



RANK-1 SIMILARITY MATRIX DECOMPOSITION FOR MODELING CHANGES IN ANTIVIRUS CONSENSUS THROUGH TIME

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ANTIVIRUS CORRELATION

- Some groups of AVs known to make correlated labeling decisions
- Conventional wisdom in industry has a few explanations:
 - Copying results of leading vendors
 - Different AV products using the same engine
 - Signature sharing
- All explanations involve “first order” interactions
 - Creates direct link between labeling decisions of two AVs

WHY DOES THIS MATTER?

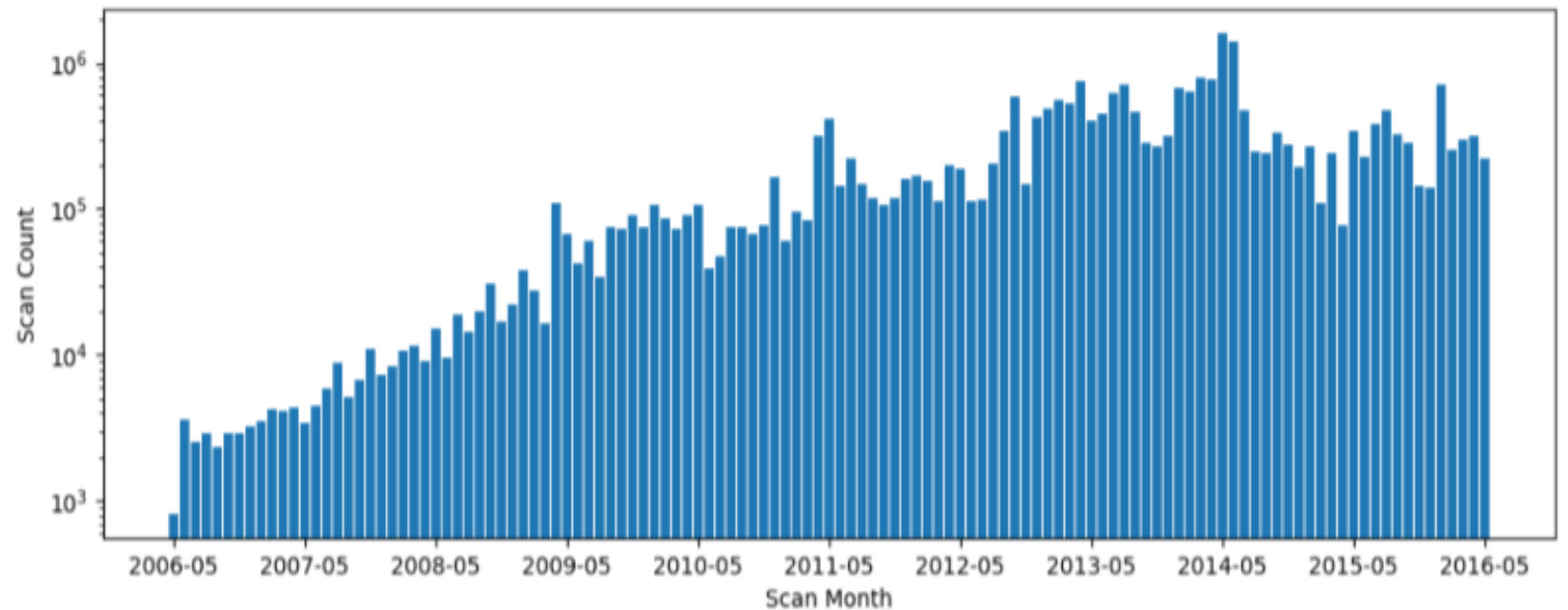
- Aggregated results from a collection of AVs is much better than using a single AV
 - Detection – is it malicious or benign?
 - Classification – which family does it belong to?
- Correlations between AVs can influence voting and other aggregation approaches

RESEARCH QUESTIONS

- Are existing assumptions about AV correlation correct?
- Is AV agreement predominantly due to first-order interactions?
 - When detecting files as malware?
 - When classifying malware by family?
- How do first-order interactions between AVs change over time?

