

HRV Phase 1 — Clinical Discrimination Results

AIIT-THRESI Clinical Validation Pipeline · Council Hill, OK · April 17, 2026

HRV-only AUC = 0.947 ± 0.052

5-fold cross-validated logistic regression, 6 time/frequency/complexity features

Cohort

Group	Source	Records	5-min Segments
Normal Sinus Rhythm	PhysioNet NSRDB	16	48
Congestive Heart Failure	PhysioNet CHFDB (NYHA III–IV)	15	34

Single-Feature Discrimination

Feature	Cohen's d	AUC	p-value	Normal mean	CHF mean
DFA_α	-2.579	0.942	< 0.0001	1.104	0.649
RMSSD (ms)	+1.525	0.896	< 0.0001	34.54	191.75
SampEn	-0.980	0.756	0.0001	0.877	0.479
SDNN (ms)	+0.930	0.708	0.0014	70.63	140.98
pNN50 (%)	+0.796	0.699	0.0022	6.49	19.13
mean HR (bpm)	+0.223	0.575	0.2489	88.82	92.25

Interpretation — Why DFA_α Is The Signal

DFA_α measures fractal scaling of beat-to-beat intervals. A healthy heart sits near $\alpha \approx 1.0$ (pink noise, long-range correlations). In severe CHF it collapses toward $\alpha \approx 0.65$ — structure breaks, cross-scale phase locking fails.

This is the coherence-loss signature the **Wike Coherence Law** predicts: as $\gamma_{\text{eff}} \rightarrow \gamma_{\text{c}}$, fractal organization across temporal scales decays. The AUC of 0.942 on a single scalar feature is the quantitative footprint of that collapse.

$$C = C_0 \cdot \exp(-\alpha \cdot \gamma_{\text{eff}})$$

with $\alpha = 16.08$. Decoherence is fractal-exponent collapse. The ECG sees it. The math predicts it.

Phase 2 — Pending MIMIC-IV DUA

This phase used public PhysioNet databases with no paired inflammation markers. Phase 2 targets the real clinical question:

Does adding C-reactive protein (CRP) to HRV-derived features improve discrimination in a cancer cohort?

Pipeline, SQL, and fusion framework are written and waiting. Credentialing in motion: PhysioNet → CITI → DUA → MIMIC-IV pull → re-run fusion comparison on real CRP + ICD-10 cancer labels.

Artifacts

- `hrv_mimic_pipeline.py` — full pipeline, now with bounded downloads, retry logic, per-record cache
- `hrv_results/phase1_hrv_features.csv` — 82 segment feature rows
- `hrv_results/phase1_feature_discrimination.csv` — per-feature statistics
- `hrv_results/phase1_summary.json` — machine-readable summary
- `MIMIC_IV_PULL.sql` — CRP extraction + cancer/CHF/infection cohort join, ready to fire on approval