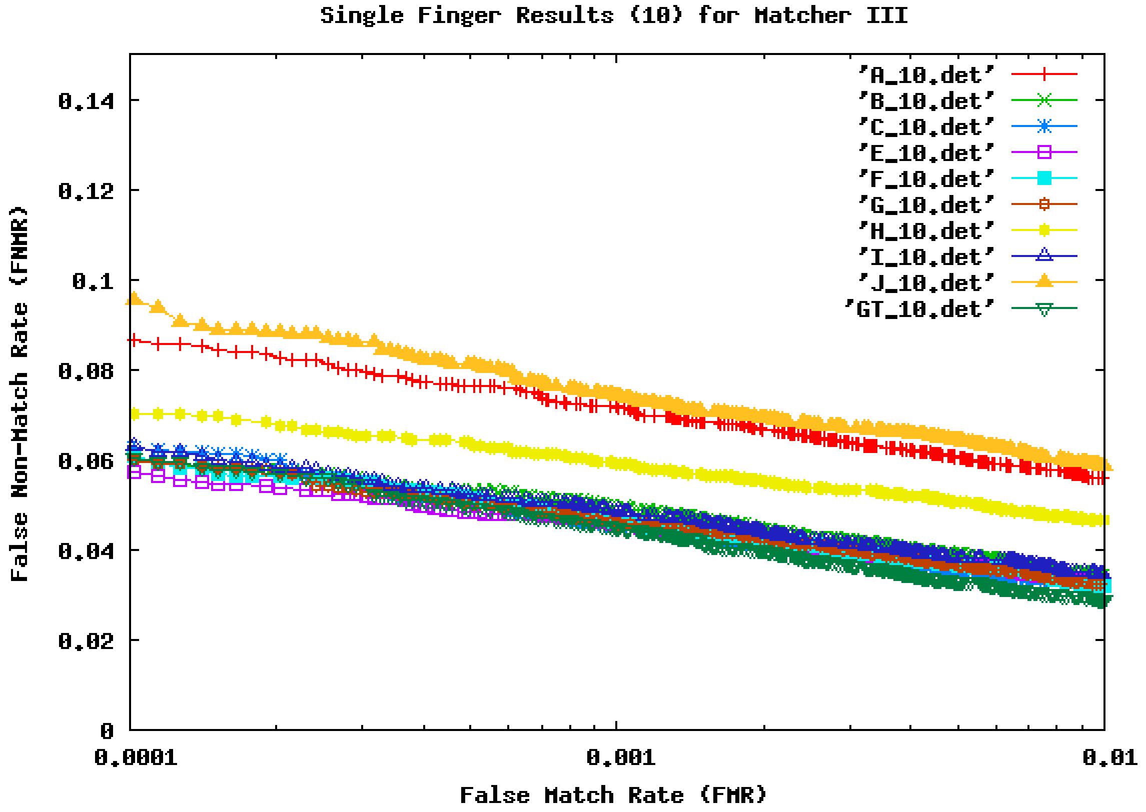
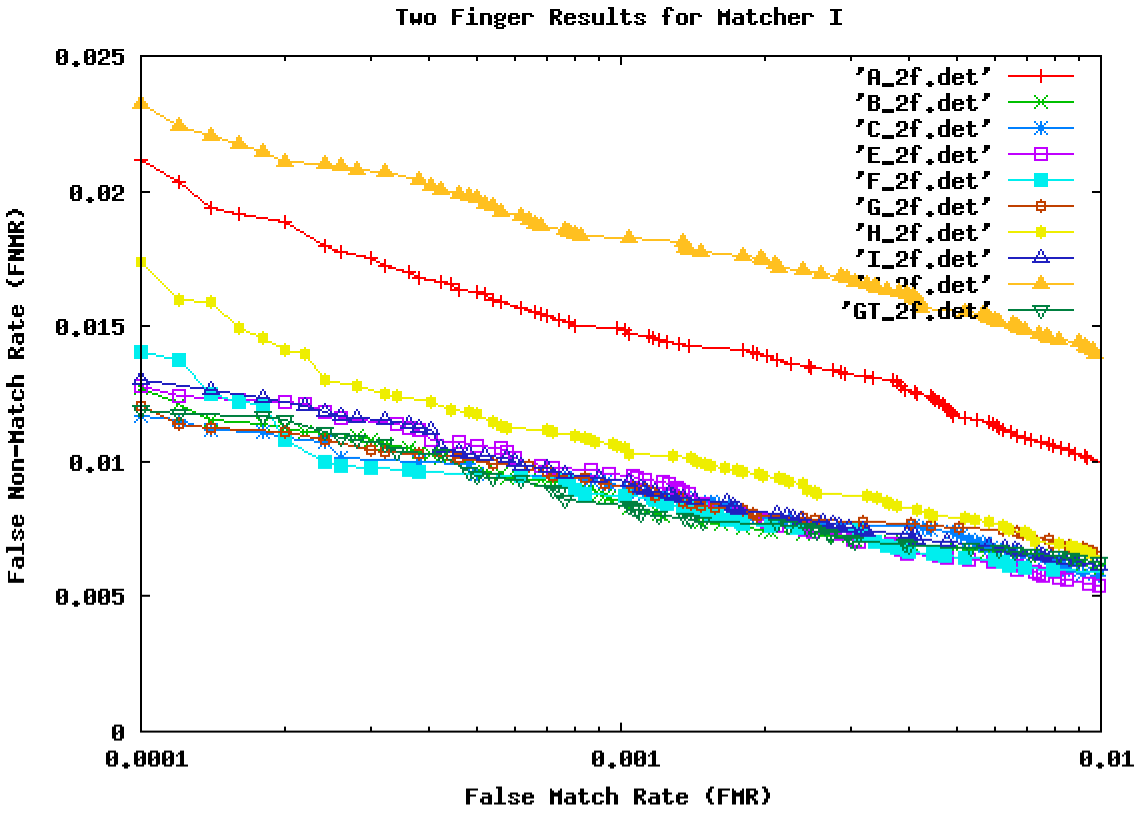
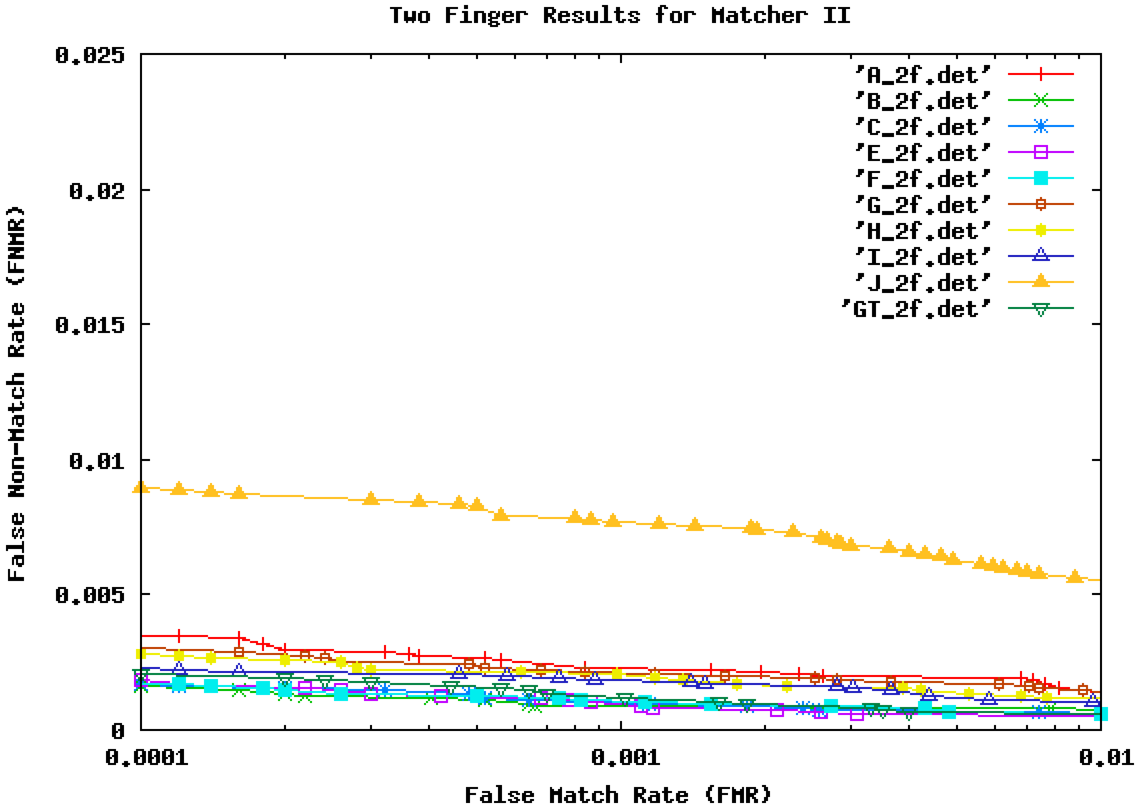
False Match Rate (FMR)
'A_07.det'
'B_07.det'
'C_07.det'
'E_07.det'
'F_07.det'
'G_07.det'
'H_07.det'
'I_07.det'
'J_07.det'
'GT_07.det'

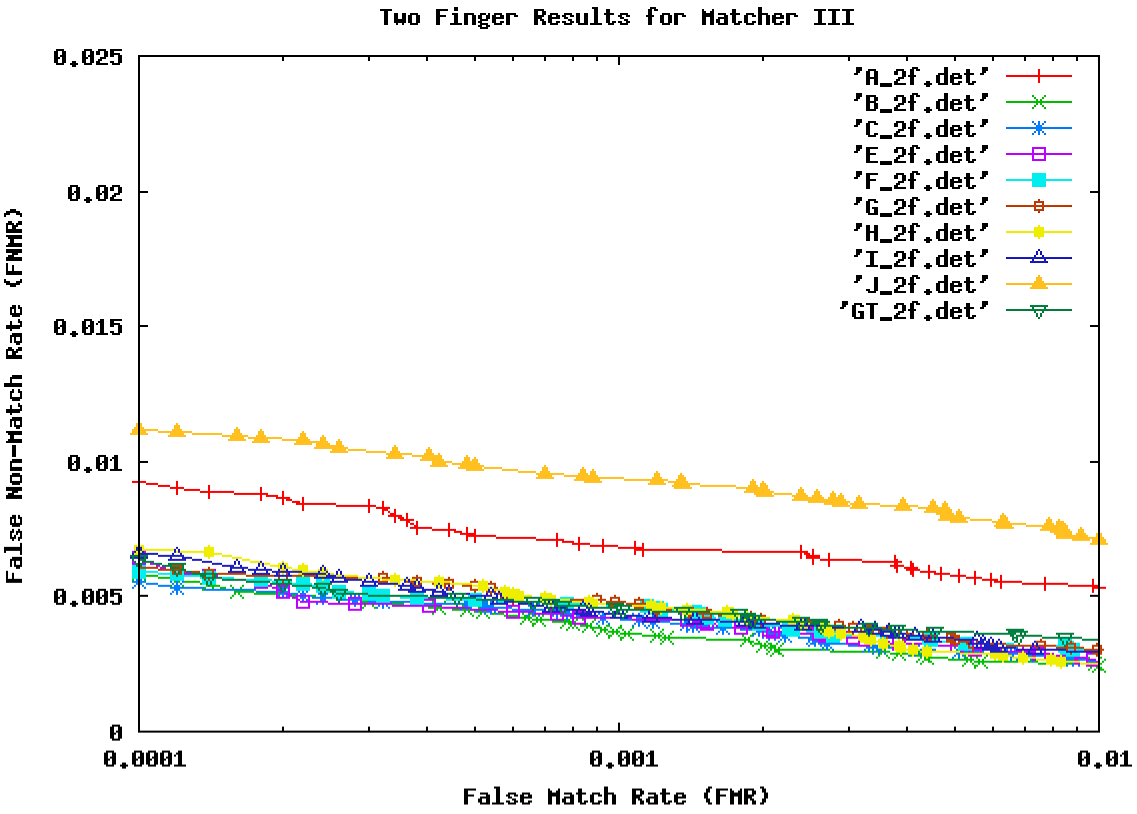

Single Finger Results (08) for Matcher III
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
'A_08.det'
'B_08.det'
'C_08.det'
'E_08.det'
'F_08.det'
'G_08.det'
'H_08.det'
'I_08.det'
'J_08.det'
'GT_08.det'

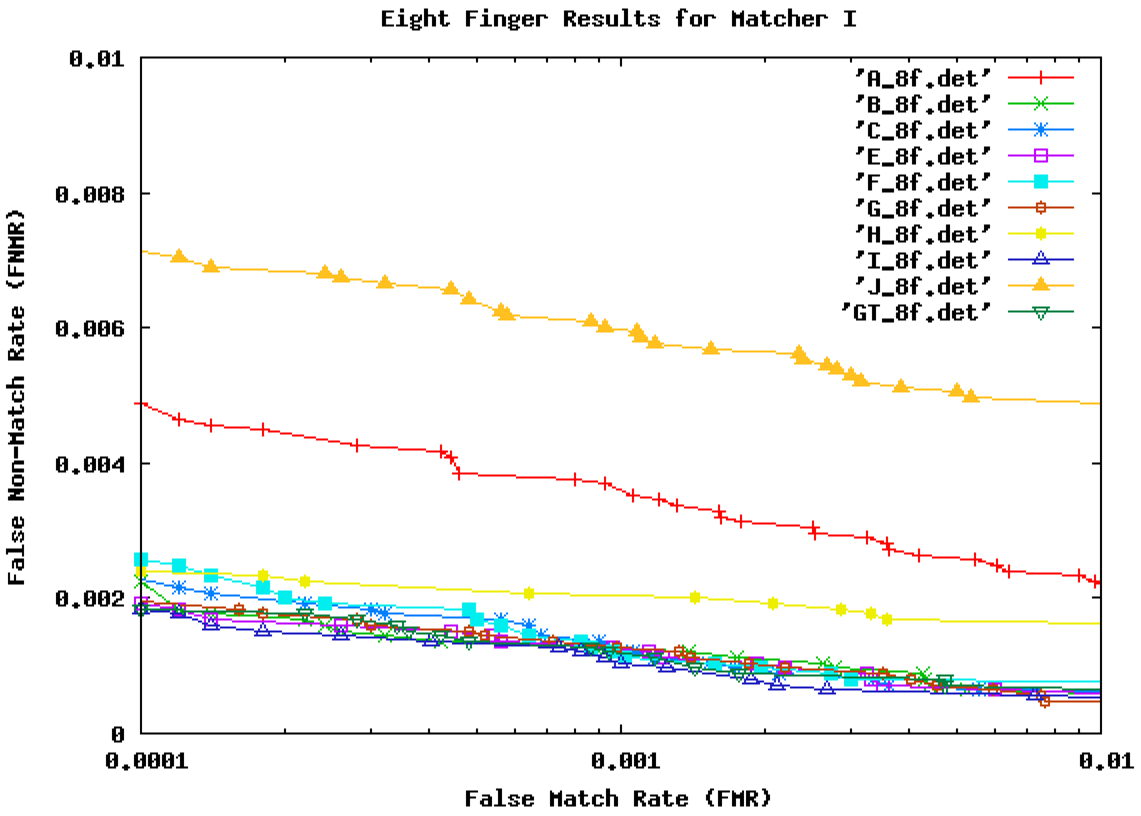

Single Finger Results (09) for Matcher III
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
'A_09.det'
'B_09.det'
'C_09.det'
'E_09.det'
'F_09.det'
'G_09.det'
'H_09.det'
'I_09.det'
'J_09.det'
'GT_09.det'