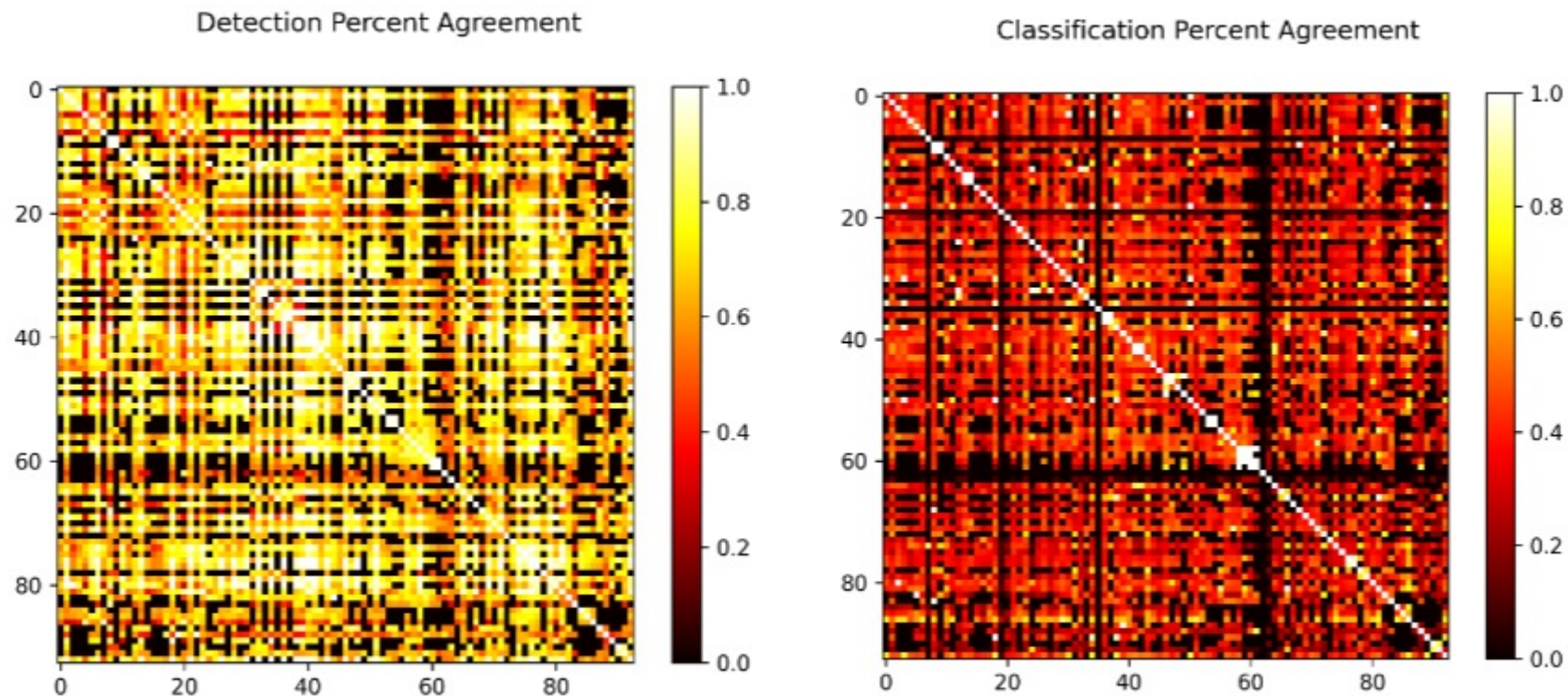
THE DATA

- Using 25,100,286 VirusTotal scan reports over 10-year period
- Malware samples are from the VirusShare dataset
- 93 distinct AVs



