

CONTRIBUTIONS

- The **first work to use a similarity measure to select positive pairs** in time-series contrastive learning
- Our **learned measure** captures motif similarity and **predicts mutual class membership**
- Our REBAR approach achieves **SOTA performance against a suite of representative benchmarks** that only differ by their learning objective.

MOTIVATION

Strong Opportunity in SSL for Health Sensors

- Many advances within wearable health sensor technology (e.g. Oura Ring, Apple Watch, Zio ECG monitor)
- But the cost of labeling this data remains high.

Contrastive SSL for Time-Series is Underexplored

- Augmentation-based methods (e.g. TF-C and TS2Vec) use an inconsistent set of augmentations.
- Sampling-based approaches (e.g. TNC and T-loss) naively choose positive pairs based on temporal proximity.

How can we identify meaningful positive pairs?

Time-series Motifs are Indicative of Semantic Properties

- Examples include the QRS complex in ECG, the Hand swinging motion in HAR, Dicrotic notch in PPG, etc.

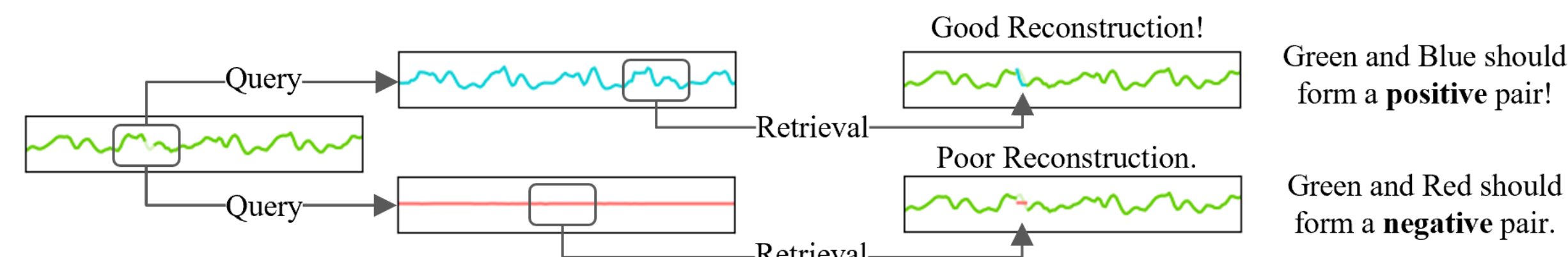
Key idea: If two sequences share similar motifs, then they are a good candidate to form positive pairs

INTUITION

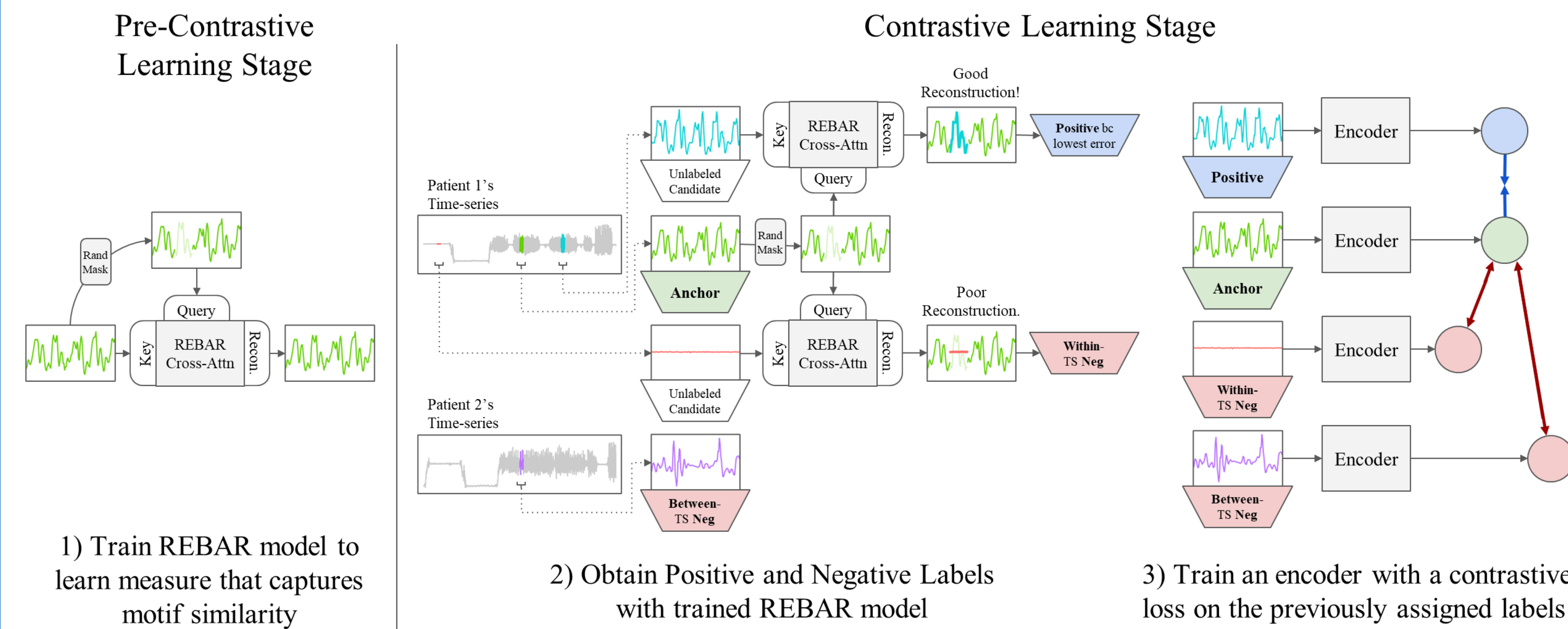
Given this accelerometry signal, with *Walk Subseq 1* as our anchor, we would rather identify *Walk Subseq 2* as our positive instance rather than *Sit Subseq*.