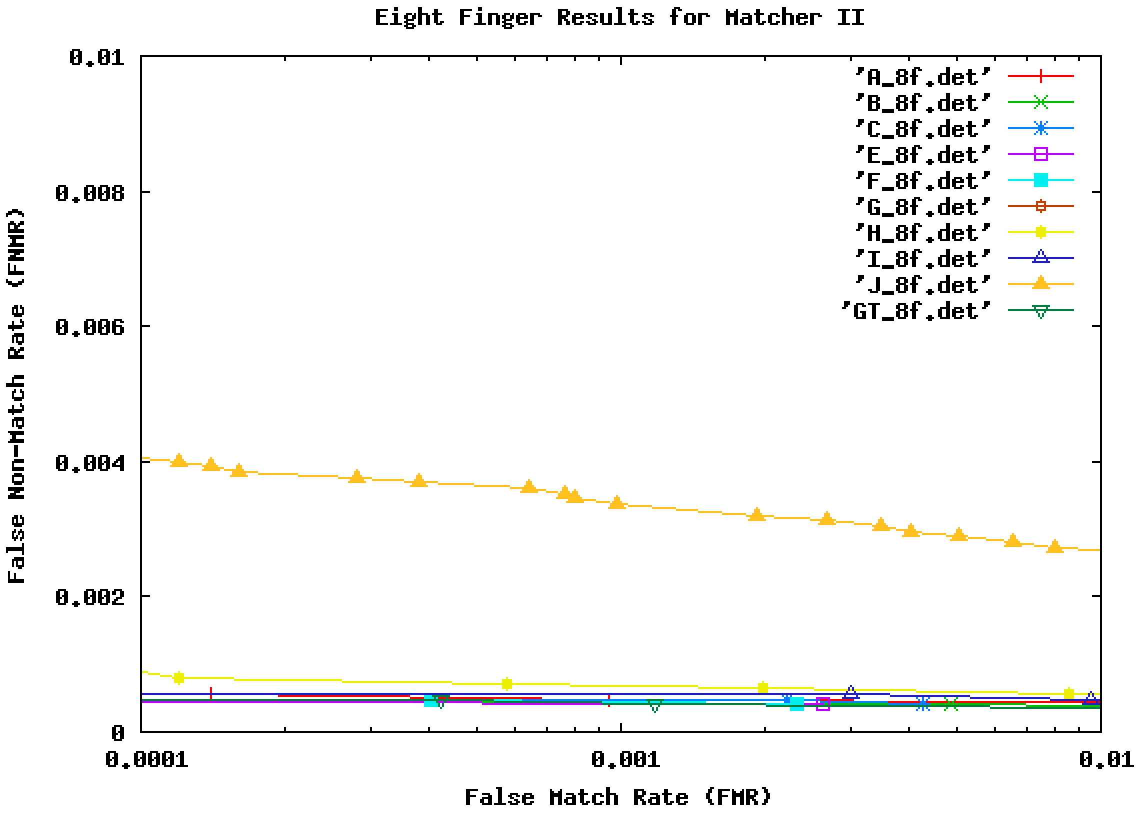

Single Finger Results (10) for Matcher III
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
'A_10.det'
'B_10.det'
'C_10.det'
'E_10.det'
'F_10.det'
'G_10.det'
'H_10.det'
'I_10.det'
'J_10.det'
'GT_10.det'

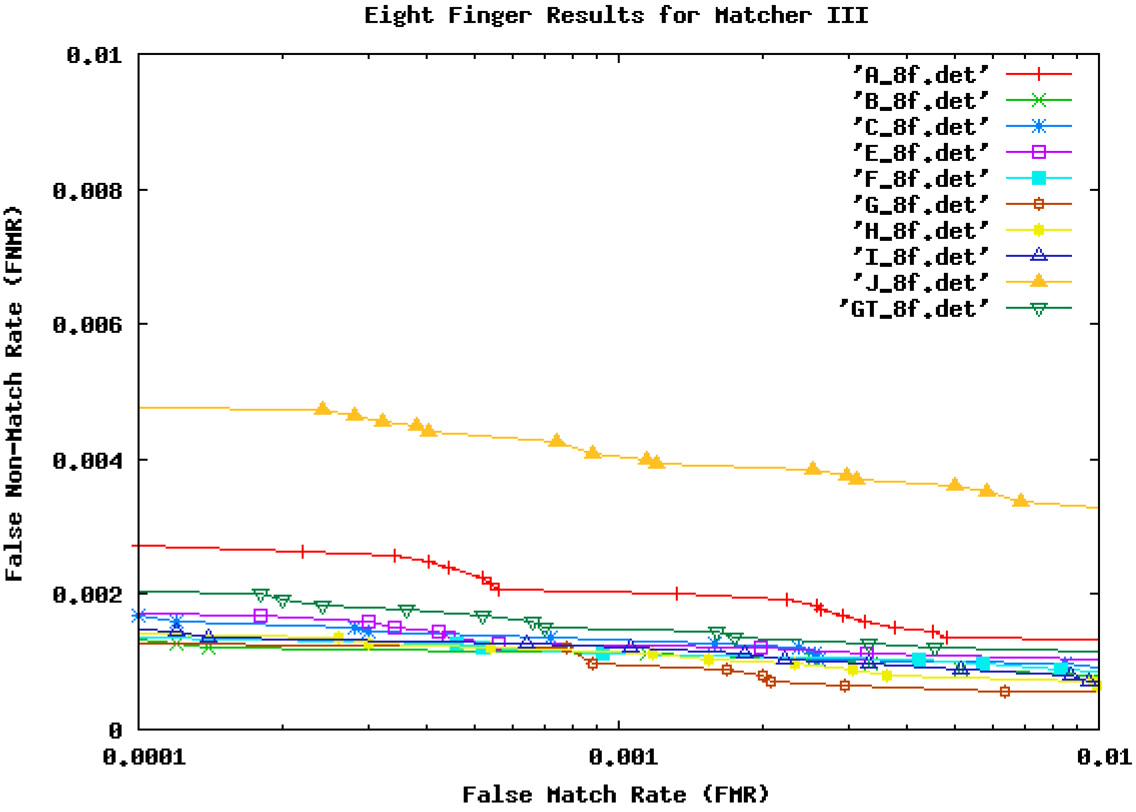

Two Finger Results for Matcher I
0.025
0.02
0.015
0.01
0.005
0
0.0001
0.001
0.01
False Non-Match Rate (FNMR)
False Match Rate (FMR)
'A_2f.det'
'B_2f.det'
'C_2f.det'
'E_2f.det'
'F_2f.det'
'G_2f.det'
'H_2f.det'
'I_2f.det'
'J_2f.det'
'GT_2f.det'


Two Finger Results for Matcher II
0.025
0.02
0.015
0.01
0.005
0
0.0001
0.001
0.01
False Non-Match Rate (FNMR)
False Match Rate (FMR)
'A_2f.det'
'B_2f.det'
'C_2f.det'
'E_2f.det'
'F_2f.det'
'G_2f.det'
'H_2f.det'
'I_2f.det'
'J_2f.det'
'GT_2f.det'


Two Finger Results for Matcher III
False Non-Match Rate (FNMR)
0.025
0.02
0.015
0.01
0.005
0
0.0001
0.001
0.01
False Match Rate (FMR)
'A_2f.det'
'B_2f.det'
'C_2f.det'
'E_2f.det'
'F_2f.det'
'G_2f.det'
'H_2f.det'
'I_2f.det'
'J_2f.det'
'GT_2f.det'


Eight Finger Results for Matcher I
0.01
0.008
0.006
0.004
0.002
0
0.0001
0.001
0.01
False Non-Match Rate (FNMR)
False Match Rate (FMR)
'A_8f.det'
'B_8f.det'
'C_8f.det'
'E_8f.det'
'F_8f.det'
'G_8f.det'
'H_8f.det'
'I_8f.det'
'J_8f.det'
'GT_8f.det'


Eight Finger Results for Matcher II
0.01
0.008
0.006
0.004
0.002
0
0.0001
0.001
0.01
False Non-Match Rate (FNMR)
False Match Rate (FMR)
'A_8f.det'
'B_8f.det'
'C_8f.det'
'E_8f.det'
'F_8f.det'
'G_8f.det'
'H_8f.det'
'I_8f.det'
'J_8f.det'
'GT_8f.det'


Eight Finger Results for Matcher III
False Non-Match Rate (FNMR)
False Match Rate (FMR)
0.01
0.008
0.006
0.004
0.002
0
0.0001
0.001
0.01
'A_8f.det'
'B_8f.det'
'C_8f.det'
'E_8f.det'
'F_8f.det'
'G_8f.det'
'H_8f.det'
'I_8f.det'
'J_8f.det'
'GT_8f.det'

Appendix E

This appendix has plots of False Non-Match Rate (FNMR) vs False Match Rate (FMR) for single finger, two finger, and eight finger combinations using three different matching algorithms. The segmentation boxes were the hand marked boxes (GT), the minimum tolerance limits allowed in SlapSegII (GTL), and 16 pixels inside the minimum tolerance limits (GTL2). The minimum tolerance allowed in SlapSegII was -32 pixels for the left and right sides, -64 pixels for the top, and -64 pixels for the bottom. Note that the y-axis (FNMR) scale changes between the single finger, two finger and eight finger plots.

The three matching algorithms were high-end performers in the Proprietary Fingerprint Template (PFT)[1] evaluation but with different speed and template size characteristics. Matcher-I had the smallest feature template and was the fastest in both template extractions and matching. Matcher-II was two times slower than Matcher-I in template extractions, had larger templates, and was only slightly slower in matching speed. Matcher-III was 3-4 times slower than Matcher-I for template extraction, had the largest template size, and was 2-3 times as slow in matching speed.