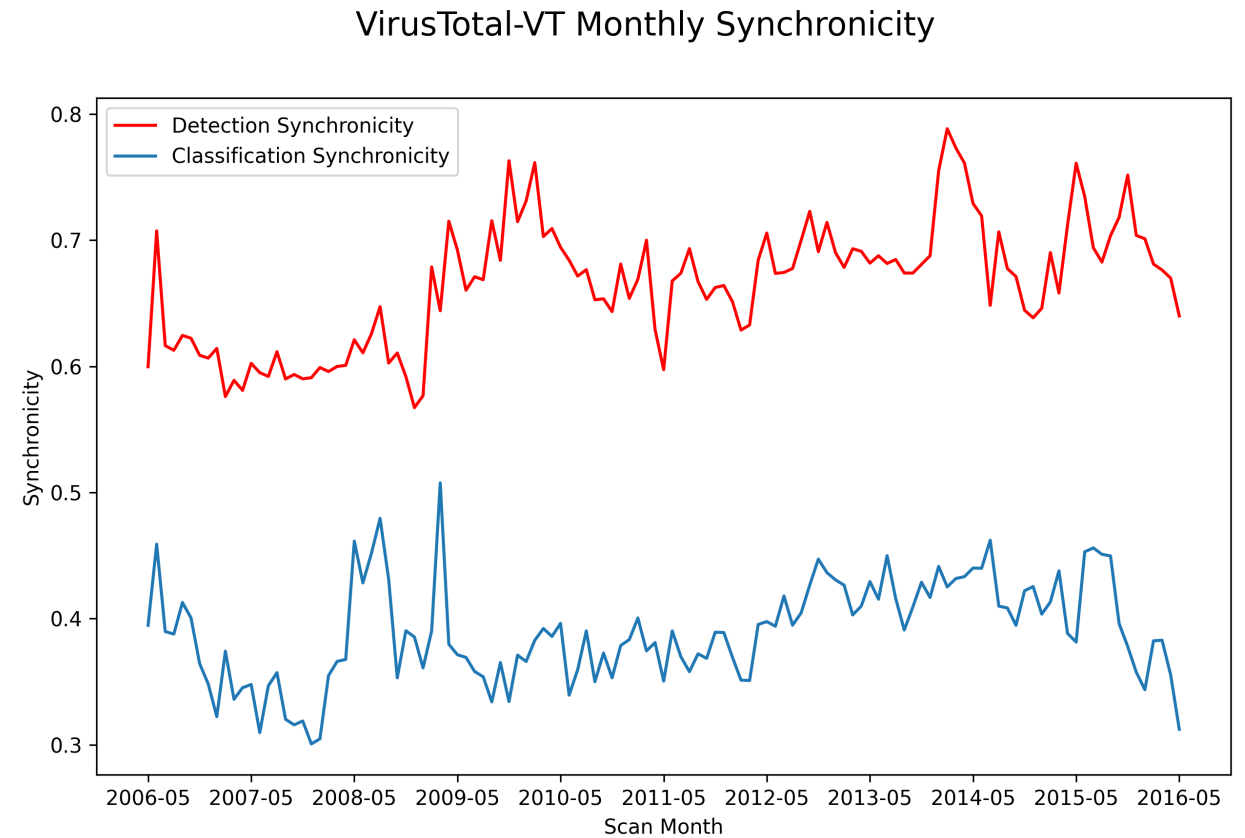
ANTIVIRUS AGREEMENT

- Before we look into first-order interactions, we need to measure how frequently AVs agree with each other



ANTIVIRUS SYNCHRONICITY

- Synchronicity is the average pairwise agreement between all AVs
- Extremely variable on a monthly timescale



