

Supplementary information.

Appendix A Supplementary Information



Fig. A1: Sars-CoV-2 fit parameters executions

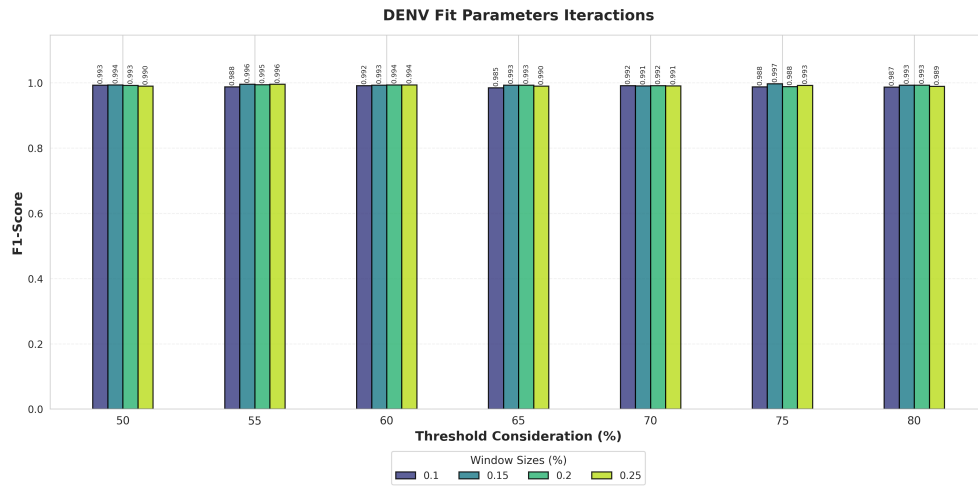


Fig. A2: DENV fit parameters executions

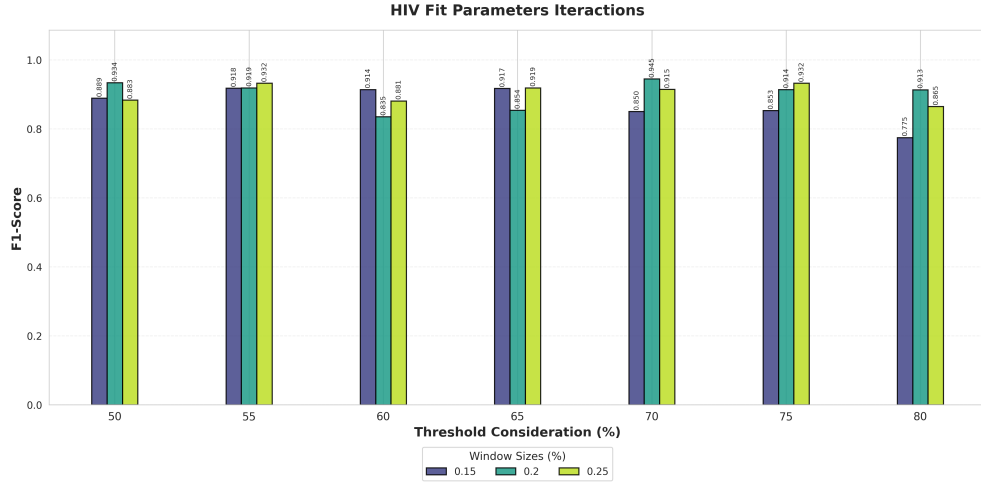


Fig. A3: HIV fit parameters executions

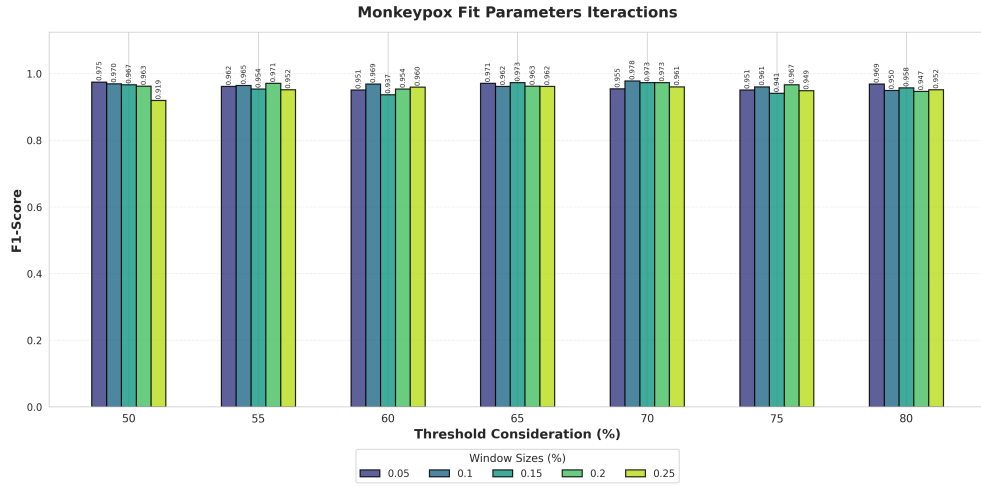


Fig. A4: Monkeypox fit parameters executions

CASTOR SARS-COV-2 (Reduced) Confusion Matrix										
True label	Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
	99.1% ±0.6%	0.1% ±0.2%	0.1% ±0.2%	0.0% ±0.1%	0.2% ±0.4%	0.1% ±0.3%	0.1% ±0.1%	0.1% ±0.1%	0.1% ±0.2%	0.1% ±0.2%
	0.1% ±0.2%	98.2% ±1.1%	0.0% ±0.1%	0.3% ±0.6%	0.2% ±0.3%	0.2% ±0.5%	0.6% ±0.6%	0.1% ±0.4%	0.1% ±0.4%	0.1% ±0.2%
	0.1% ±0.3%	0.0% ±0.2%	98.2% ±0.9%	0.1% ±0.2%	0.1% ±0.2%	0.1% ±0.2%	0.3% ±0.3%	0.7% ±0.6%	0.1% ±0.3%	0.4% ±0.5%
	0.0% ±0.0%	0.2% ±0.3%	0.1% ±0.2%	99.1% ±0.6%	0.1% ±0.5%	0.0% ±0.1%	0.2% ±0.2%	0.2% ±0.2%	0.2% ±0.2%	0.0% ±0.0%
	0.3% ±0.7%	0.2% ±0.4%	0.1% ±0.3%	0.0% ±0.4%	98.8% ±1.2%	0.1% ±0.4%	0.2% ±0.6%	0.1% ±0.5%	0.1% ±0.3%	0.0% ±0.1%
	0.1% ±0.1%	0.3% ±0.5%	0.0% ±0.1%	0.0% ±0.1%	0.1% ±0.1%	99.1% ±0.6%	0.2% ±0.2%	0.1% ±0.2%	0.1% ±0.1%	0.2% ±0.2%
	0.0% ±0.0%	0.4% ±0.4%	0.0% ±0.1%	0.2% ±0.4%	0.1% ±0.1%	0.1% ±0.1%	99.0% ±0.6%	0.1% ±0.3%	0.2% ±0.3%	0.0% ±0.1%
	0.1% ±0.3%	0.0% ±0.0%	0.0% ±0.3%	0.1% ±0.5%	0.1% ±0.4%	0.0% ±0.0%	0.1% ±0.4%	99.8% ±1.2%	0.1% ±0.5%	0.0% ±0.0%
	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.1%	0.1% ±0.5%	0.0% ±0.3%	0.0% ±0.0%	0.1% ±0.3%	0.0% ±0.1%	99.5% ±0.8%	0.1% ±0.3%
	0.0% ±0.1%	0.0% ±0.1%	0.1% ±0.2%	0.0% ±0.0%	0.0% ±0.2%	0.1% ±0.1%	0.0% ±0.2%	0.1% ±0.4%	0.3% ±0.5%	99.3% ±0.5%