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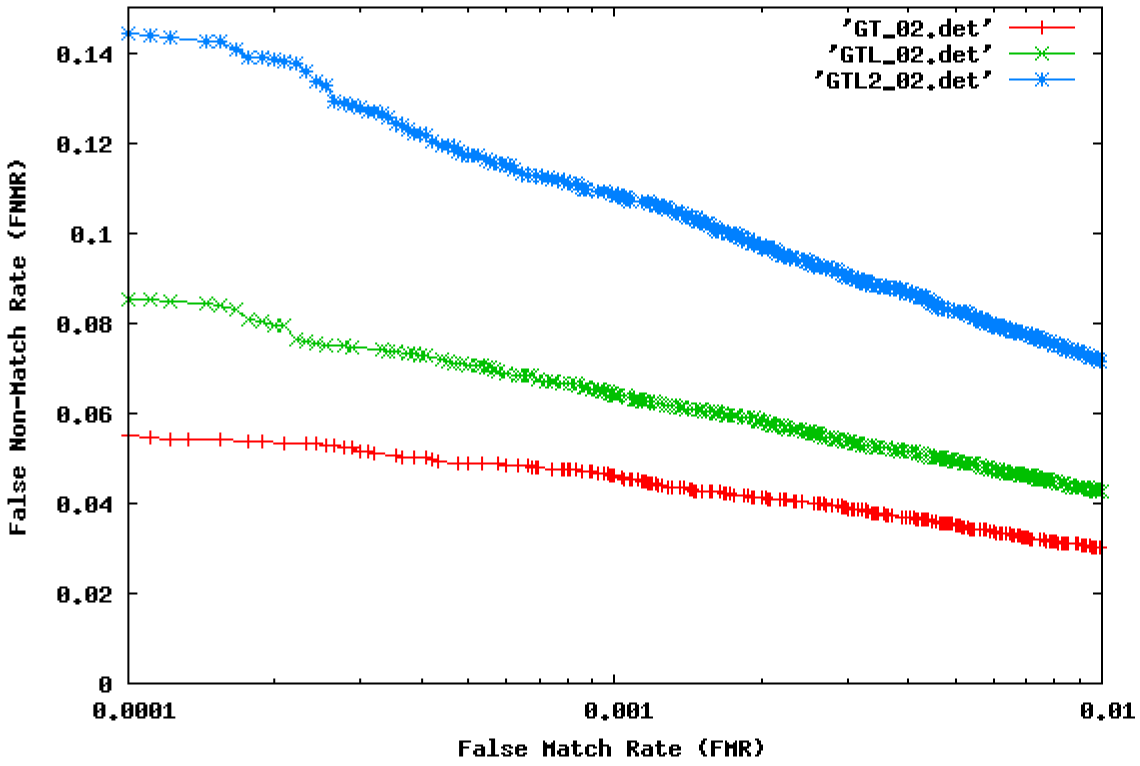
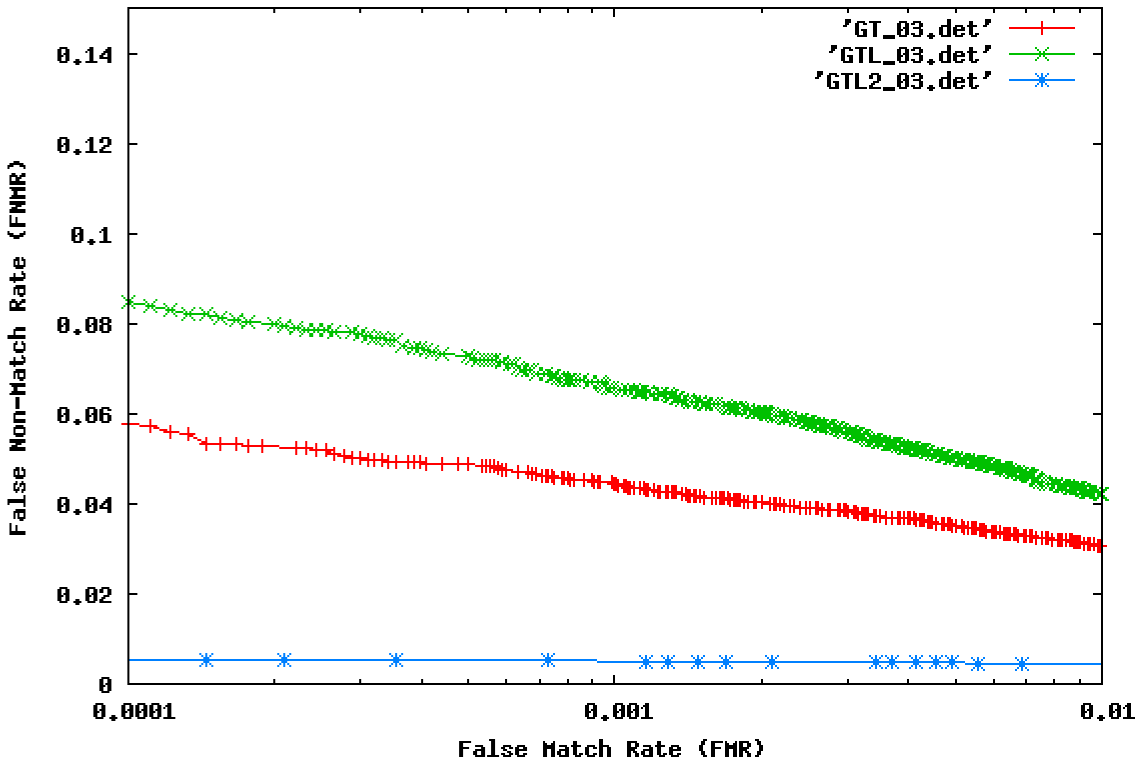
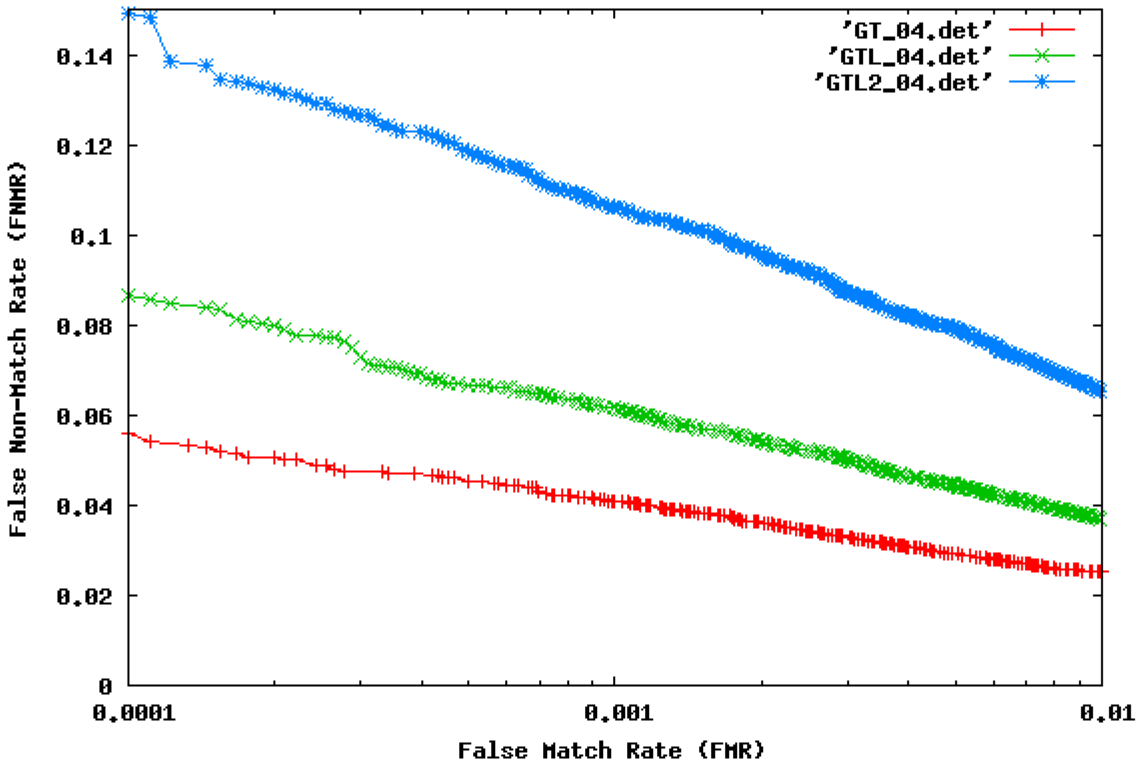
[1] http://www.nist.gov/itl/iad/ig/pft.cfm

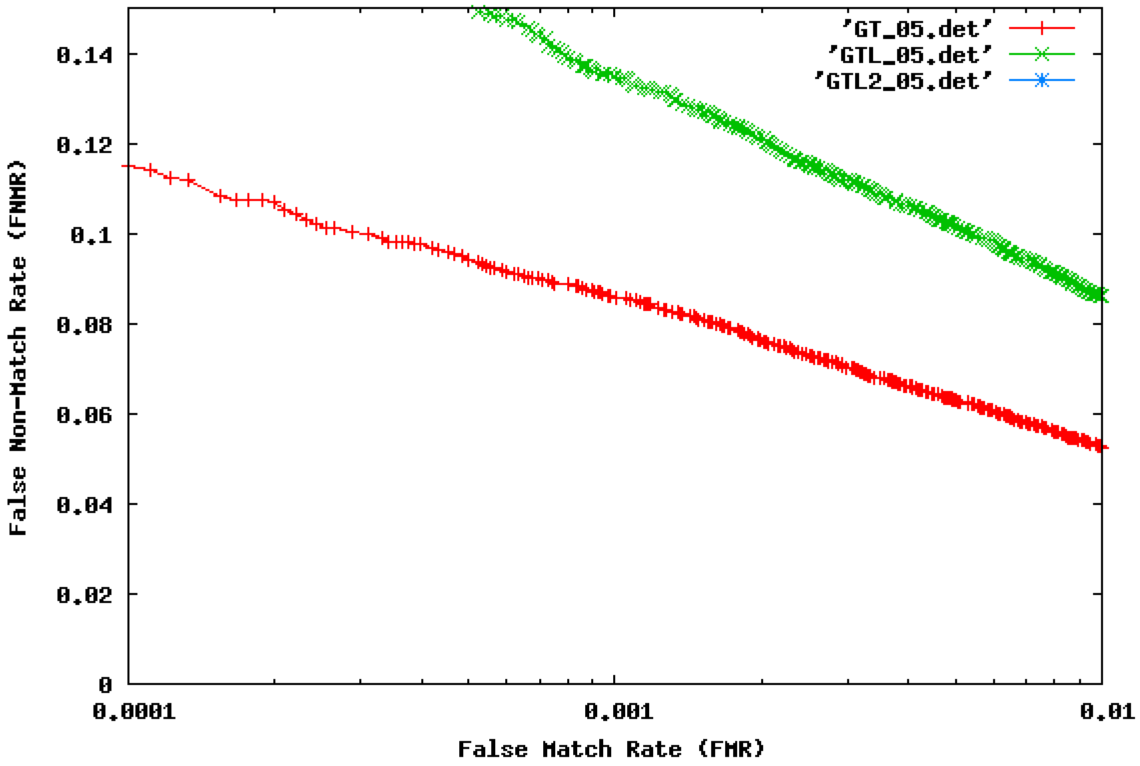
Hand Marked - Single Finger Results (02) for Matcher I



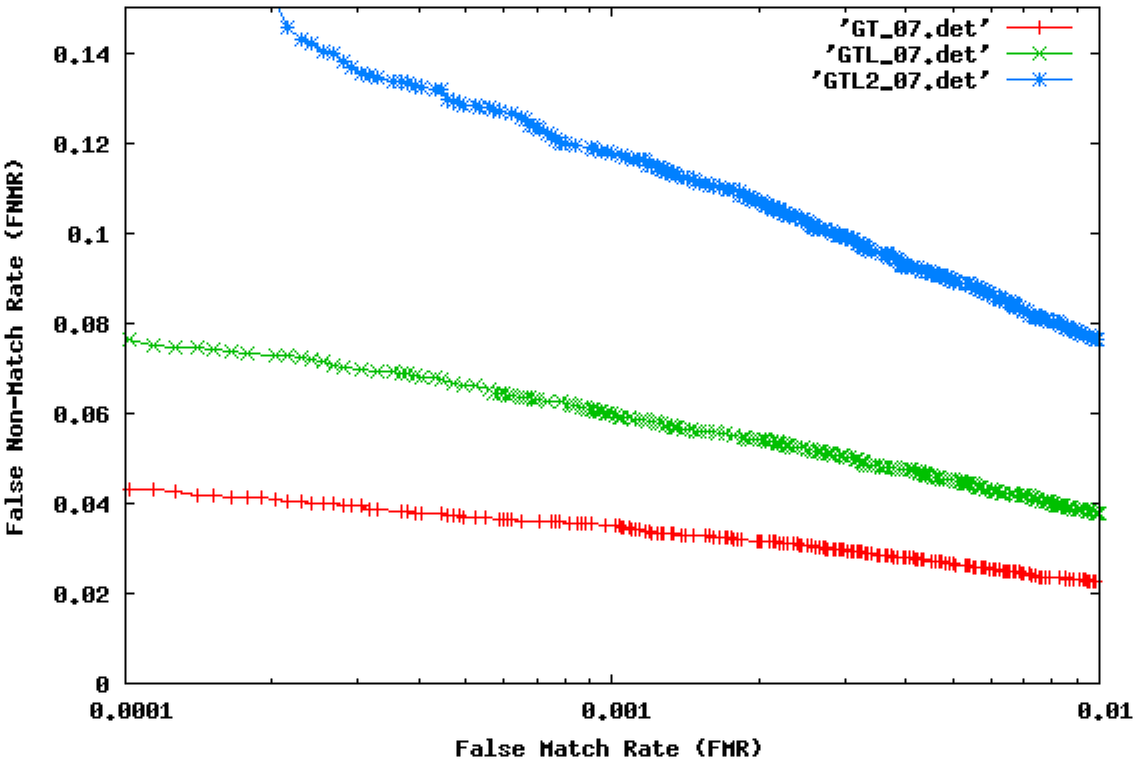
Hand Marked - Single Finger Results (03) for Matcher I