THE R1SM DECOMPOSITION

- Rank-1 Similarity Matrix Decomposition
- $D = \sum_1^k \text{triu}(\mathbf{r}_i \mathbf{r}_i^T, 1)$
- Decomposes a similarity matrix D into a sum of k rank-1 outer products with shared, non-negative weights
 - Because the components $\mathbf{r}_1, \mathbf{r}_2 \dots \mathbf{r}_k$ have rank 1, they manifest first-order interactions between objects

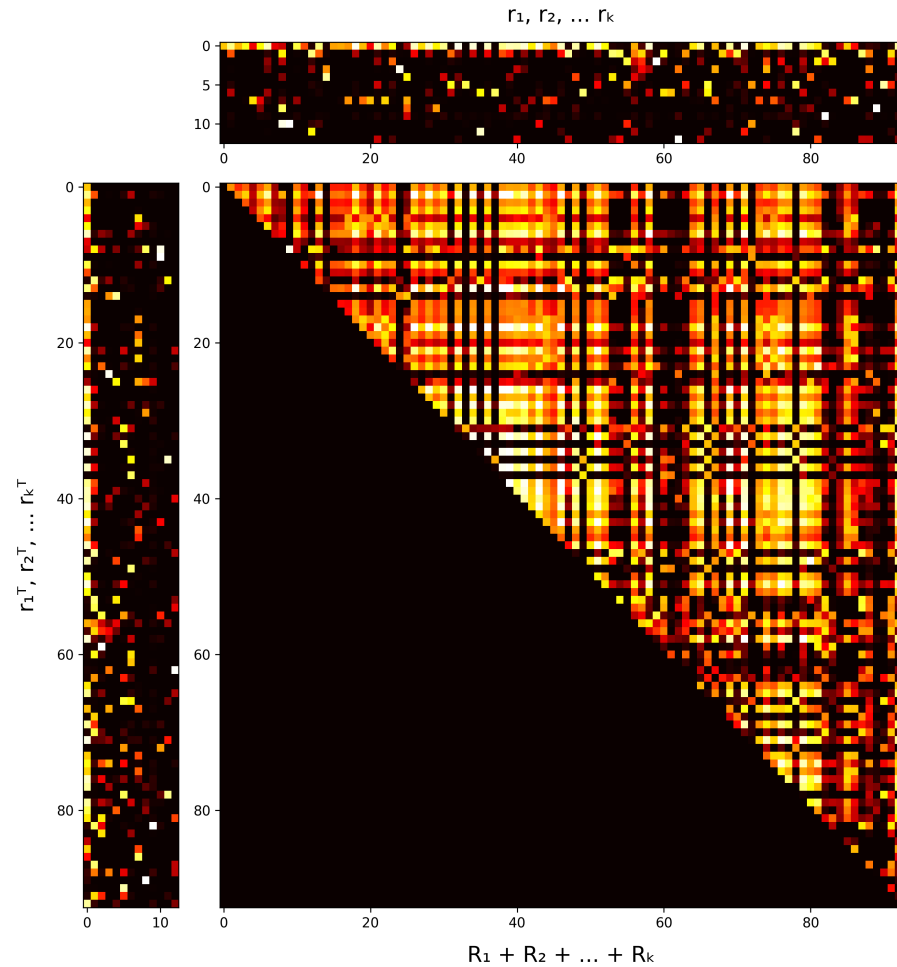
SOLVING THE R1SM DECOMPOSITION

- The R1SM decomposition typically has multiple solutions
- We developed a greedy algorithm for solving R1SM
 - At each iteration, identifies a component that explains as much of the remaining similarity matrix as possible
 - Stops when a component fails to explain a small percentage δ of the similarity matrix ($\delta = 0.1\%$ by default)
- More details in paper!