KEVOLVE SARS-COV-2 (Reduced) Confusion Matrix										
True label	Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
	22.6% ±38.3%	7.7% ±23.1%	15.5% ±32.4%	3.8% ±15.9%	22.1% ±37.5%	3.1% ±14.2%	6.9% ±22.6%	6.2% ±21.8%	3.4% ±16.1%	8.7% ±24.8%
	5.7% ±18.5%	28.3% ±38.9%	11.3% ±26.2%	10.4% ±25.7%	17.0% ±32.3%	1.6% ±9.6%	7.0% ±20.5%	5.3% ±18.0%	4.4% ±16.5%	9.1% ±22.9%
	7.0% ±20.5%	7.3% ±21.3%	33.0% ±39.5%	6.8% ±19.5%	10.5% ±23.1%	2.6% ±11.1%	12.2% ±27.0%	6.9% ±18.1%	5.6% ±16.8%	8.1% ±22.2%
	4.9% ±19.1%	8.2% ±22.5%	10.2% ±23.5%	28.8% ±40.1%	15.5% ±30.3%	2.3% ±12.1%	12.4% ±26.3%	6.7% ±21.7%	1.7% ±9.8%	9.2% ±24.3%
	7.3% ±21.1%	5.1% ±18.2%	16.7% ±32.5%	9.3% ±24.5%	31.6% ±40.0%	2.4% ±12.7%	5.7% ±18.0%	5.7% ±19.2%	6.1% ±20.2%	10.1% ±25.3%
	8.8% ±23.7%	8.0% ±24.9%	9.1% ±23.9%	8.5% ±23.7%	13.5% ±27.8%	8.1% ±35.0%	8.7% ±22.6%	4.8% ±24.1%	12.3% ±18.5%	12.3% ±29.0%
	5.4% ±16.8%	6.7% ±17.3%	10.1% ±23.0%	7.2% ±17.1%	11.8% ±24.1%	7.4% ±37.4%	29.0% ±17.5%	5.0% ±21.8%	3.7% ±18.5%	13.7% ±24.8%
	5.7% ±15.5%	6.4% ±21.2%	8.5% ±24.0%	9.5% ±26.1%	13.8% ±29.3%	2.8% ±13.3%	11.0% ±28.0%	26.0% ±30.9%	5.8% ±19.3%	10.6% ±24.9%
	4.7% ±16.8%	6.0% ±19.2%	11.1% ±27.8%	7.7% ±24.0%	18.2% ±33.5%	3.4% ±15.4%	10.8% ±19.3%	5.0% ±17.2%	20.1% ±37.6%	12.9% ±29.9%
	3.7% ±12.2%	8.0% ±21.8%	10.6% ±23.5%	8.3% ±23.2%	15.7% ±31.2%	2.2% ±11.6%	5.8% ±17.3%	3.4% ±15.1%	5.2% ±17.2%	37.0% ±41.2%

(a) CASTOR-KRFE on the SARS-CoV-2 reduced dataset. (b) KEVOLVE on the SARS-CoV-2 reduced dataset.

Fig. A13: Confusion matrix classification average accuracy and standard deviation over 100 iterations using the reduced dataset produced only with the regions extracted by GREAC.