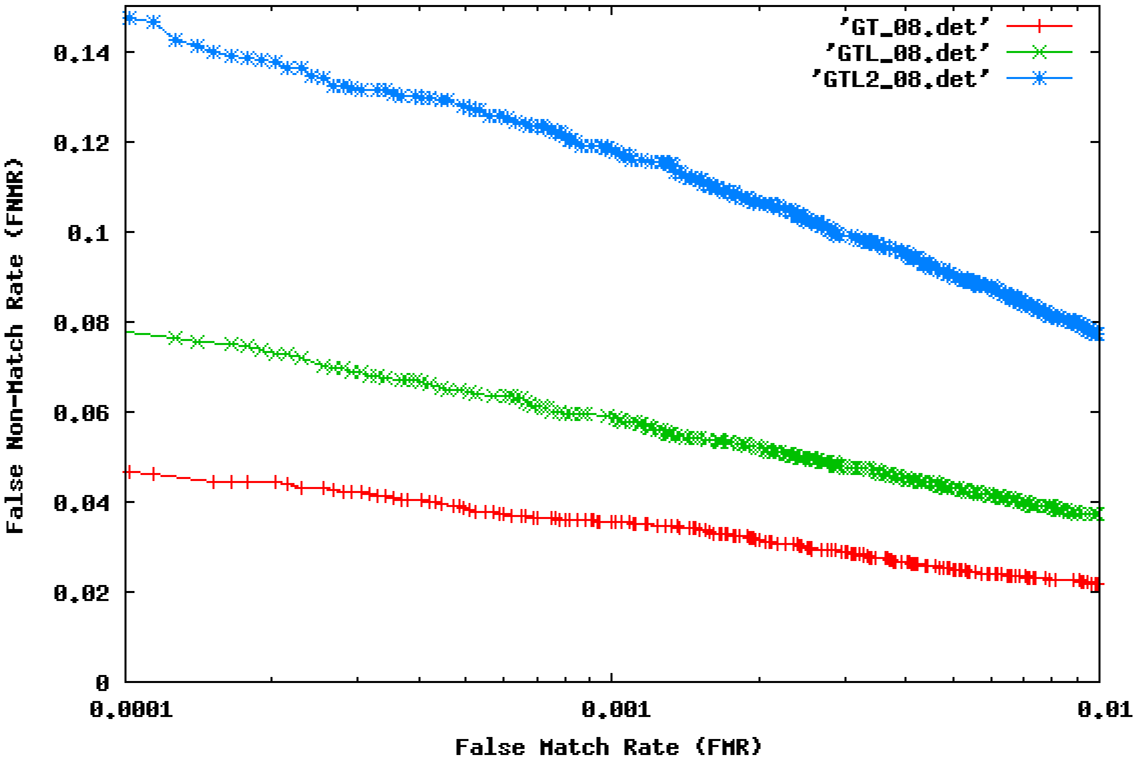

Hand Marked - Single Finger Results (04) for Matcher I

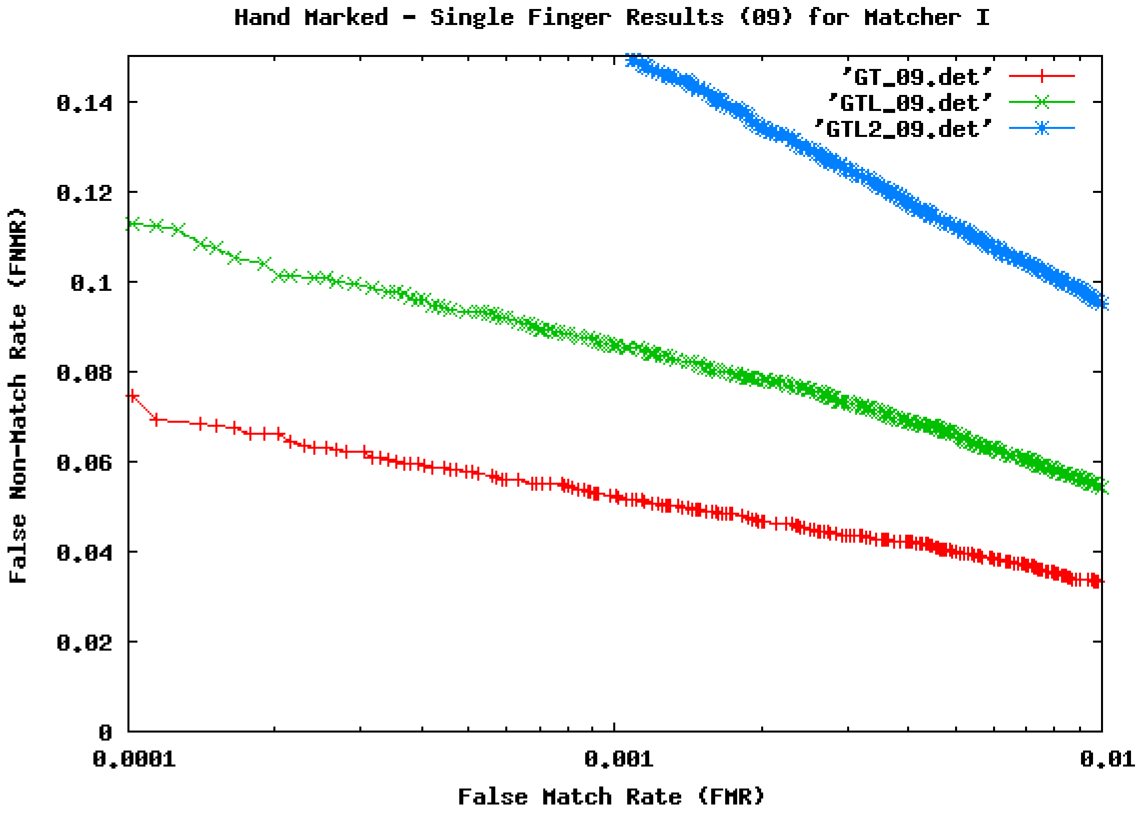

Hand Marked - Single Finger Results (05) for Matcher I

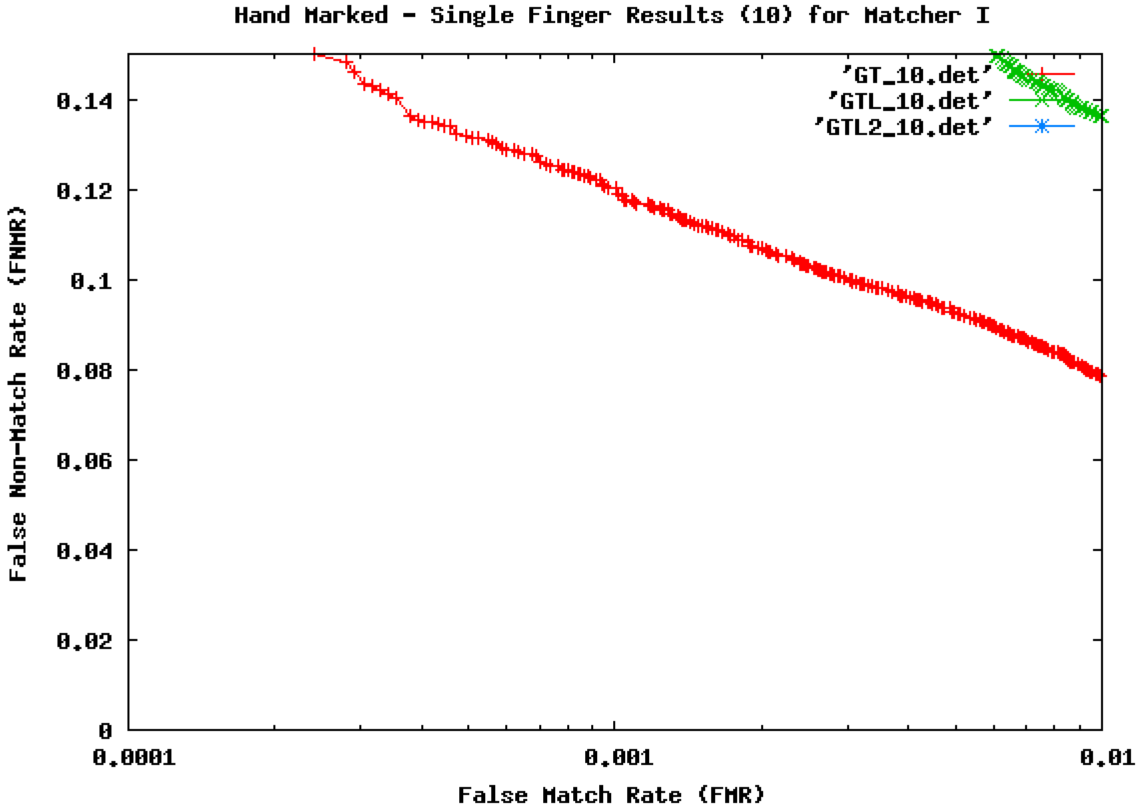
Hand Marked - Single Finger Results (07) for Matcher I

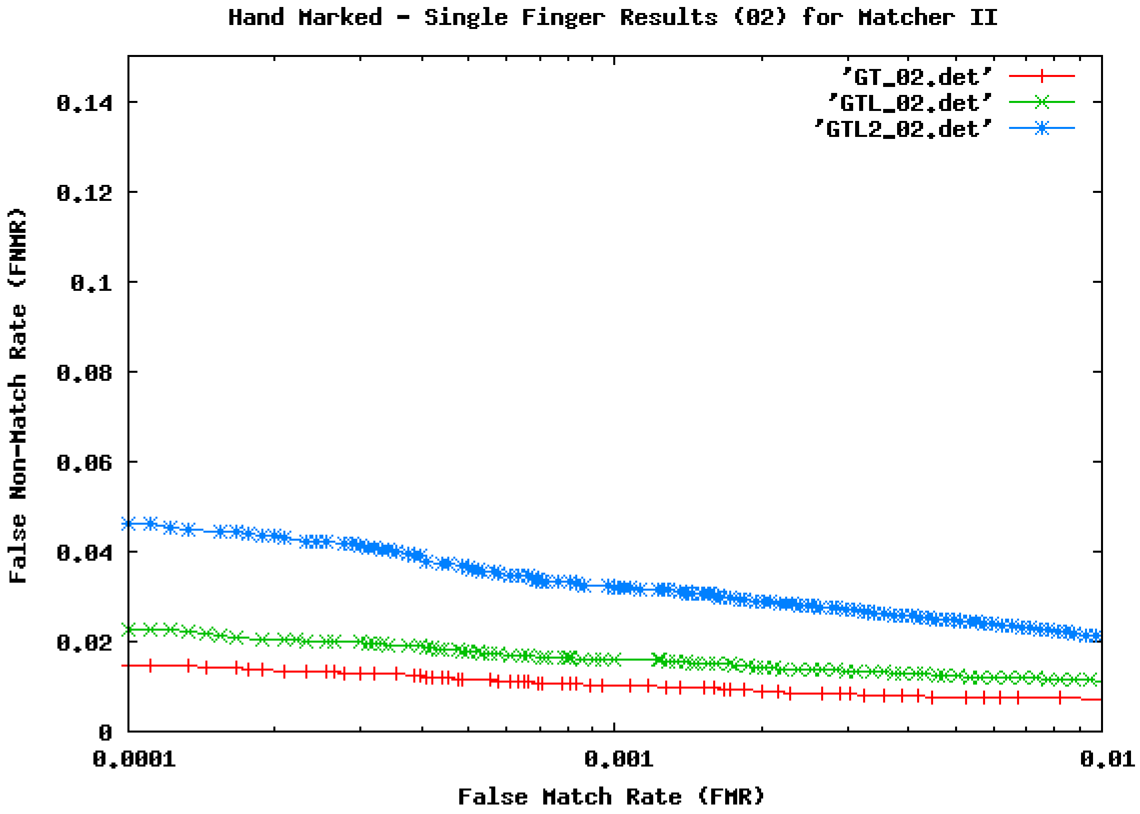


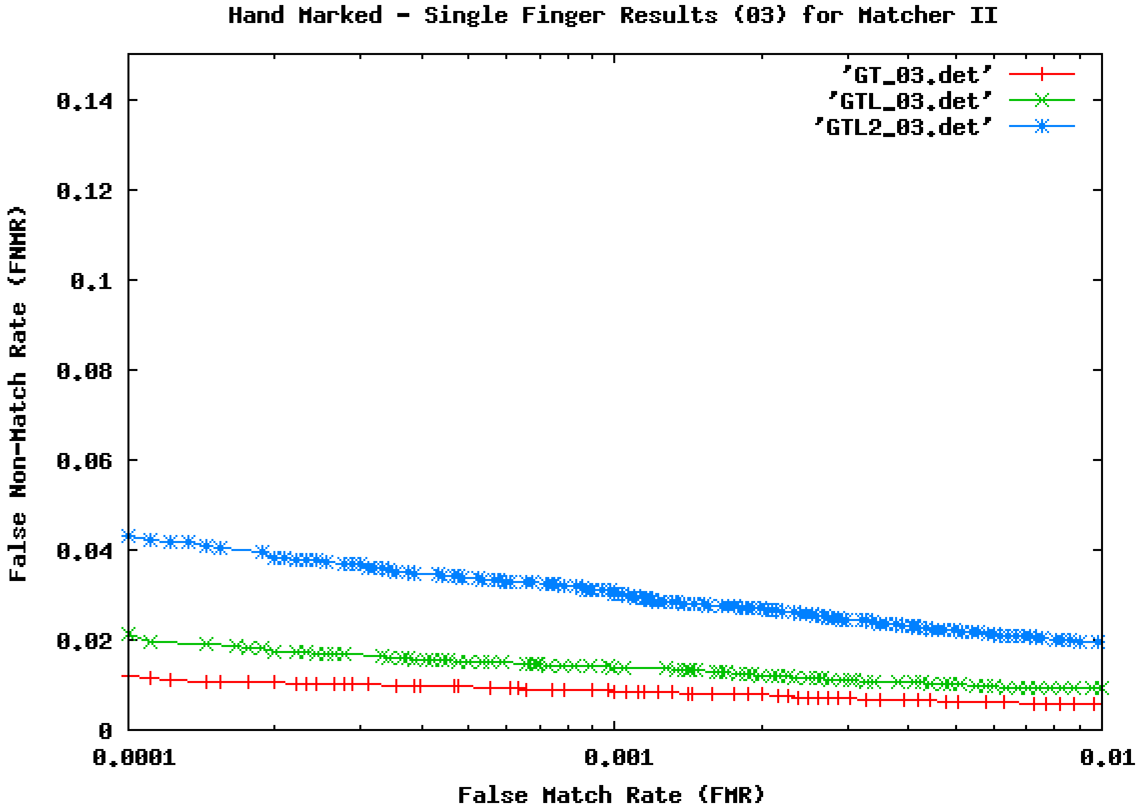
Hand Marked - Single Finger Results (08) for Matcher I



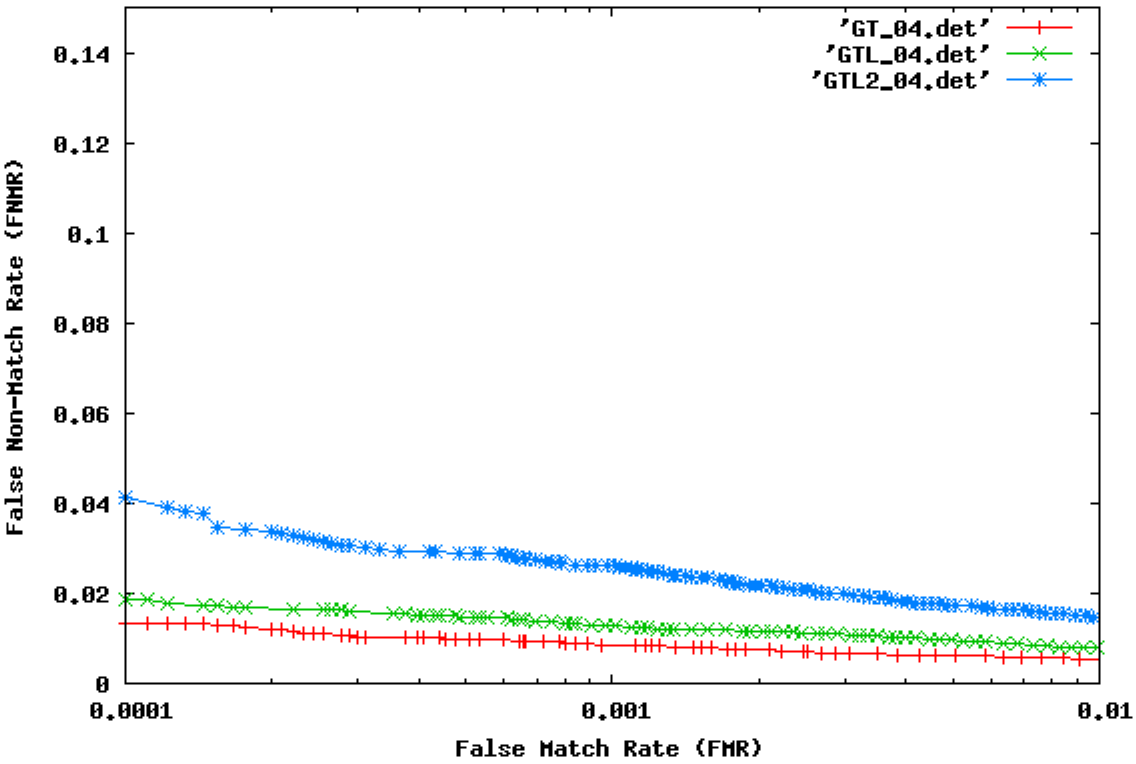

Hand Marked - Single Finger Results (09) for Matcher I
'GT_09.det'
'GTL_09.det'
'GTL2_09.det'
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)


Hand Marked - Single Finger Results (10) for Matcher I
'GT_10.det'
'GTL_10.det'
'GTL2_10.det'
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)