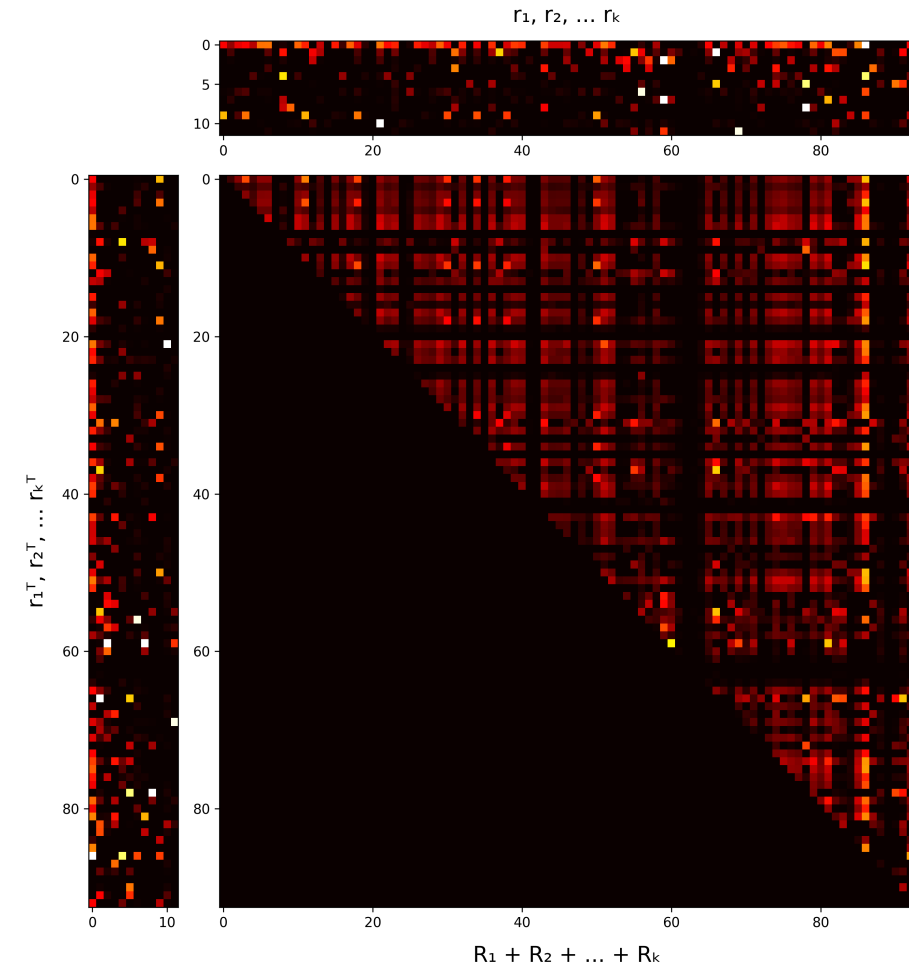
APPLYING R1SM TO ANTIVIRUS SCAN DATA

- Applied R1SM to the detection and classification percent agreement similarity matrices
- Detection percent agreement:
 - $k = 16$ components that explain 60.596% of similarity matrix
- Classification percent agreement:
 - $k = 21$ components that explain 58.394% of similarity matrix