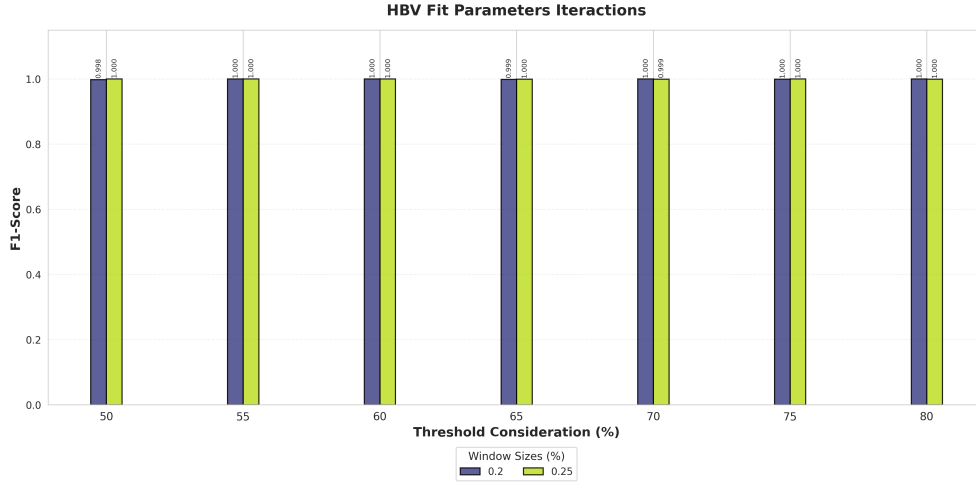
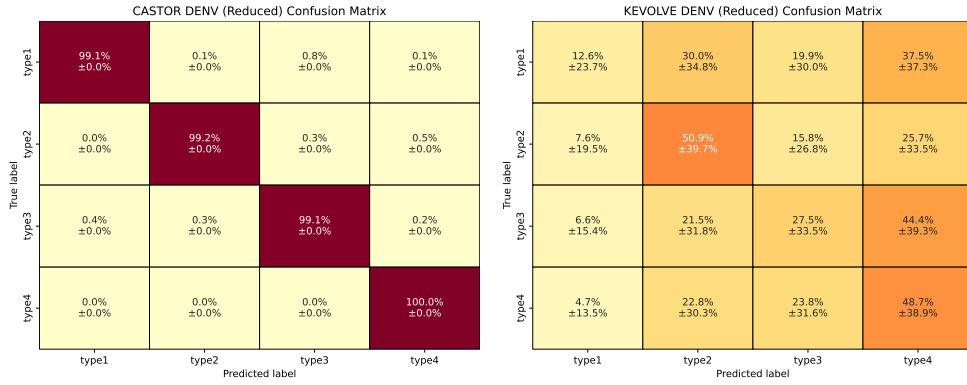


Fig. A5: HBV fit parameters executions



(a) CASTOR-KRFE on the DENV reduced dataset. (b) KEVOLVE on the DENV reduced dataset.

Fig. A14: Confusion matrix classification average accuracy and standard deviation over 100 iterations using the reduced dataset produced only with the regions extracted by GREAC.

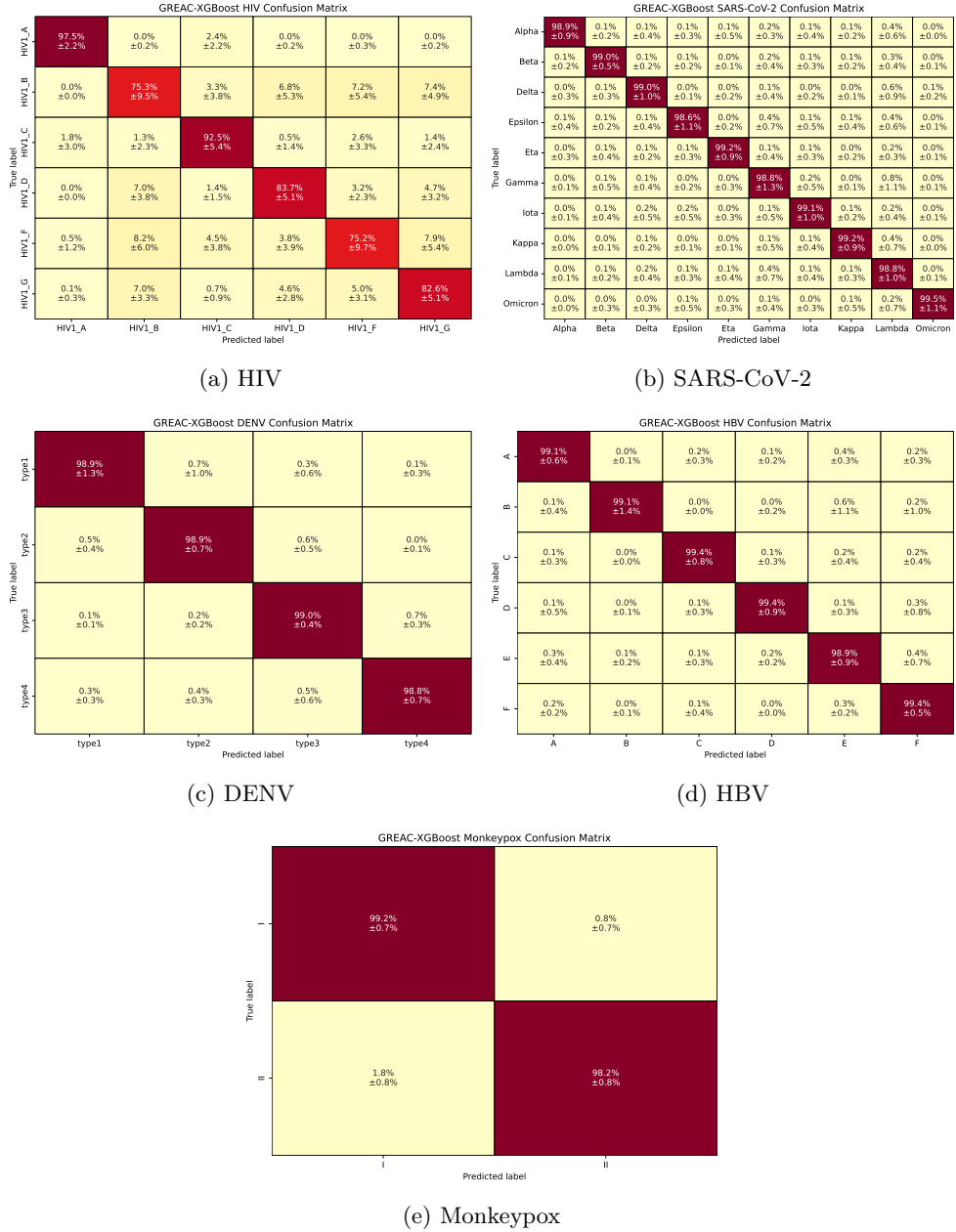


Fig. A6: Organisms XGBoost confusion matrix classification average accuracy percentage and standard deviation over 100 iterations. (A6a) HIV results. (A6b) SARS-CoV-2 results. (A6c) DENV results. (A6d) HBV results. (A6e) Monkeypox results.