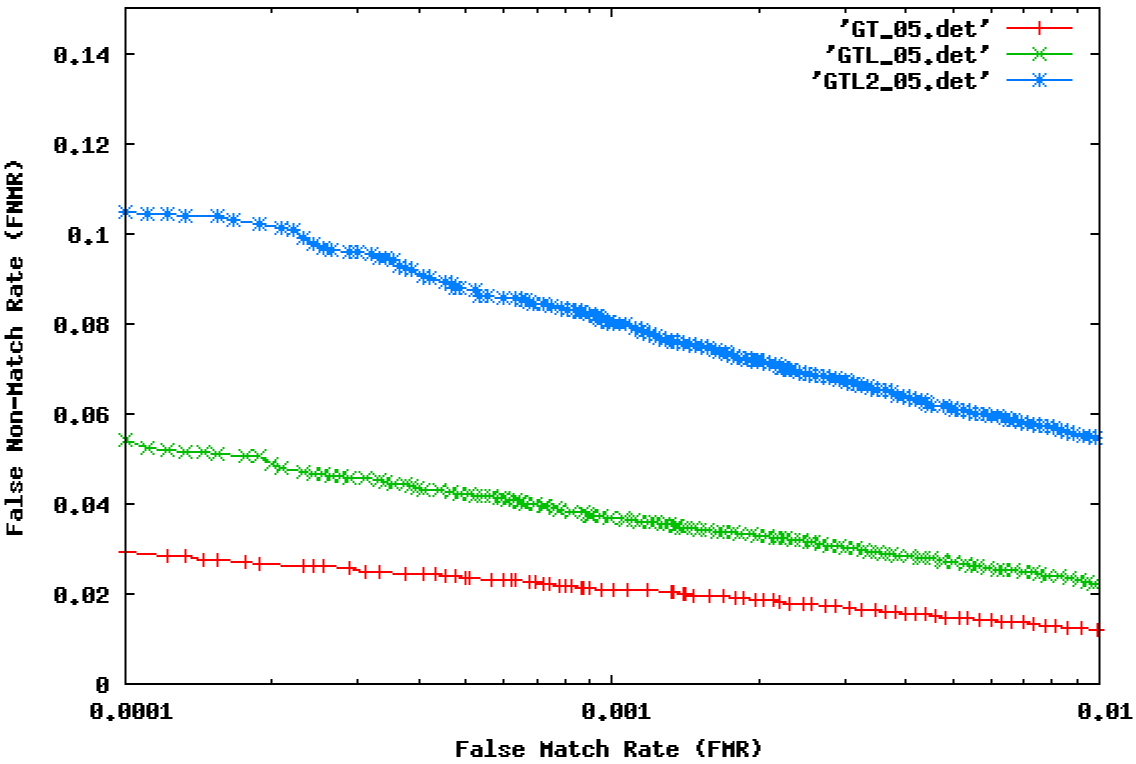

Hand Marked - Single Finger Results (02) for Matcher II
'GT_02.det'
'GTL_02.det'
'GTL2_02.det'
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)

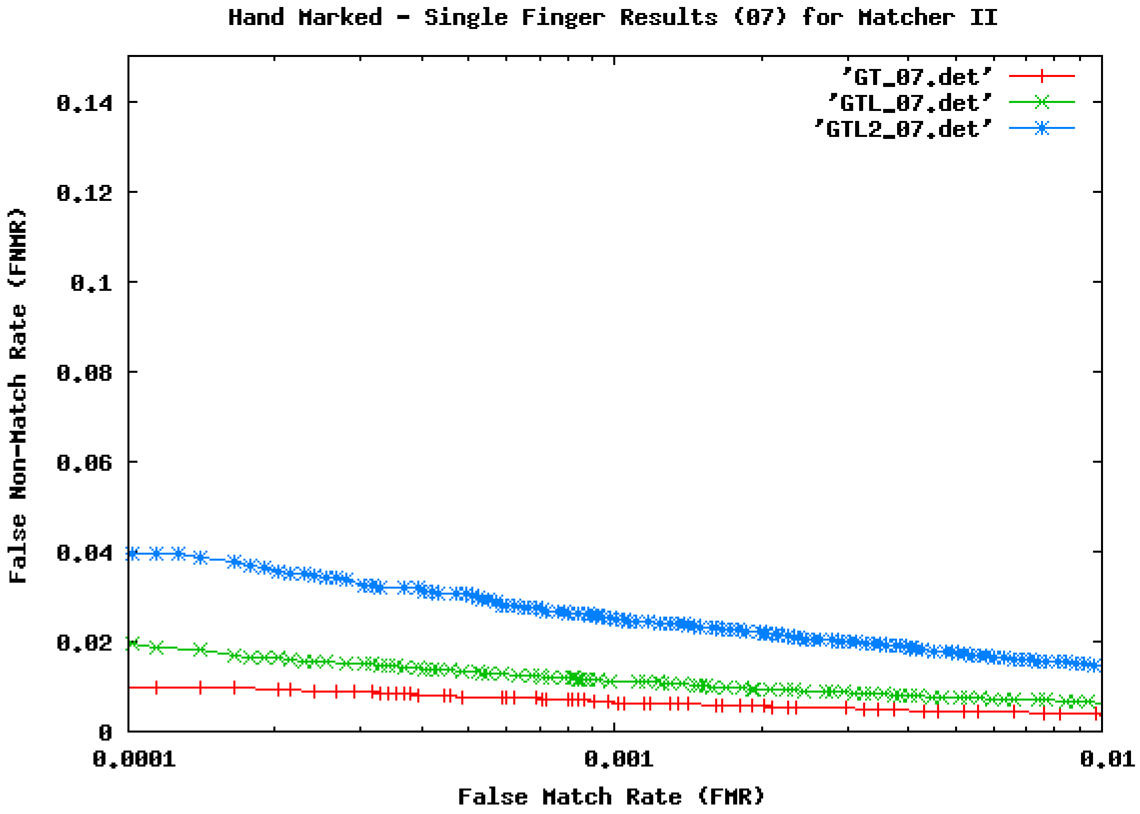

Hand Marked - Single Finger Results (03) for Matcher II
'GT_03.det'
'GTL_03.det'
'GTL2_03.det'
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)

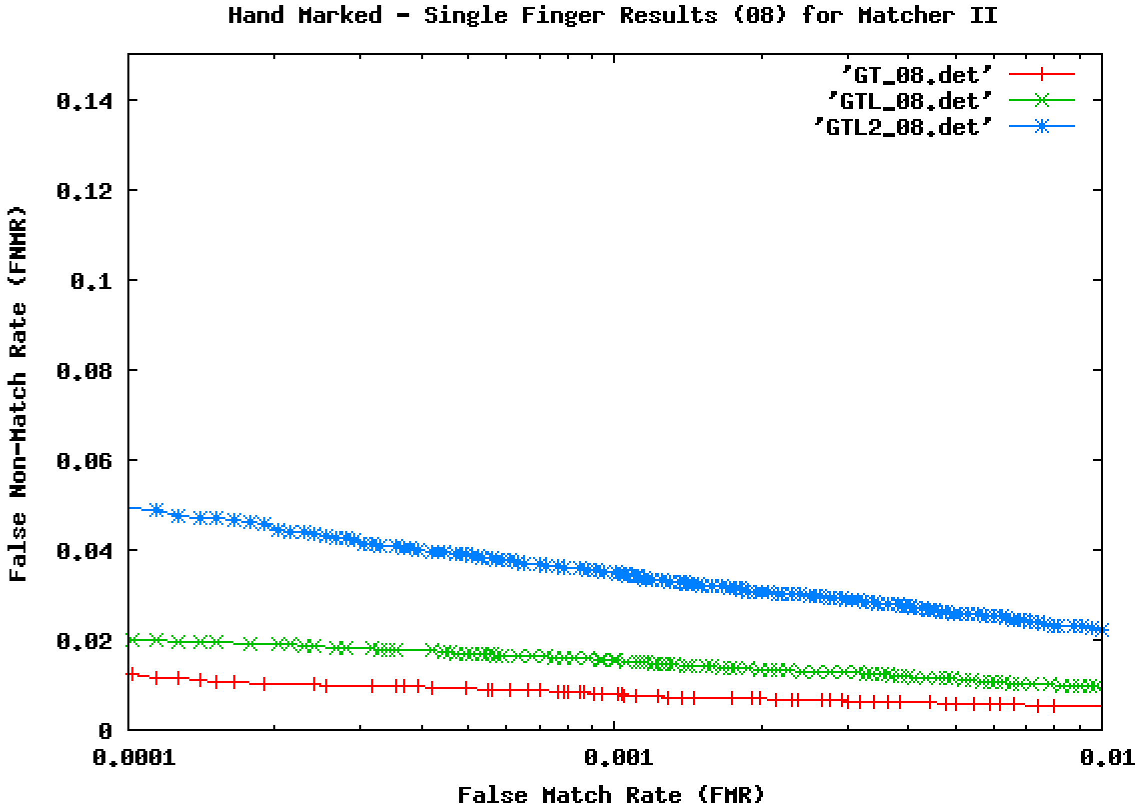
Hand Marked - Single Finger Results (04) for Matcher II



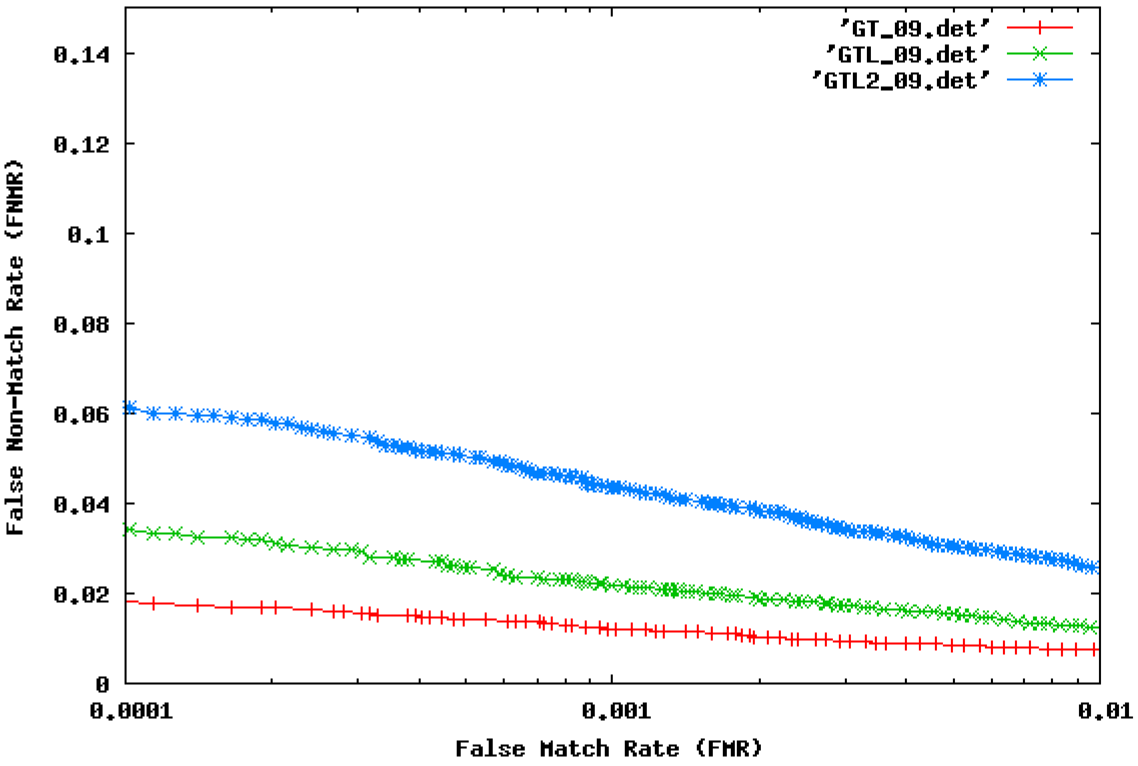
Hand Marked - Single Finger Results (05) for Matcher II