APPLYING R1SM TO ANTIVIRUS SCAN DATA



Detection Percent Agreement



Classification Percent Agreement

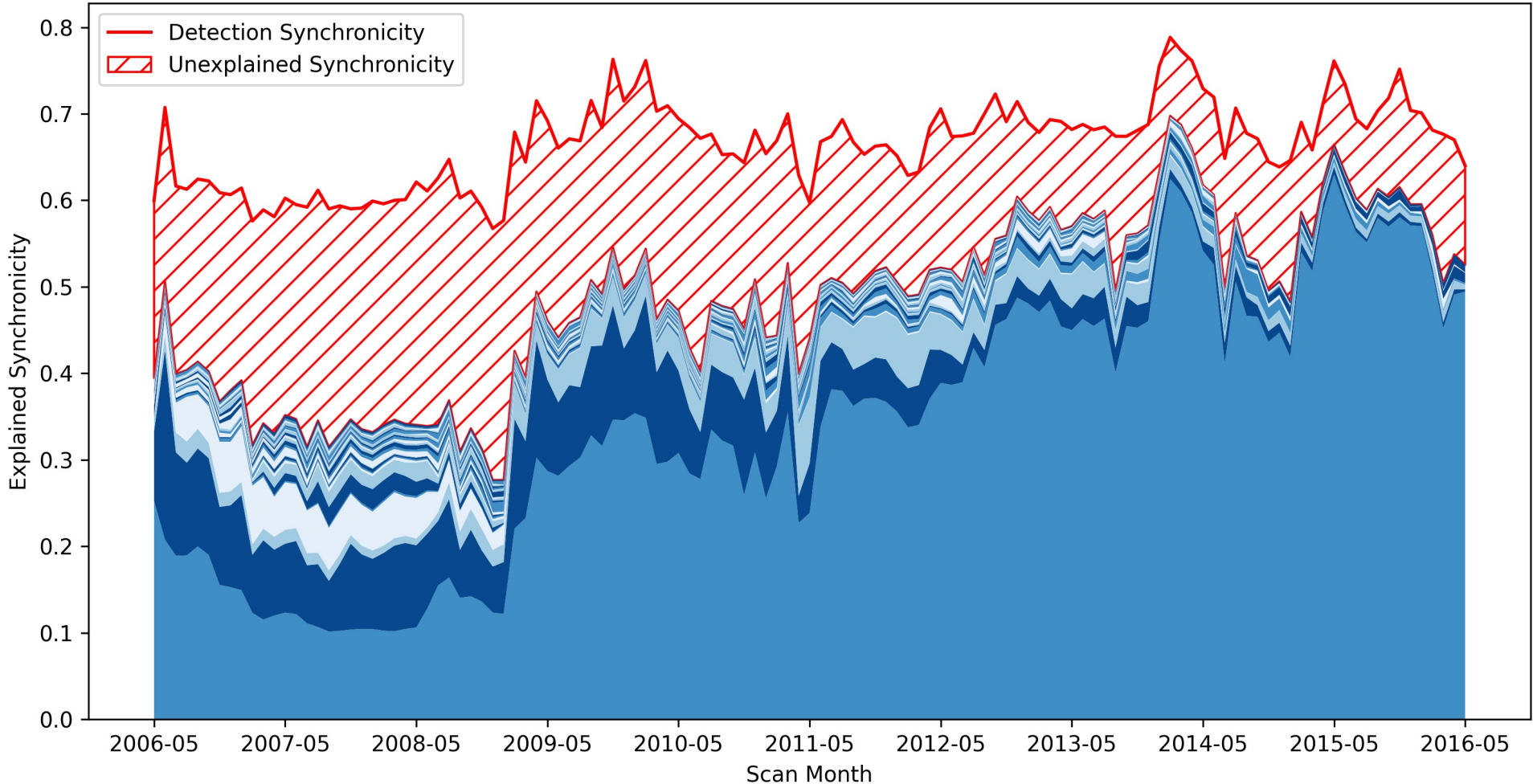
R1SM-T: EXTENDING R1SM TO TIME-SERIES DATA

- R1SM decomposition of a time-series of similarity matrices
- Shares information across all matrices as a function of their spatial relationships in time
- Implemented as a deep neural network over positional embeddings