GREAC-Gaussian HIV Confusion Matrix

	HIV1_A	HIV1_B	HIV1_C	HIV1_D	HIV1_F	HIV1_G
HIV1_A	98.0% ±1.4%	0.0% ±0.0%	2.0% ±1.4%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%
HIV1_B	0.1% ±0.5%	28.9% ±9.4%	3.4% ±4.1%	20.9% ±9.5%	21.7% ±8.2%	25.1% ±7.9%
HIV1_C	4.2% ±4.8%	3.3% ±4.6%	66.4% ±12.6%	0.3% ±1.2%	14.4% ±11.0%	11.3% ±10.1%
HIV1_D	0.0% ±0.2%	22.4% ±7.1%	0.7% ±0.9%	44.3% ±8.1%	16.0% ±6.9%	16.6% ±8.0%
HIV1_F	0.0% ±0.0%	21.4% ±8.8%	5.8% ±5.7%	14.6% ±9.9%	31.9% ±11.3%	26.4% ±10.2%
HIV1_G	0.0% ±0.1%	25.7% ±9.0%	1.5% ±1.3%	16.7% ±6.7%	14.2% ±8.9%	41.9% ±9.4%
	Predicted label					

(a) HIV Gaussian Membership Results

GREAC-Gaussian SARS-CoV-2 Confusion Matrix

	Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
Alpha	98.7% ±0.6%	0.0% ±0.0%	0.0% ±0.0%	0.6% ±0.7%	0.0% ±0.0%	0.6% ±0.7%	0.0% ±0.0%	0.1% ±0.3%	0.0% ±0.0%	0.0% ±0.0%
Beta	0.0% ±0.0%	99.1% ±0.3%	0.0% ±0.1%	0.1% ±0.2%	0.0% ±0.0%	0.6% ±0.5%	0.0% ±0.0%	0.2% ±0.3%	0.0% ±0.0%	0.0% ±0.0%
Delta	0.0% ±0.0%	0.0% ±0.0%	98.4% ±0.7%	0.2% ±0.4%	0.0% ±0.0%	0.7% ±0.8%	0.0% ±0.1%	0.0% ±0.1%	0.7% ±0.9%	0.0% ±0.0%
Epsilon	0.0% ±0.1%	0.0% ±0.0%	0.0% ±0.0%	99.4% ±1.0%	0.0% ±0.0%	0.4% ±0.7%	0.0% ±0.0%	0.2% ±0.8%	0.0% ±0.0%	0.0% ±0.0%
Eta	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.5% ±1.2%	97.0% ±1.2%	1.1% ±1.2%	0.0% ±0.0%	0.5% ±0.8%	0.0% ±0.0%	0.0% ±0.0%
Gamma	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.2% ±1.0%	0.0% ±0.0%	99.5% ±1.6%	0.0% ±0.0%	0.0% ±0.0%	0.4% ±1.3%	0.0% ±0.0%
Iota	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.2% ±0.6%	0.0% ±0.0%	1.4% ±1.7%	97.9% ±1.7%	0.0% ±0.0%	0.5% ±1.0%	0.0% ±0.0%
Kappa	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.2%	0.0% ±0.0%	0.5% ±0.9%	0.0% ±0.0%	98.6% ±1.3%	0.8% ±1.1%	0.0% ±0.0%
Lambda	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.2% ±0.2%	0.0% ±0.0%	0.8% ±1.3%	0.0% ±0.0%	99.1% ±1.3%	0.0% ±0.0%	0.0% ±0.0%
Omicron	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.3%	0.0% ±0.0%	0.0% ±0.0%	5.2% ±3.7%	94.8% ±3.7%
	Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
	Predicted label									

(b) SARS-CoV-2 Gaussian Membership Results

GREAC-Gaussian DENV Confusion Matrix

	type1	type2	type3	type4
type1	98.4% ±1.1%	0.4% ±0.7%	0.4% ±0.6%	0.8% ±0.7%
type2	0.6% ±0.6%	98.2% ±1.3%	0.0% ±0.0%	1.1% ±1.1%
type3	0.0% ±0.0%	0.1% ±0.1%	99.1% ±0.1%	0.8% ±0.1%
type4	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.0%	100.0% ±0.1%
	type1	type2	type3	type4
	Predicted label			

(c) DENV Gaussian Membership Results

GREAC-Gaussian HBV Confusion Matrix

	A	B	C	D	E	F
A	99.9% ±0.2%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.1% ±0.2%	0.0% ±0.0%
B	0.0% ±0.0%	100.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%
C	0.0% ±0.0%	0.0% ±0.0%	100.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%
D	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	100.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%
E	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	100.0% ±0.0%	0.0% ±0.0%
F	0.0% ±0.1%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.7% ±0.6%	99.2% ±0.6%
	A	B	C	D	E	F
	Predicted label					

(d) HBV Gaussian Membership Results

GREAC-Gaussian Monkeypox Confusion Matrix

	I	II
I	99.9% ±0.2%	0.1% ±0.2%
II	13.7% ±0.6%	86.3% ±0.6%
	I	II
	Predicted label	

(e) Monkeypox Gaussian Membership Results

Fig. A7: Experiment using GRAMEP k-mer set using Gaussian Membership Classifications, confusion matrix results, average accuracy percentage, and standard deviation over 100 iterations.