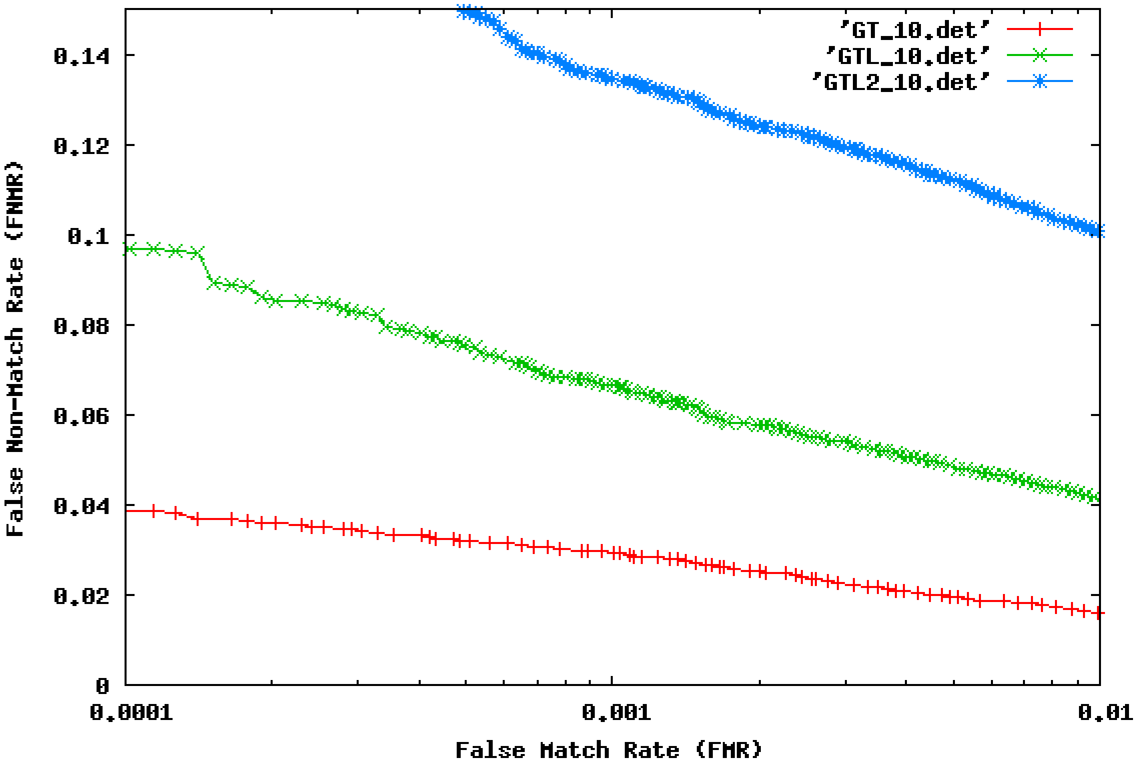

Hand Marked - Single Finger Results (07) for Matcher II

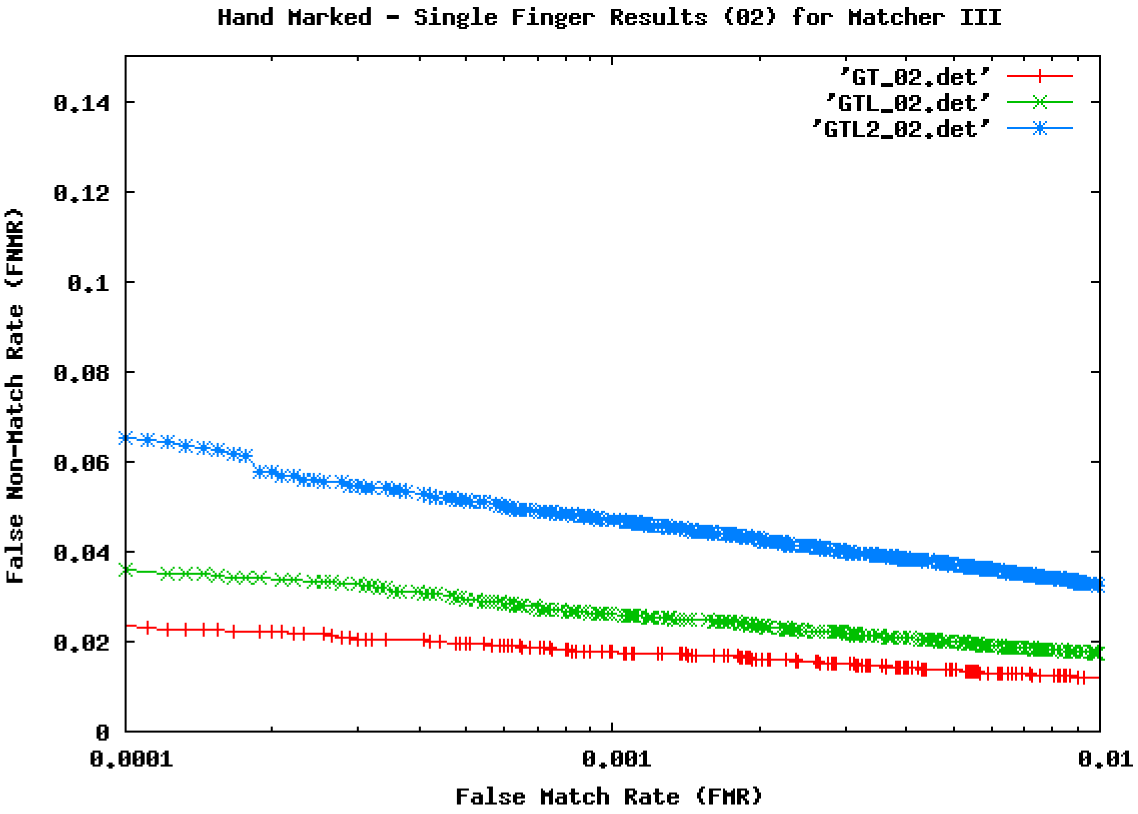

Hand Marked - Single Finger Results (08) for Matcher II

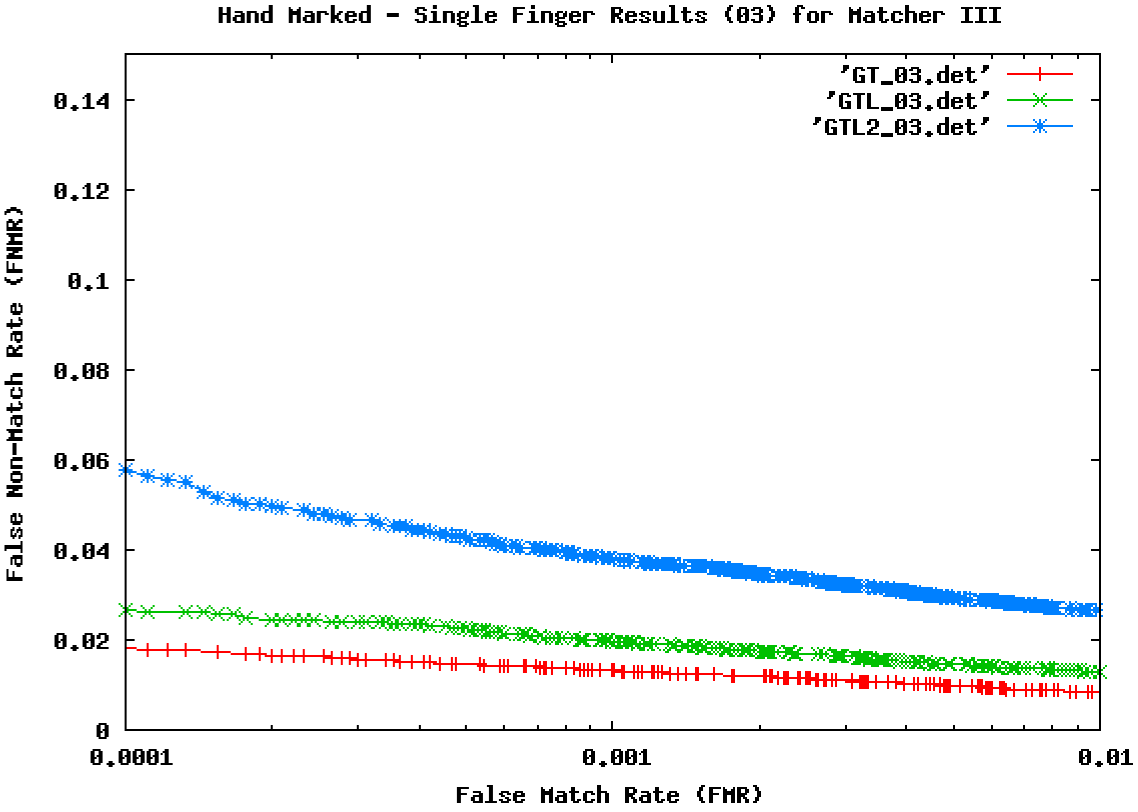
Hand Marked - Single Finger Results (09) for Matcher II

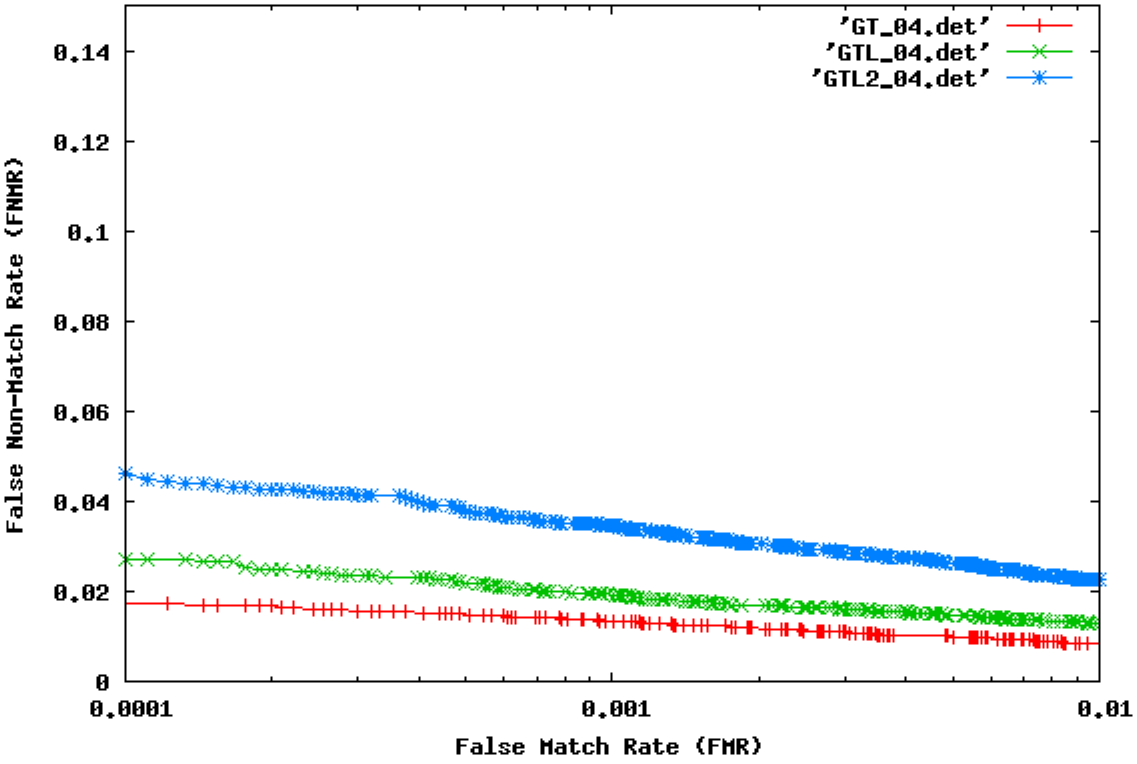


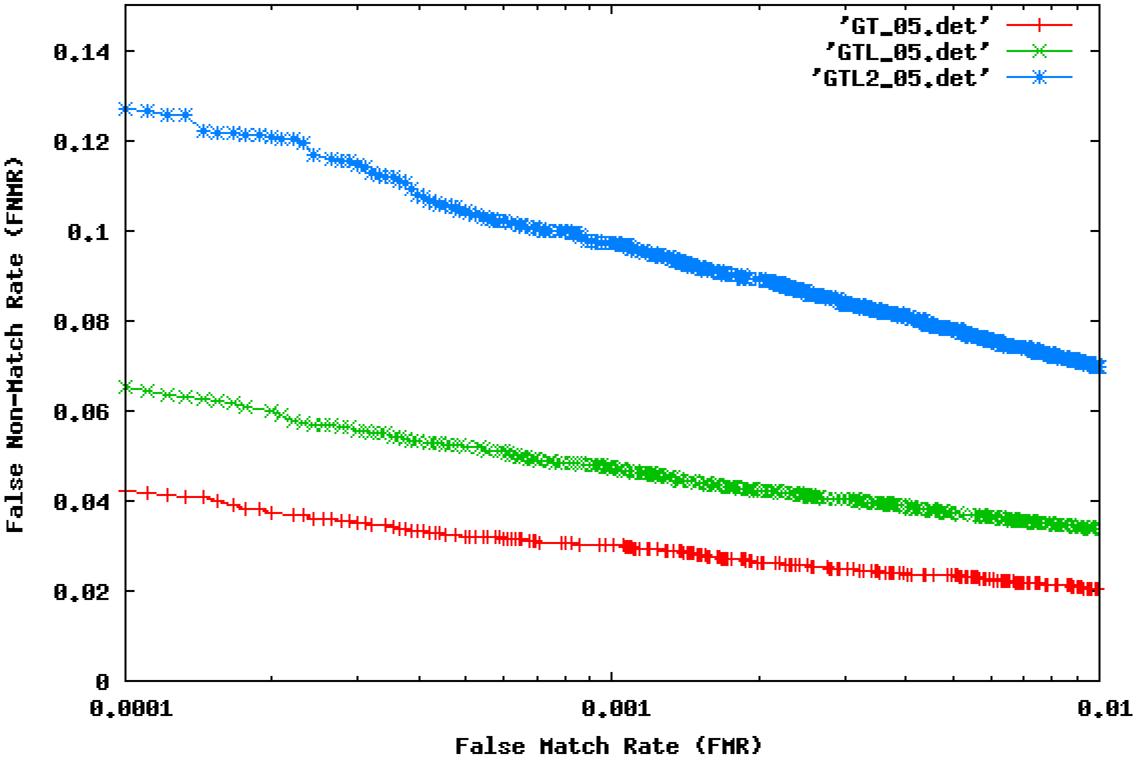
Hand Marked - Single Finger Results (10) for Matcher II



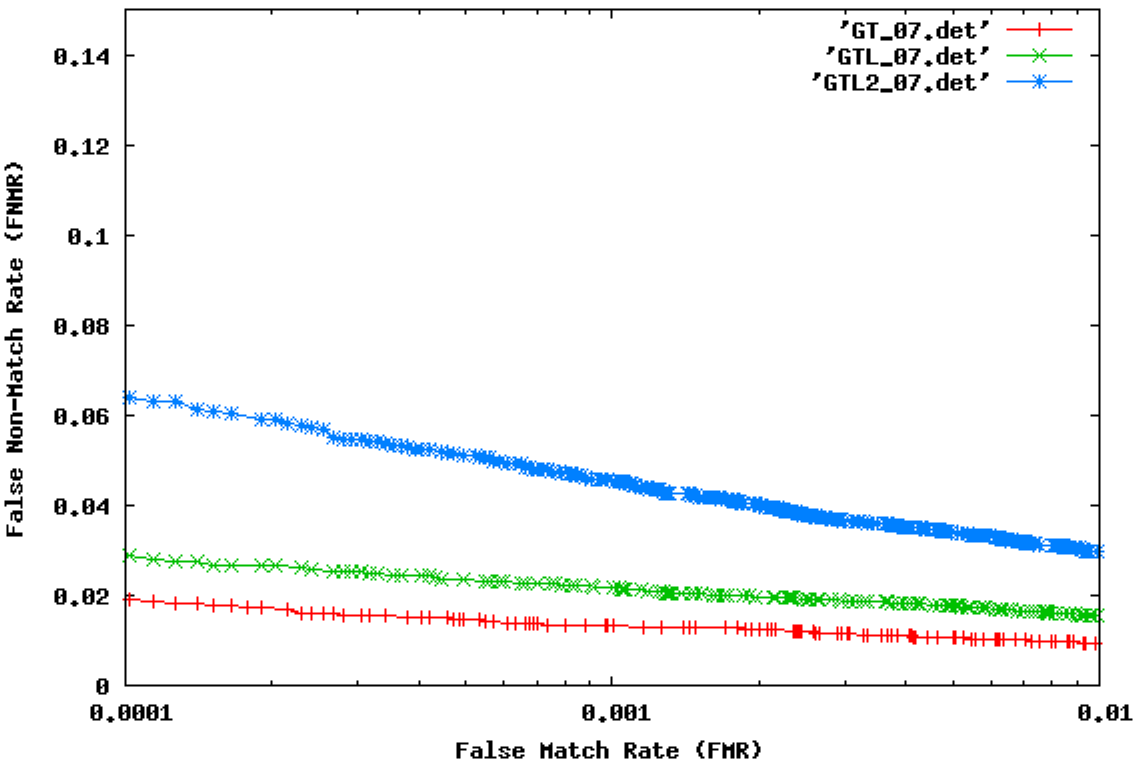

Hand Marked - Single Finger Results (02) for Matcher III
'GT_02.det'
'GTL_02.det'
'GTL2_02.det'
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
False Non-Match Rate (FNMR)