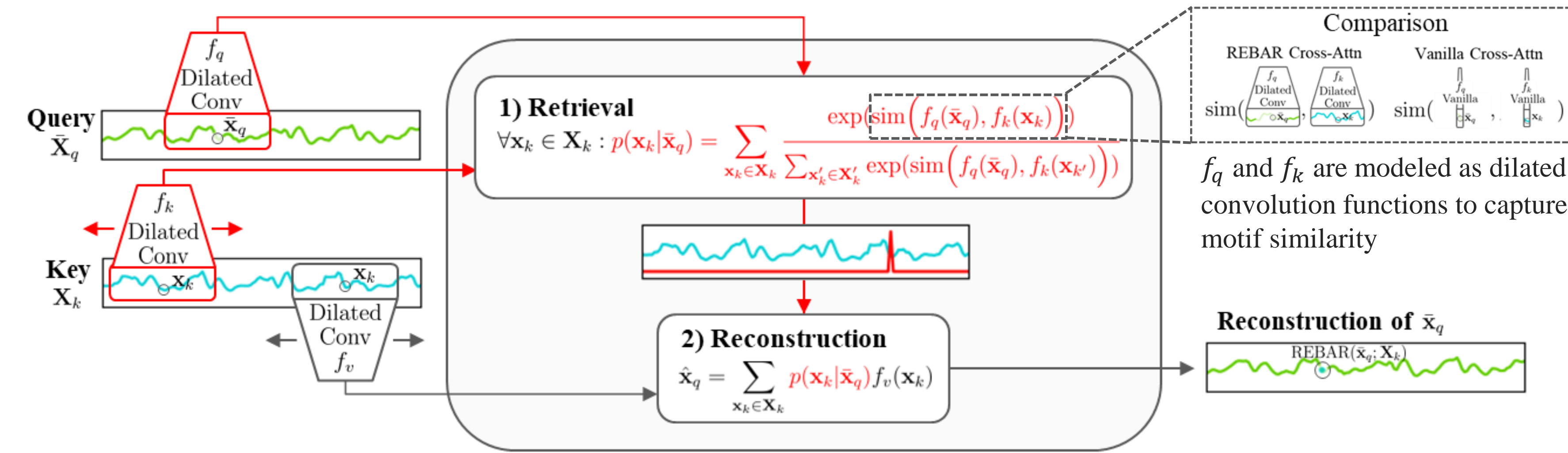
If we can successfully retrieve motif info from the candidate to aid in reconstruction, then it should be the positive.



APPROACH



REBAR Cross-Attention



Retrieval

Identifies where in the key is useful for reconstruction based on motif similarity.