KEVOLVE SARS-CoV-2 Confusion Matrix											
True label	Alpha	9.2% ±27.9%	11.0% ±30.4%	10.9% ±34.7%	7.0% ±32.5%	13.6% ±28.1%	9.1% ±34.0%	13.9% ±30.7%	11.1% ±26.0%	7.8% ±24.8%	6.9%
	Beta	4.8% ±19.4%	10.2% ±26.9%	9.7% ±28.6%	18.6% ±38.0%	5.7% ±20.8%	10.4% ±28.5%	11.5% ±30.3%	5.7% ±21.8%	12.4% ±31.0%	7.4%
	Delta	4.0% ±15.6%	6.1% ±20.1%	12.8% ±30.0%	10.2% ±27.0%	14.0% ±31.7%	11.3% ±32.3%	14.1% ±31.2%	14.7% ±20.0%	5.4% ±22.7%	7.4%
	Epsilon	6.7% ±22.4%	7.5% ±23.5%	12.5% ±30.5%	12.7% ±31.1%	10.9% ±27.8%	7.6% ±24.8%	16.5% ±33.5%	13.2% ±33.0%	5.1% ±19.1%	7.3%
	Eta	4.1% ±18.0%	6.7% ±23.8%	10.2% ±29.4%	13.0% ±32.7%	16.3% ±35.6%	13.4% ±32.7%	14.0% ±33.8%	11.2% ±29.6%	4.1% ±19.2%	7.0%
	Gamma	7.9% ±25.9%	7.0% ±24.6%	13.0% ±32.9%	11.1% ±30.6%	13.9% ±33.7%	8.7% ±26.8%	12.4% ±31.9%	14.9% ±34.7%	5.1% ±21.4%	6.2%
	Iota	9.9% ±26.1%	12.8% ±28.9%	10.2% ±26.1%	10.4% ±29.8%	13.3% ±27.7%	10.8% ±30.3%	13.6% ±25.9%	9.7% ±14.5%	3.5% ±20.7%	5.8%
	Kappa	8.6% ±26.3%	6.5% ±23.3%	9.2% ±28.0%	10.0% ±29.0%	11.7% ±30.8%	9.1% ±27.1%	12.8% ±32.3%	20.7% ±39.3%	6.6% ±23.4%	4.9%
	Lambda	8.0% ±26.2%	5.0% ±20.9%	11.0% ±30.5%	4.3% ±19.2%	14.9% ±34.6%	13.9% ±34.1%	11.9% ±31.2%	14.1% ±33.9%	4.3% ±18.8%	12.7%
	Omicron	5.6% ±20.4%	14.4% ±31.4%	14.3% ±31.9%	5.1% ±19.5%	11.0% ±28.2%	8.4% ±24.5%	11.9% ±29.3%	10.6% ±27.4%	7.5% ±24.8%	11.2%
		Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
		Predicted label									

CASTOR SARS-CoV-2 Confusion Matrix											
True label	Alpha	99.8% ±0.8%	0.2% ±0.4%	0.1% ±0.1%	0.0% ±0.0%	0.2% ±0.4%	0.2% ±0.3%	0.1% ±0.3%	0.1% ±0.3%	0.1% ±0.1%	0.1% ±0.2%
	Beta	0.2% ±0.3%	97.8% ±1.3%	0.0% ±0.2%	0.6% ±0.9%	0.3% ±0.4%	0.4% ±0.6%	0.4% ±0.6%	0.1% ±0.2%	0.1% ±0.4%	0.0% ±0.2%
	Delta	0.1% ±0.1%	0.0% ±0.1%	98.2% ±0.7%	0.2% ±0.3%	0.2% ±0.3%	0.1% ±0.2%	0.1% ±0.2%	0.8% ±0.5%	0.1% ±0.3%	0.0% ±0.3%
	Epsilon	0.0% ±0.0%	0.2% ±0.2%	0.1% ±0.1%	99.2% ±0.4%	0.0% ±0.1%	0.0% ±0.1%	0.1% ±0.2%	0.3% ±0.2%	0.1% ±0.2%	0.0% ±0.1%
	Eta	0.2% ±0.4%	0.2% ±0.5%	0.1% ±0.3%	0.0% ±0.1%	98.9% ±0.9%	0.2% ±0.4%	0.2% ±0.4%	0.1% ±0.5%	0.1% ±0.3%	0.0% ±0.2%
	Gamma	0.1% ±0.2%	0.3% ±0.4%	0.0% ±0.1%	0.0% ±0.2%	0.1% ±0.2%	99.0% ±0.8%	0.1% ±0.6%	0.1% ±0.1%	0.1% ±0.2%	0.1% ±0.2%
	Iota	0.1% ±0.2%	0.2% ±0.3%	0.0% ±0.0%	0.1% ±0.2%	0.0% ±0.1%	0.1% ±0.5%	99.3% ±0.2%	0.1% ±0.3%	0.2% ±0.3%	0.1% ±0.2%
	Kappa	0.0% ±0.3%	0.1% ±0.5%	0.0% ±0.3%	0.2% ±0.8%	0.0% ±0.3%	0.0% ±0.4%	0.1% ±1.3%	99.3% ±0.6%	0.1% ±0.4%	0.1% ±0.4%
	Lambda	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.2% ±0.4%	0.0% ±0.2%	99.4% ±0.6%	0.2% ±0.3%
	Omicron	0.1% ±0.7%	0.0% ±0.1%	0.1% ±0.2%	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.1% ±0.1%	0.2% ±0.3%	99.4% ±0.8%
		Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
		Predicted label									