Hand Marked - Single Finger Results (03) for Matcher III
'GT_03.det'
'GTL_03.det'
'GTL2_03.det'
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)
False Non-Match Rate (FNMR)

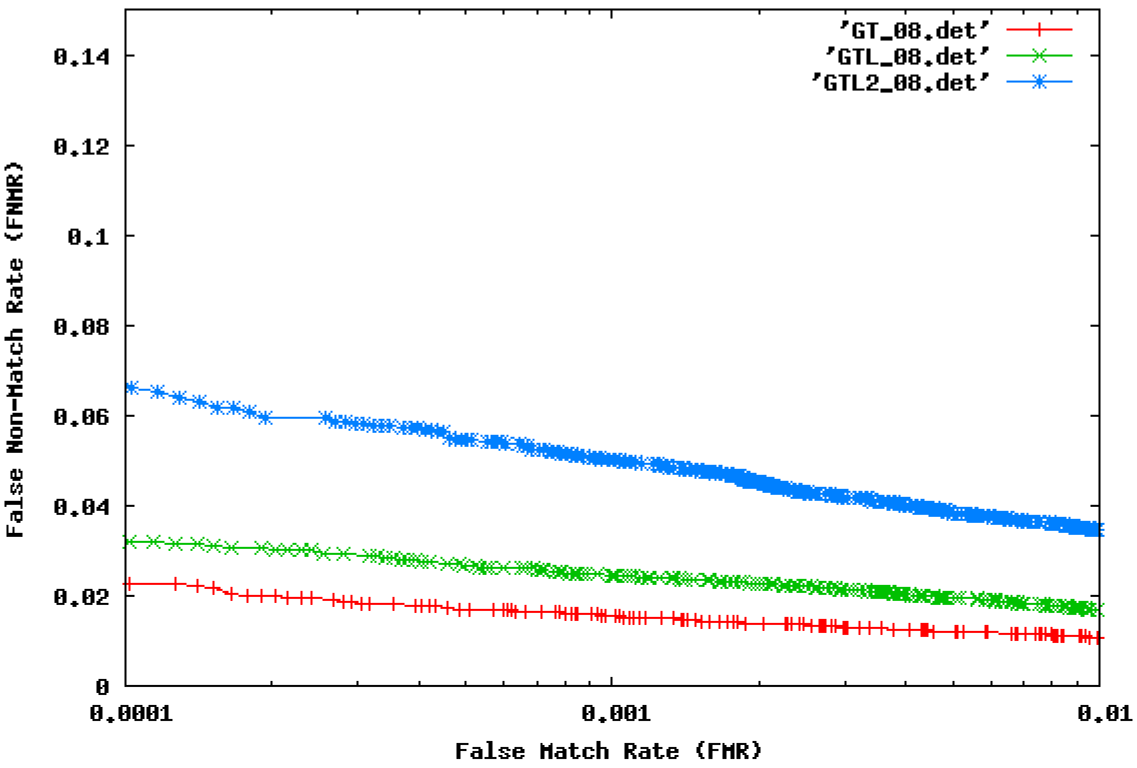

Hand Marked - Single Finger Results (04) for Matcher III

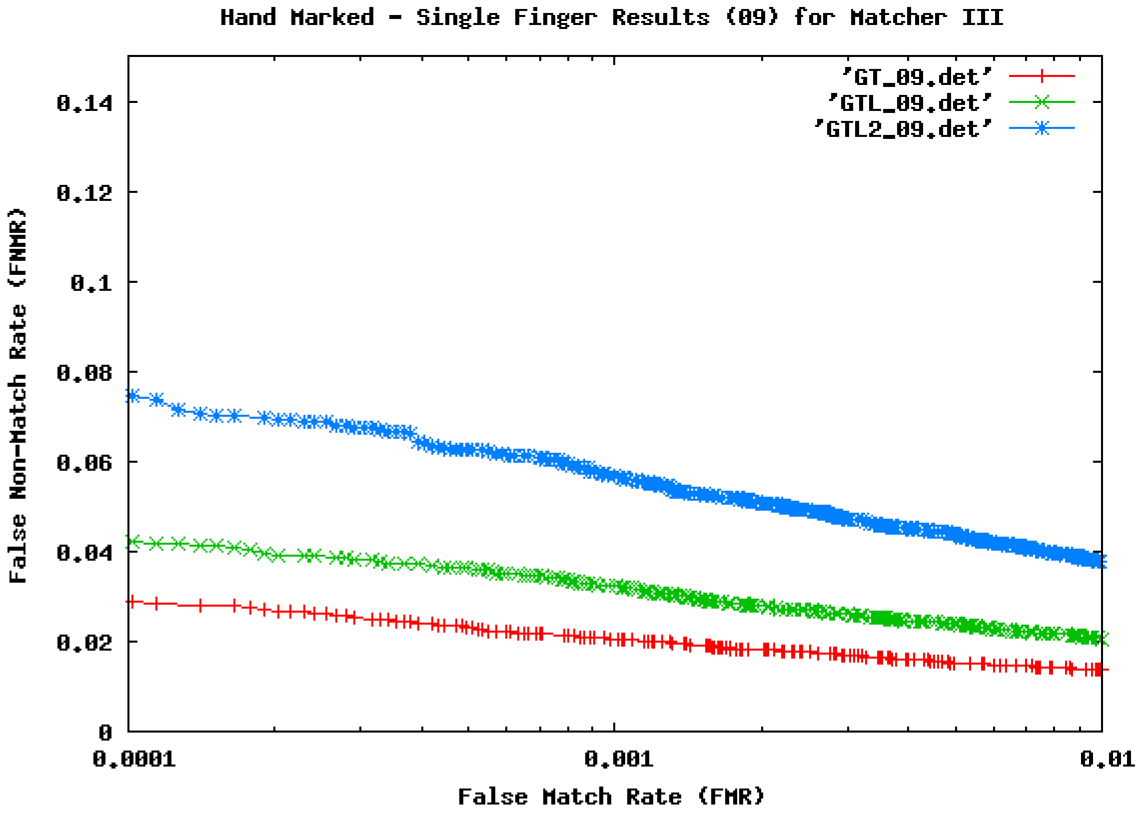

Hand Marked - Single Finger Results (05) for Matcher III

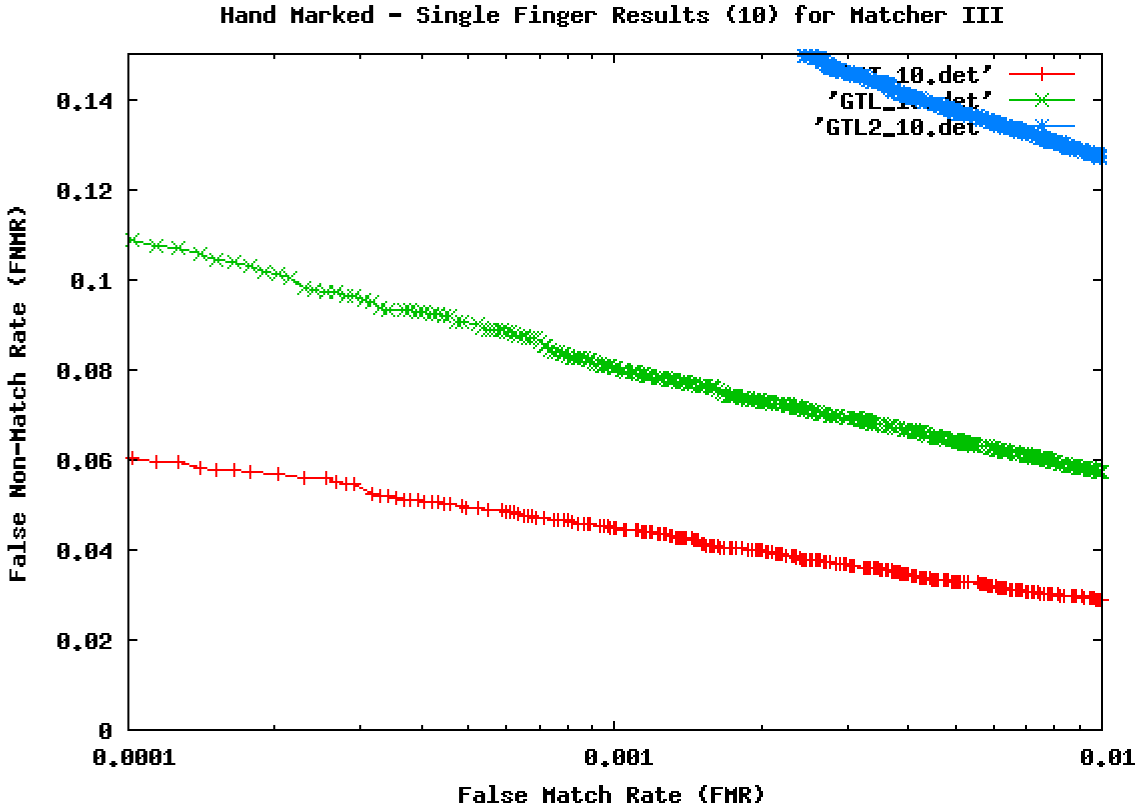
Hand Marked - Single Finger Results (07) for Matcher III

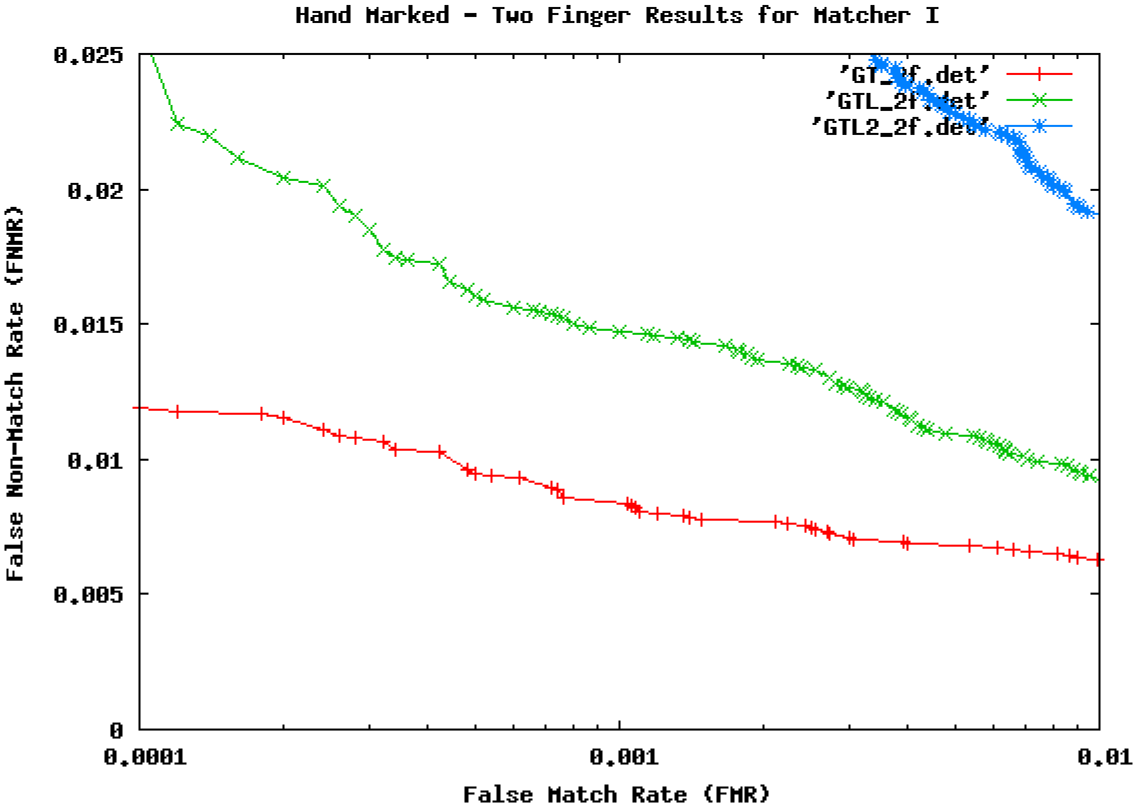


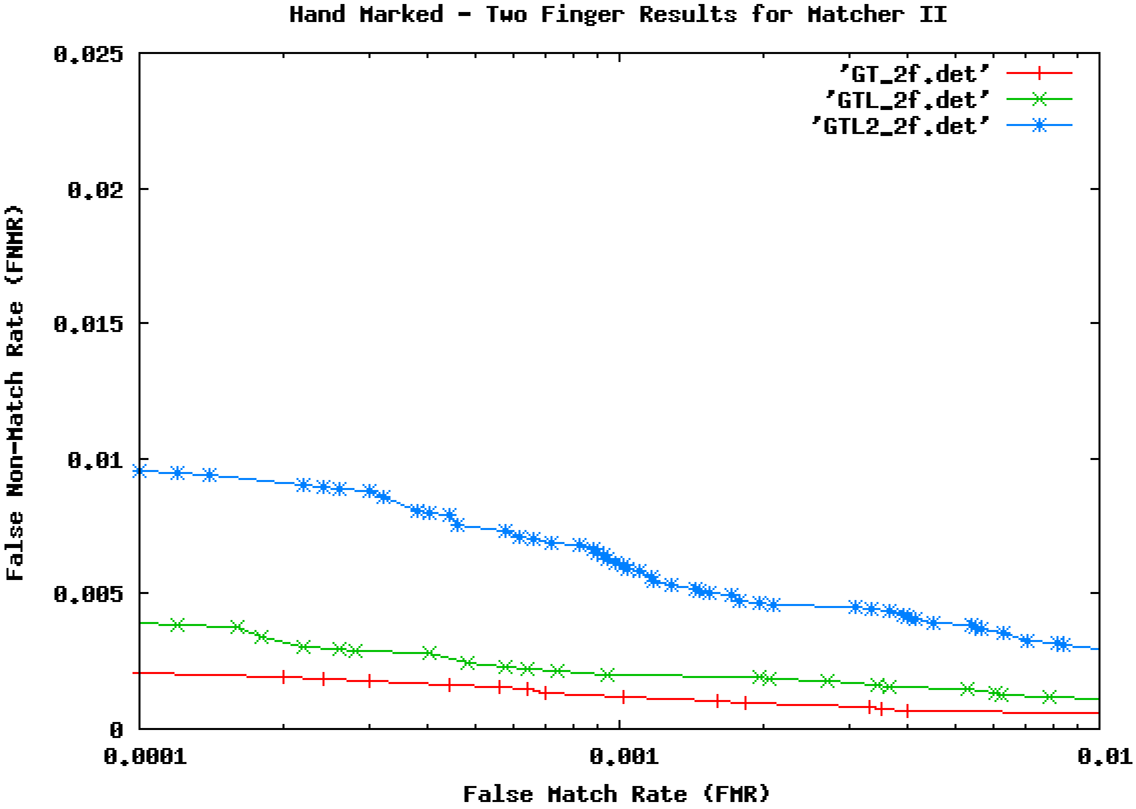
Hand Marked - Single Finger Results (08) for Matcher III