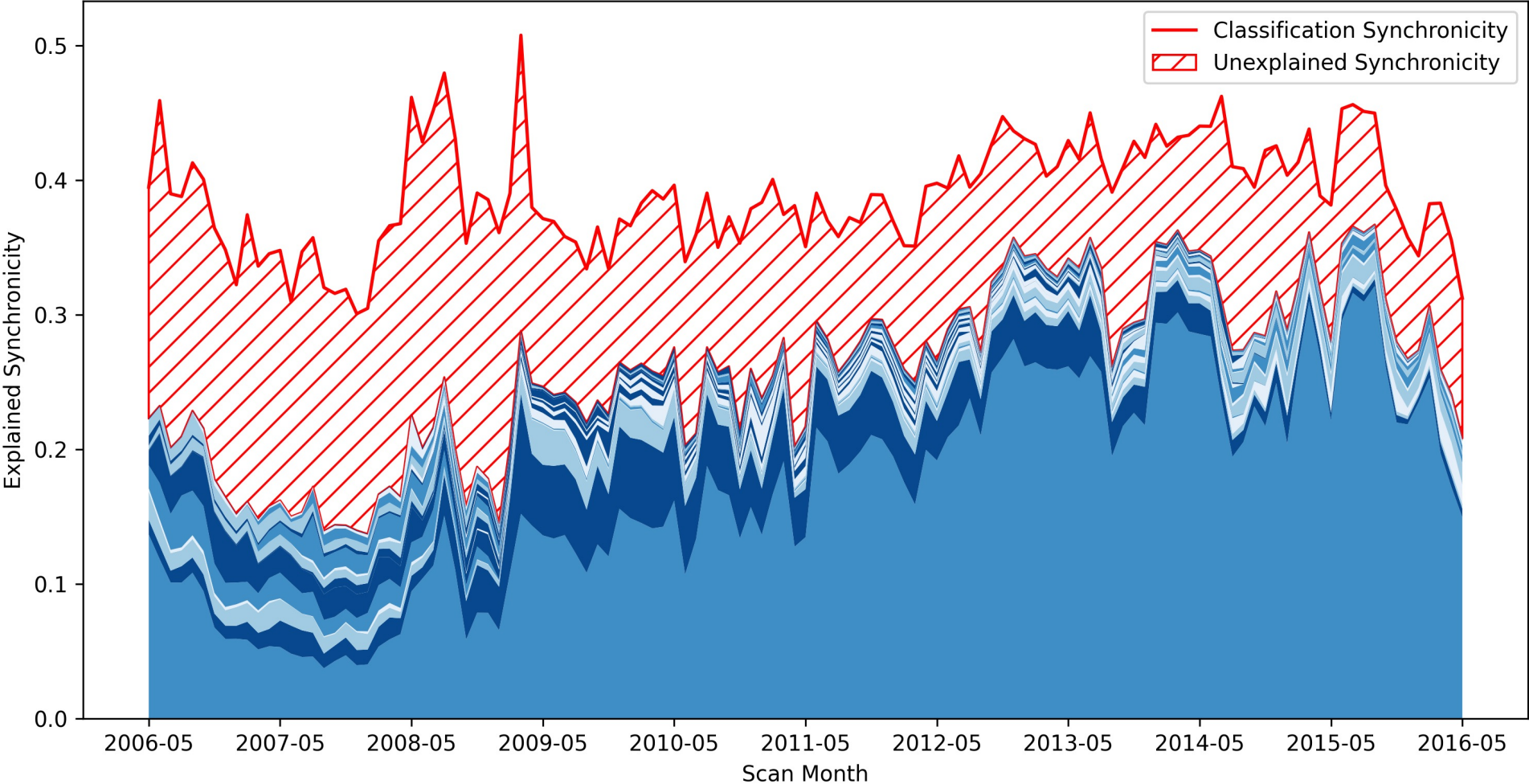
APPLYING R1SM-T TO ANTIVIRUS SCAN DATA

- Decomposed a time-series of similarity matrices representing monthly detection and classification agreement
- Detection percent agreement:
 - $k = 26$ components that explain 73.709% of time-series
- Classification percent agreement:
 - $k = 26$ components that explain 67.196% of time-series