(a) KEVOLVE

(b) CASTOR-KRFE

GREAC SARS-CoV-2 Confusion Matrix											
True label	Alpha	99.7% ±0.3%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.0%	0.1% ±0.1%	0.1% ±0.2%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.1%
	Beta	0.0% ±0.1%	99.6% ±0.6%	0.0% ±0.1%	0.1% ±0.2%	0.0% ±0.2%	0.2% ±0.4%	0.0% ±0.1%	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.1%
	Delta	0.0% ±0.0%	0.0% ±0.0%	99.7% ±0.2%	0.0% ±0.0%	0.1% ±0.1%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.0%	0.1% ±0.1%
	Epsilon	0.0% ±0.0%	0.1% ±0.3%	0.0% ±0.0%	99.8% ±0.3%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%
	Eta	0.0% ±0.0%	0.0% ±0.2%	0.1% ±0.3%	0.0% ±0.0%	99.6% ±1.0%	0.2% ±0.5%	0.0% ±0.0%	0.0% ±0.5%	0.1% ±0.5%	0.1% ±0.5%
	Gamma	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.2%	0.0% ±0.0%	0.0% ±0.0%	99.8% ±0.3%	0.0% ±0.2%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.2%
	Iota	0.0% ±0.0%	0.1% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.2% ±0.2%	99.7% ±0.2%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%
	Kappa	0.0% ±0.0%	0.0% ±0.0%	0.2% ±0.7%	0.0% ±0.3%	0.0% ±0.3%	0.0% ±0.0%	0.0% ±0.0%	99.7% ±0.8%	0.0% ±0.0%	0.0% ±0.0%
	Lambda	0.0% ±0.0%	0.0% ±0.0%	0.1% ±0.2%	0.0% ±0.0%	0.1% ±0.2%	0.1% ±0.5%	0.1% ±0.2%	0.0% ±0.0%	99.6% ±0.7%	0.0% ±0.2%
	Omicron	0.0% ±0.0%	0.0% ±0.0%	0.1% ±0.2%	0.0% ±0.0%	0.1% ±0.2%	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.1%	0.2% ±0.3%	99.7% ±0.3%
		Alpha	Beta	Delta	Epsilon	Eta	Gamma	Iota	Kappa	Lambda	Omicron
		Predicted label									

(c) GREAC

Fig. A8: SARS-CoV-2 confusion matrices, classifications, average accuracy percentage, and standard deviation over 100 iterations. (A8a) KEVOLVE results. (A8b) CASTOR-KRFE results. (A8c) GREAC results.

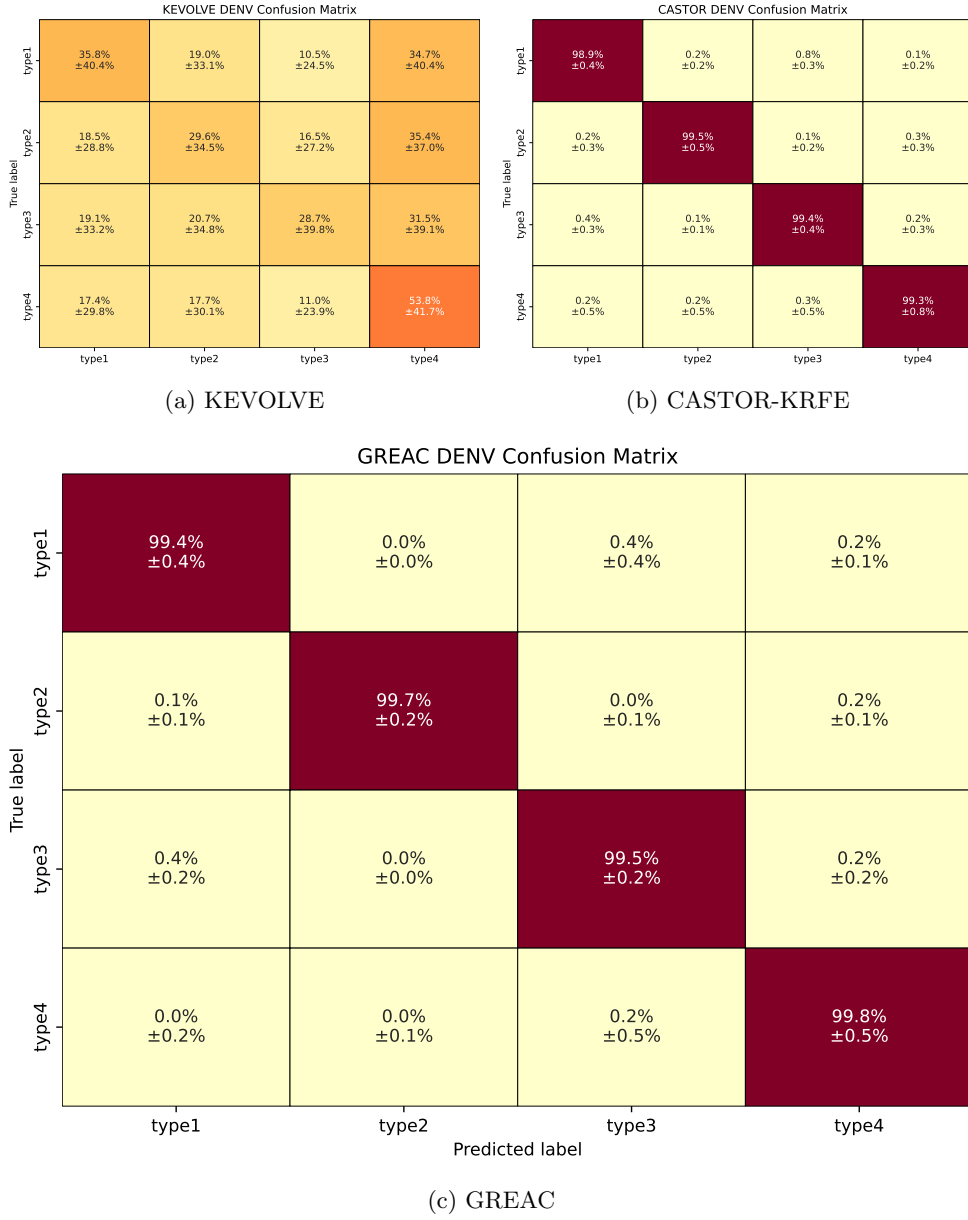


Fig. A9: DENV confusion matrices, classifications, average accuracy percentage, and standard deviation over 100 iterations. (A9a) KEVOLVE results. (A9b) CASTOR-KRFE results.(A9c) GREAC results.