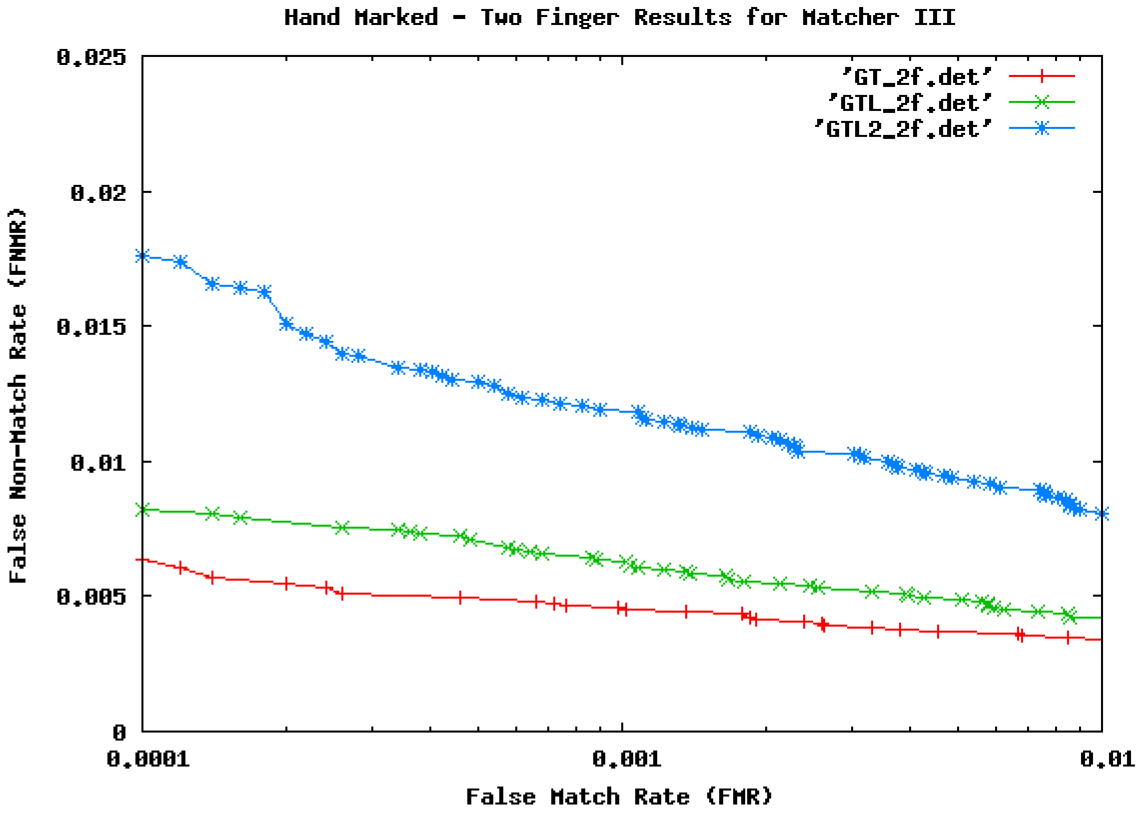


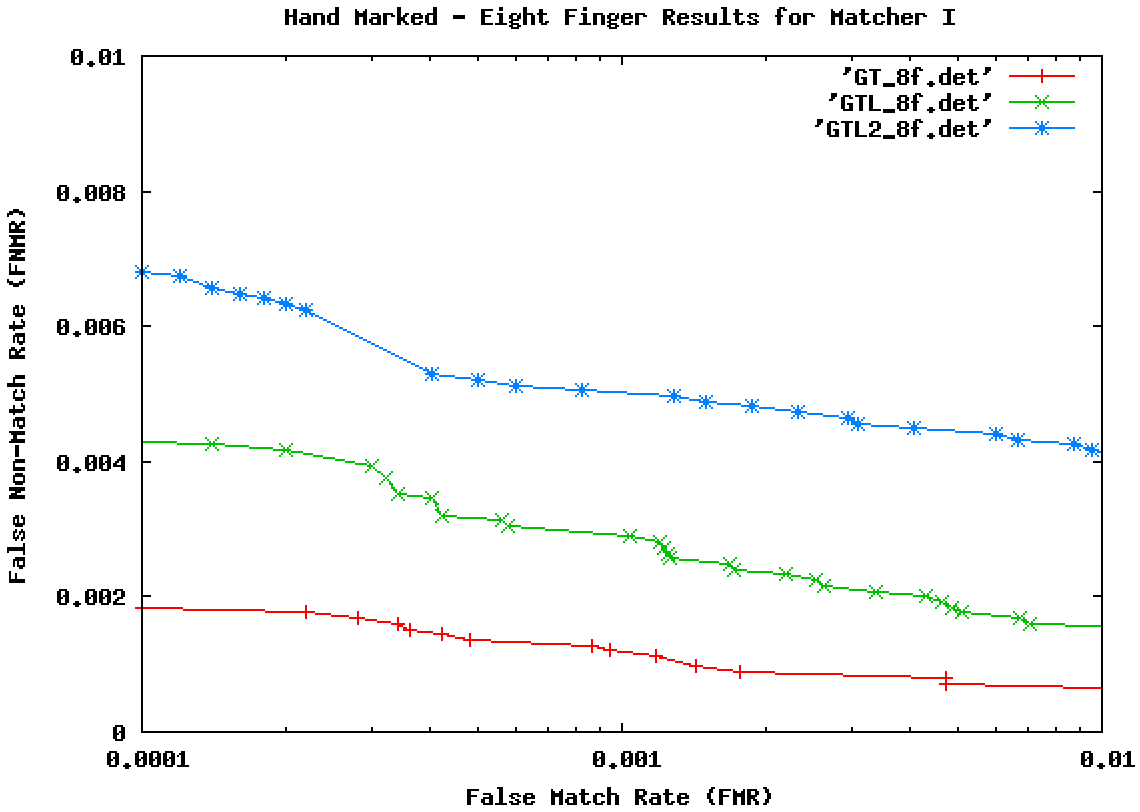

Hand Marked - Single Finger Results (09) for Matcher III
'GT_09.det'
'GTL_09.det'
'GTL2_09.det'
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)

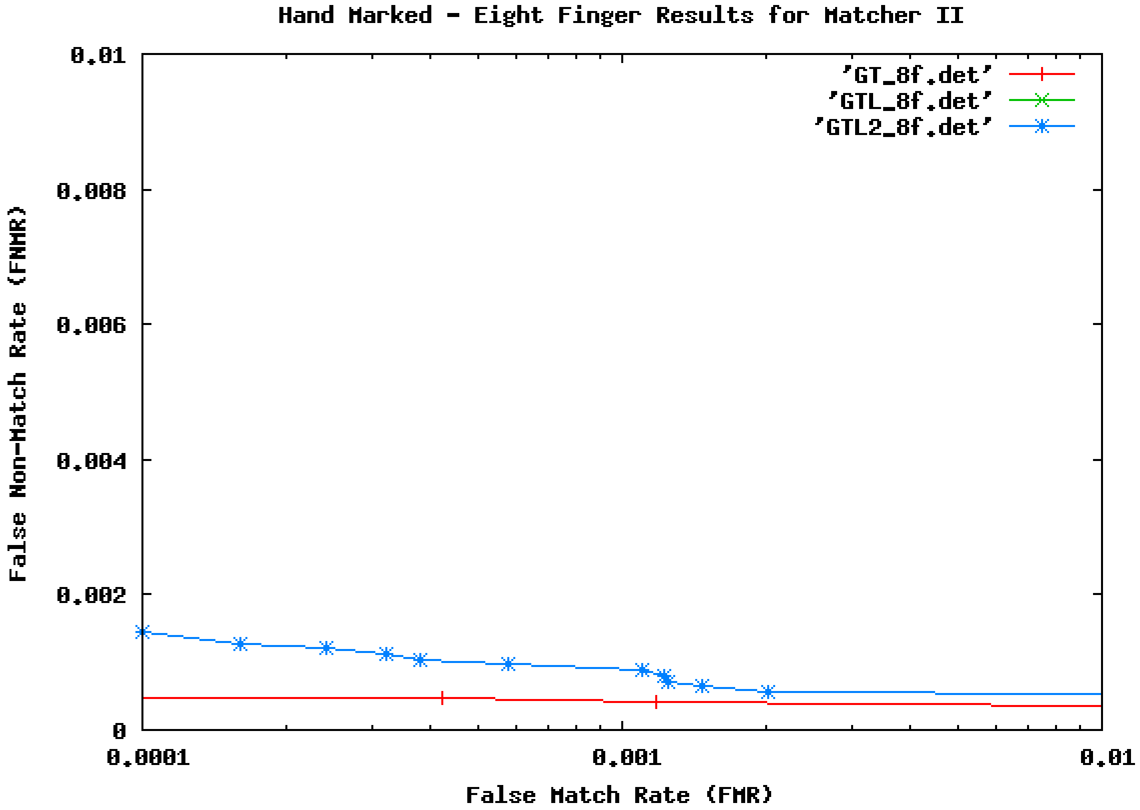

Hand Marked - Single Finger Results (10) for Matcher III
T_10.det'
'GTL_1
et'
'GTL2_10.det
False Non-Match Rate (FNMR)
0.14
0.12
0.1
0.08
0.06
0.04
0.02
0
0.0001
0.001
0.01
False Match Rate (FMR)

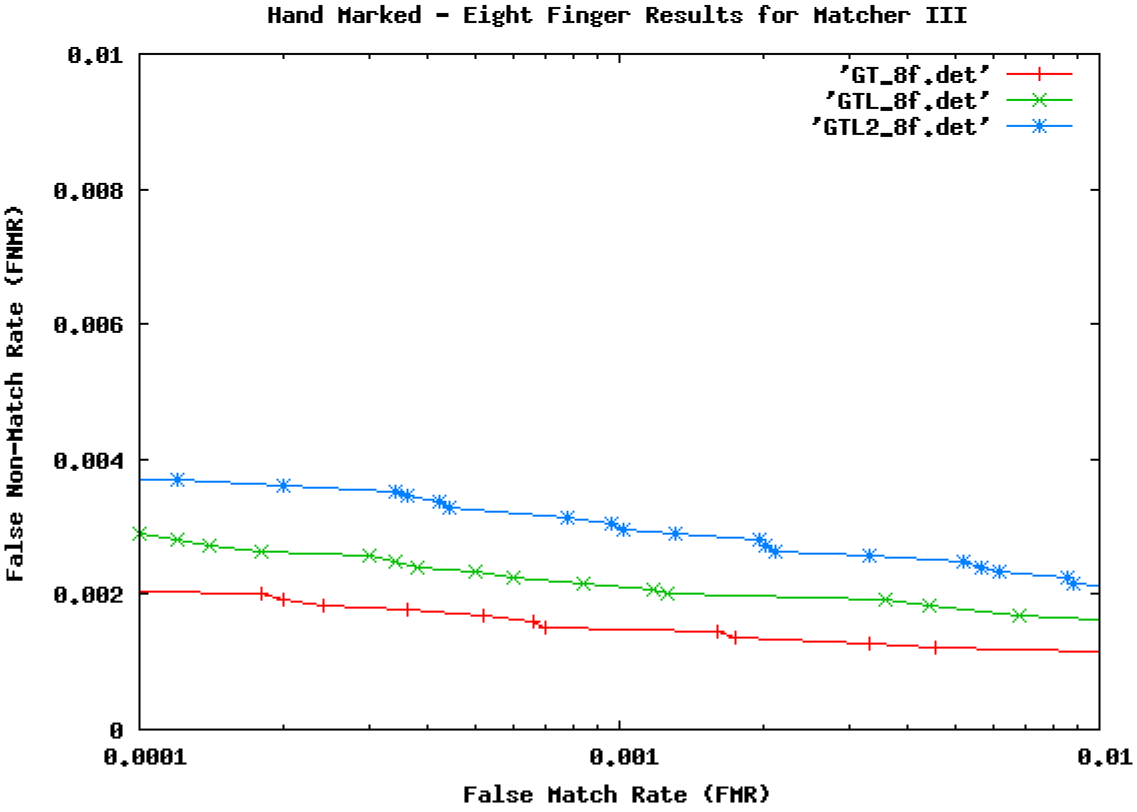

Hand Marked - Two Finger Results for Matcher I


Hand Marked - Two Finger Results for Matcher II


Hand Marked - Two Finger Results for Matcher III
'GT_2f.det'
'GTL_2f.det'
'GTL2_2f.det'
False Non-Match Rate (FNMR)
0.025
0.02
0.015
0.01
0.005
0
0.0001
0.001
0.01
False Match Rate (FMR)


Hand Marked - Eight Finger Results for Matcher I
'GT_8f.det'
'GTL_8f.det'
'GTL2_8f.det'
False Non-Match Rate (FNMR)
0.01
0.008
0.006
0.004
0.002
0
0.0001
0.001
0.01
False Match Rate (FMR)


Hand Marked - Eight Finger Results for Matcher II
'GT_8f.det'
'GTL_8f.det'
'GTL2_8f.det'
False Non-Match Rate (FNMR)
0.01
0.008
0.006
0.004
0.002
0
0.0001
0.001
0.01
False Match Rate (FMR)



Hand Marked - Eight Finger Results for Matcher III