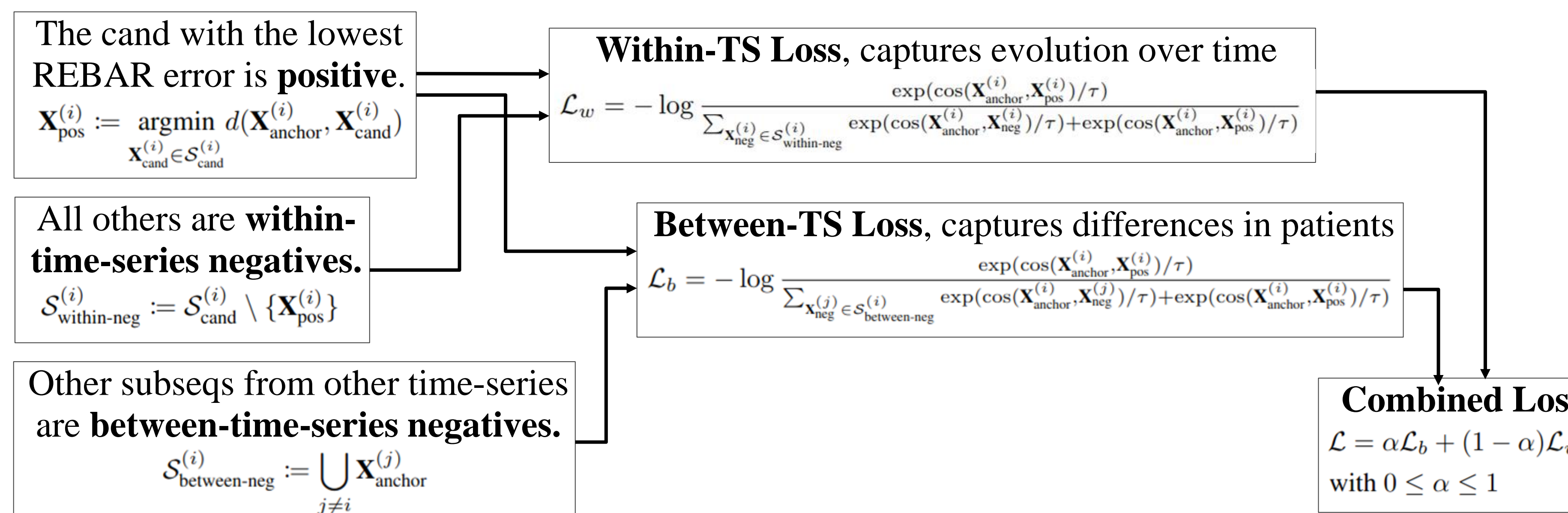
Reconstruction

A weighted average of the retrieved regions from the key is used for reconstruction of the query

Reconstruction is directly dependent on the motif similarity of the query with the key. When the reconstruction error is lower, the pair is more likely to share semantic information.

Applying REBAR to Contrastive Learning

Randomly sample a set of candidate subseqs and an anchor subseq from a time-series, then:

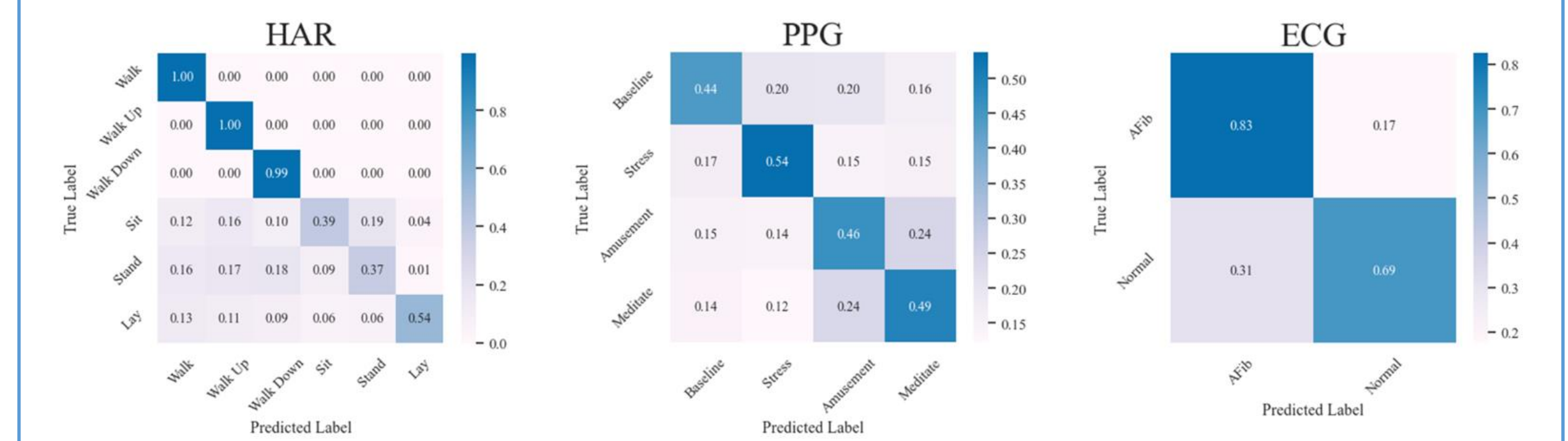


VALIDATION EXPERIMENT

After sampling a candidate from each class, label the anchor with a nearest neighbor classifier, with distance measured by REBAR error.

$$P(c_{\text{pred}} = c | c_{\text{true}}) = \mathbb{E}_{\mathbf{A}^{(i)} \sim D} \left[\mathbb{E}_{\mathbf{X}^{(i)} \sim \mathbf{A}^{(i)}} \left[\mathbb{1}_{c_{\text{true}}} \left(\underset{c \in \{1, \dots, C\}}{\text{argmin}} d(\mathbf{x}_{\text{anchor}, c_{\text{true}}}^{(i)}, \mathbf{x}_{\text{cand}, c}^{(i)}) \right) \right] \right]$$

The high diagonal concentration demonstrate REBAR's ability to predict mutual class membership.