KEVOLVE HBV Confusion Matrix						
True label	A	B	C	D	E	F
	32.0% ±39.3%	11.7% ±26.9%	7.9% ±21.4%	15.1% ±29.2%	14.1% ±27.2%	19.2% ±33.7%
	16.3% ±29.2%	30.9% ±38.4%	11.7% ±26.1%	8.2% ±22.1%	14.8% ±29.9%	18.0% ±32.4%
	14.9% ±28.0%	14.1% ±27.0%	24.8% ±32.6%	11.8% ±23.7%	14.9% ±28.7%	19.5% ±31.4%
	12.7% ±26.1%	14.3% ±28.4%	11.7% ±25.7%	32.2% ±38.8%	12.0% ±25.6%	17.2% ±32.0%
	12.2% ±27.1%	13.9% ±28.9%	13.2% ±27.7%	16.7% ±31.7%	30.7% ±39.2%	13.3% ±30.2%
	15.5% ±29.8%	19.2% ±33.0%	9.8% ±21.8%	11.4% ±25.4%	10.7% ±25.6%	33.5% ±41.2%

(a) KEVOLVE

CASTOR HBV Confusion Matrix						
True label	A	B	C	D	E	F
	97.6% ±1.3%	0.9% ±0.9%	1.0% ±0.8%	0.1% ±0.3%	0.2% ±0.5%	0.1% ±0.3%
	0.5% ±0.6%	98.4% ±0.9%	0.7% ±0.7%	0.2% ±0.3%	0.1% ±0.2%	0.2% ±0.3%
	0.7% ±0.8%	0.5% ±0.8%	98.0% ±1.5%	0.4% ±0.6%	0.2% ±0.3%	0.3% ±0.5%
	0.1% ±0.1%	0.2% ±0.4%	0.4% ±0.4%	98.6% ±0.9%	0.4% ±0.7%	0.3% ±0.4%
	0.1% ±0.5%	0.1% ±0.5%	0.4% ±0.7%	0.6% ±1.2%	98.3% ±1.4%	0.4% ±0.6%
	0.0% ±0.3%	0.1% ±0.5%	0.2% ±0.6%	0.2% ±0.6%	0.3% ±0.9%	99.2% ±1.3%

(b) CASTOR-KRFE

GREAC HBV Confusion Matrix						
True label	A	B	C	D	E	F
	99.9% ±0.2%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.0%	0.0% ±0.1%	0.0% ±0.0%
	0.0% ±0.1%	99.8% ±0.1%	0.1% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.0%
	0.0% ±0.1%	0.0% ±0.0%	99.9% ±0.1%	0.0% ±0.1%	0.0% ±0.1%	0.0% ±0.0%
	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.1%	99.9% ±0.6%	0.1% ±0.6%	0.0% ±0.0%
	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	100.0% ±0.0%	0.0% ±0.0%
	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	0.0% ±0.0%	100.0% ±0.0%

(c) GREAC

Fig. A10: HBV confusion matrices, classifications, average accuracy percentage, and standard deviation over 100 iterations. (A10a) KEVOLVE results. (A10b) CASTOR-KRFE results. (A10c) GREAC results.

True label \ Predicted label	HIV1_A	HIV1_B	HIV1_C	HIV1_D	HIV1_F	HIV1_G
HIV1_A	30.4% ±32.6%	5.8% ±12.7%	9.5% ±16.5%	20.8% ±27.6%	17.1% ±24.9%	16.4% ±26.1%
HIV1_B	20.1% ±28.8%	13.6% ±22.2%	9.5% ±17.3%	23.5% ±28.2%	17.6% ±27.3%	15.7% ±24.4%
HIV1_C	23.5% ±31.3%	6.5% ±14.8%	16.9% ±24.8%	20.3% ±26.1%	18.2% ±26.3%	14.6% ±26.2%
HIV1_D	20.1% ±28.1%	5.0% ±14.1%	8.7% ±16.1%	36.5% ±35.1%	16.2% ±25.2%	13.6% ±21.4%
HIV1_F	24.5% ±31.1%	7.2% ±16.1%	10.4% ±19.4%	18.9% ±24.1%	23.3% ±29.3%	15.6% ±25.7%
HIV1_G	21.6% ±30.0%	6.3% ±15.2%	12.5% ±20.0%	19.2% ±24.6%	15.2% ±23.3%	25.3% ±32.2%

(a) KEVOLVE

True label \ Predicted label	HIV1_A	HIV1_B	HIV1_C	HIV1_D	HIV1_F	HIV1_G
HIV1_A	97.2% ±2.3%	0.1% ±0.5%	0.2% ±0.6%	0.2% ±0.7%	0.9% ±1.2%	1.4% ±1.9%
HIV1_B	0.2% ±0.6%	98.0% ±2.2%	0.2% ±0.5%	1.2% ±1.7%	0.3% ±0.9%	0.1% ±0.4%
HIV1_C	0.5% ±1.0%	0.1% ±0.6%	98.5% ±1.7%	0.1% ±0.5%	0.5% ±1.0%	0.1% ±0.5%
HIV1_D	0.3% ±1.0%	0.8% ±2.0%	0.2% ±0.9%	98.5% ±2.8%	0.3% ±1.1%	0.0% ±0.4%
HIV1_F	1.5% ±2.5%	0.5% ±1.4%	0.9% ±2.0%	0.4% ±1.5%	95.8% ±4.4%	1.0% ±2.2%
HIV1_G	1.5% ±2.4%	0.2% ±0.9%	0.2% ±0.7%	0.3% ±1.0%	1.4% ±2.3%	96.4% ±3.8%

(b) CASTOR-KRFE

True label \ Predicted label	HIV1_A	HIV1_B	HIV1_C	HIV1_D	HIV1_F	HIV1_G
HIV1_A	98.4% ±1.7%	0.1% ±0.3%	0.3% ±0.6%	0.2% ±0.6%	0.8% ±1.3%	0.3% ±0.7%
HIV1_B	0.1% ±0.4%	98.9% ±1.4%	0.0% ±0.2%	0.7% ±1.2%	0.2% ±0.6%	0.0% ±0.0%
HIV1_C	0.0% ±0.0%	0.1% ±0.3%	99.8% ±0.6%	0.0% ±0.2%	0.1% ±0.4%	0.0% ±0.1%
HIV1_D	0.0% ±0.4%	0.2% ±0.8%	0.0% ±0.0%	99.6% ±1.4%	0.1% ±0.7%	0.0% ±0.4%
HIV1_F	0.4% ±1.2%	0.1% ±0.6%	0.2% ±1.0%	0.0% ±0.4%	99.0% ±1.9%	0.2% ±0.9%
HIV1_G	0.4% ±1.3%	0.1% ±0.6%	0.1% ±0.5%	0.1% ±0.6%	0.3% ±0.9%	99.0% ±1.7%

(c) GREAC

Fig. A11: HIV confusion matrices, classifications, average accuracy percentage, and standard deviation over 100 iterations. (A11a) KEVOLVE results. (A11b) CASTOR-KRFE results. (A11c) GREAC results.