RESULTS

	HAR			PPG			ECG		
Model	↑ Accuracy	↑ AUROC	↑ AUPRC	↑ Accuracy	↑ AUROC	↑ AUPRC	↑ Accuracy	↑ AUROC	↑ AUPRC
Fully Supervised	0.9535	0.9835	0.9531	0.4138	0.6241	0.3689	0.7814	0.9329	0.9260
TS2Vec	0.9324	0.9931	0.9766	0.4023	0.6428	0.3959	0.7612	0.8656	0.8516
TNC	0.9437	0.9937	0.9788	0.2989	0.6253	0.3730	0.7340	0.8405	0.8195
CPC	0.8662	0.9867	0.9438	0.3448	0.5843	0.3642	0.7775	0.8377	0.8223
SimCLR	0.9465	0.9938	0.9763	0.3448	0.6119	0.3608	0.6992	0.8254	0.8063
Sliding-MSE	0.9352	0.9931	0.9767	0.3333	0.6456	0.3831	0.7751	0.8755	0.8574
REBAR (ours)	0.9535	0.9965	0.9891	0.4138	0.6977	0.4457	0.8154	0.9146	0.8985

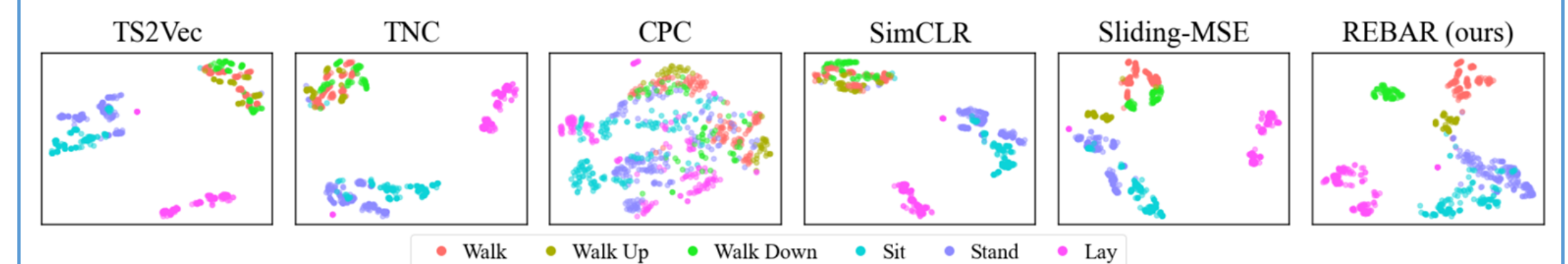
Table 1: Linear Probe Classification Results with Accuracy, AUROC, and AUPRC

REBAR consistently achieved the *strongest linear probe results*, beating a *wide range of representative* augmentation-based and sampling-based *contrastive methods*, even beating a *fully-supervised approach*.

	HAR		PPG		ECG	
Model	↑ ARI	↑ NMI	↑ ARI	↑ NMI	↑ ARI	↑ NMI
TS2Vec	0.4654	0.6115	-0.0353	0.1582	0.2087	0.1701
TNC	0.4517	0.5872	0.0958	0.1666	0.2186	0.1753
CPC	0.1603	0.2217	0.1110	0.1867	0.0532	0.0724
SimCLR	0.5805	0.6801	0.1535	0.3081	0.2182	0.1751
Sliding-MSE	0.5985	0.7019	0.1083	0.2141	-0.0081	0.0180
REBAR (ours)	0.6258	0.7721	0.1830	0.3422	0.2260	0.1796

Table 2: Clusterability Results with Adjusted Rand Index and Normalized Mutual Information

Clusterability results demonstrate that REBAR has the strongest agreement between k-mean clusters and true labels, *corroborating classification results*.



Unlike most methods, REBAR is able to *distinguish between semantically similar, but distinct, classes*

CONCLUSION

Our REBAR method offers a powerful *new perspective on how to identify positive pairings*, and we hope that this work will drive future work into understanding how to best learn representations in time-series and the greater SSL space.