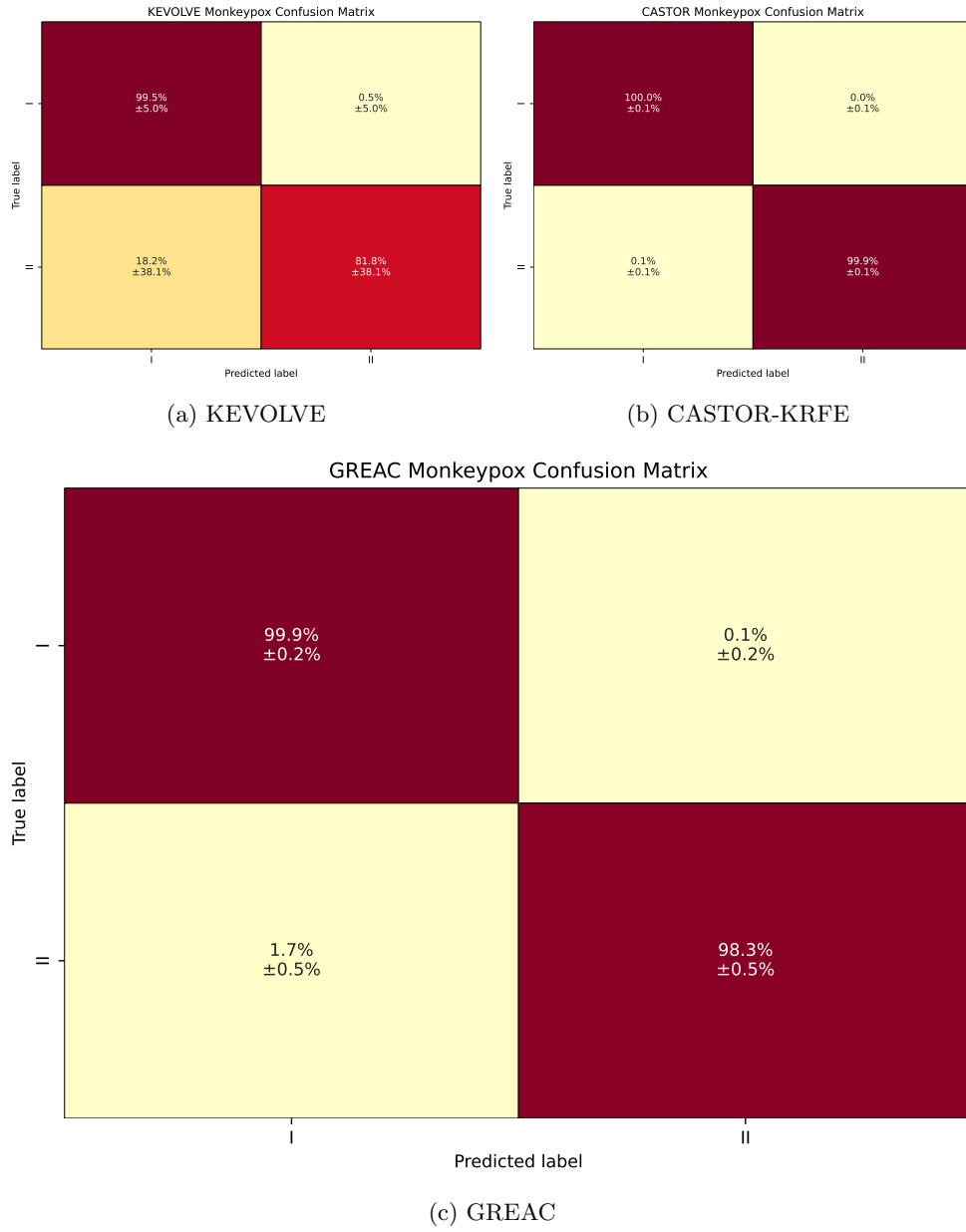
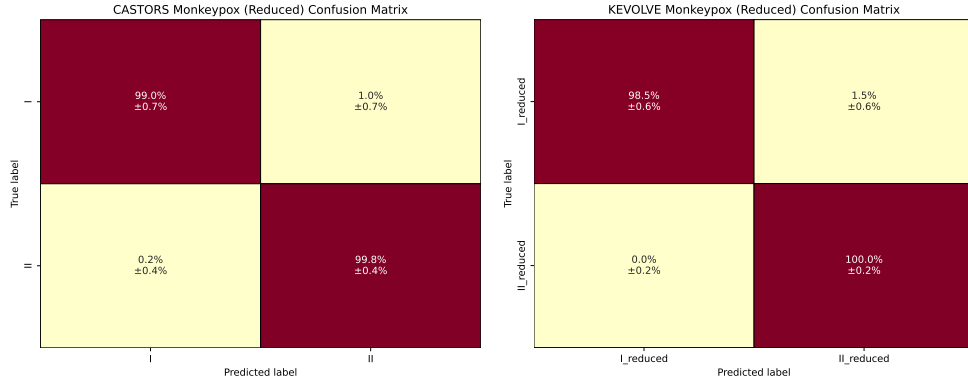


Fig. A12: Monkeypox confusion matrices classifications, average accuracy percentage, and standard deviation over 100 iterations. (A12a) KEVOLVE results. (A12b) CASTOR-KRFE results.(A12c) GREAC results.



(a) CASTOR-KRFE results on Monkeypox reduced dataset. (b) KEVOLVE results on Monkeypox reduced dataset.

Fig. A15: Confusion matrix classification average accuracy and standard deviation over 100 iterations using the reduced dataset produced only with the regions extracted by GREAC.