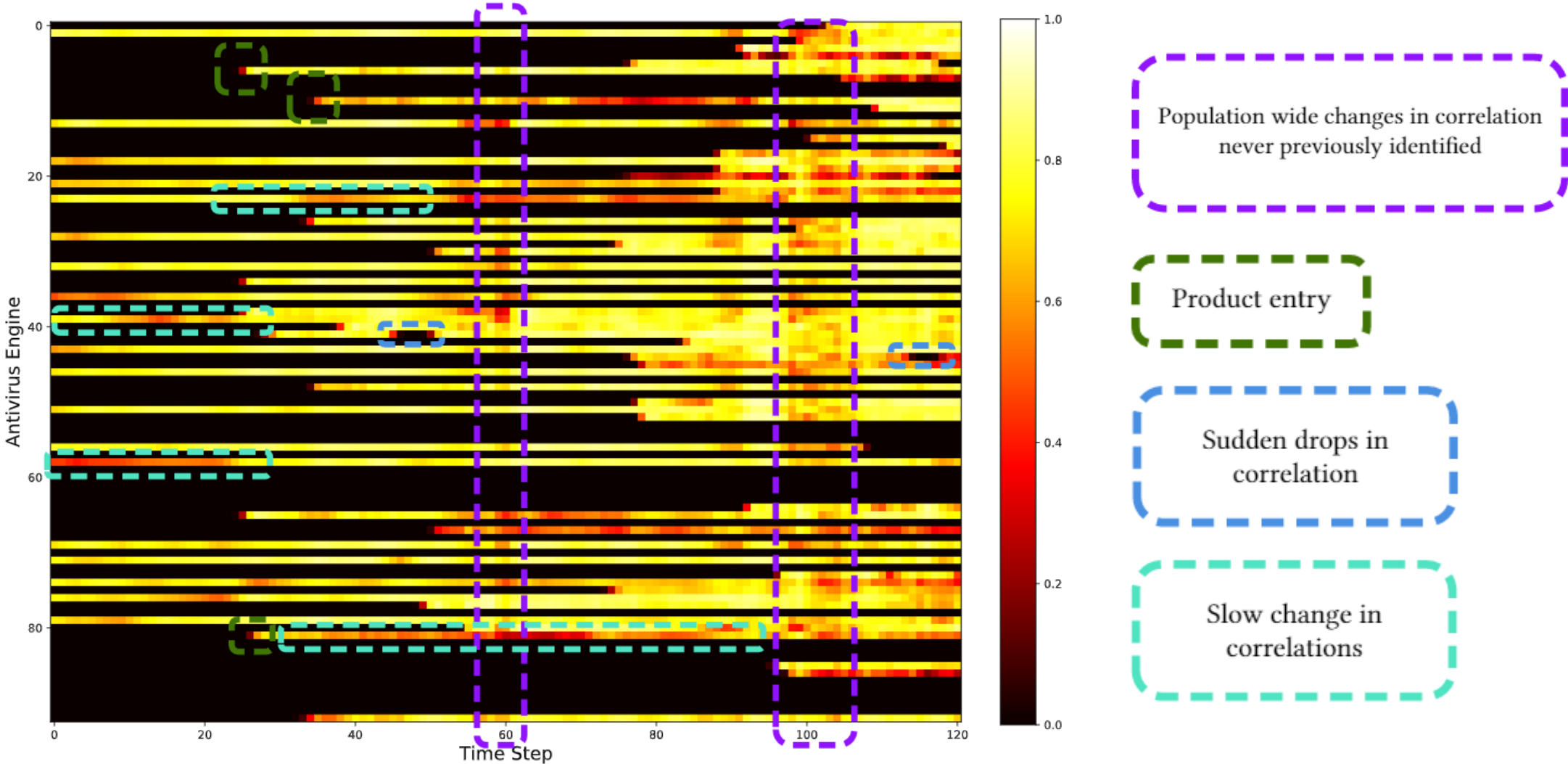
R1SM-T MONTHLY EXPLAINED DETECTION SYNCHRONICITY



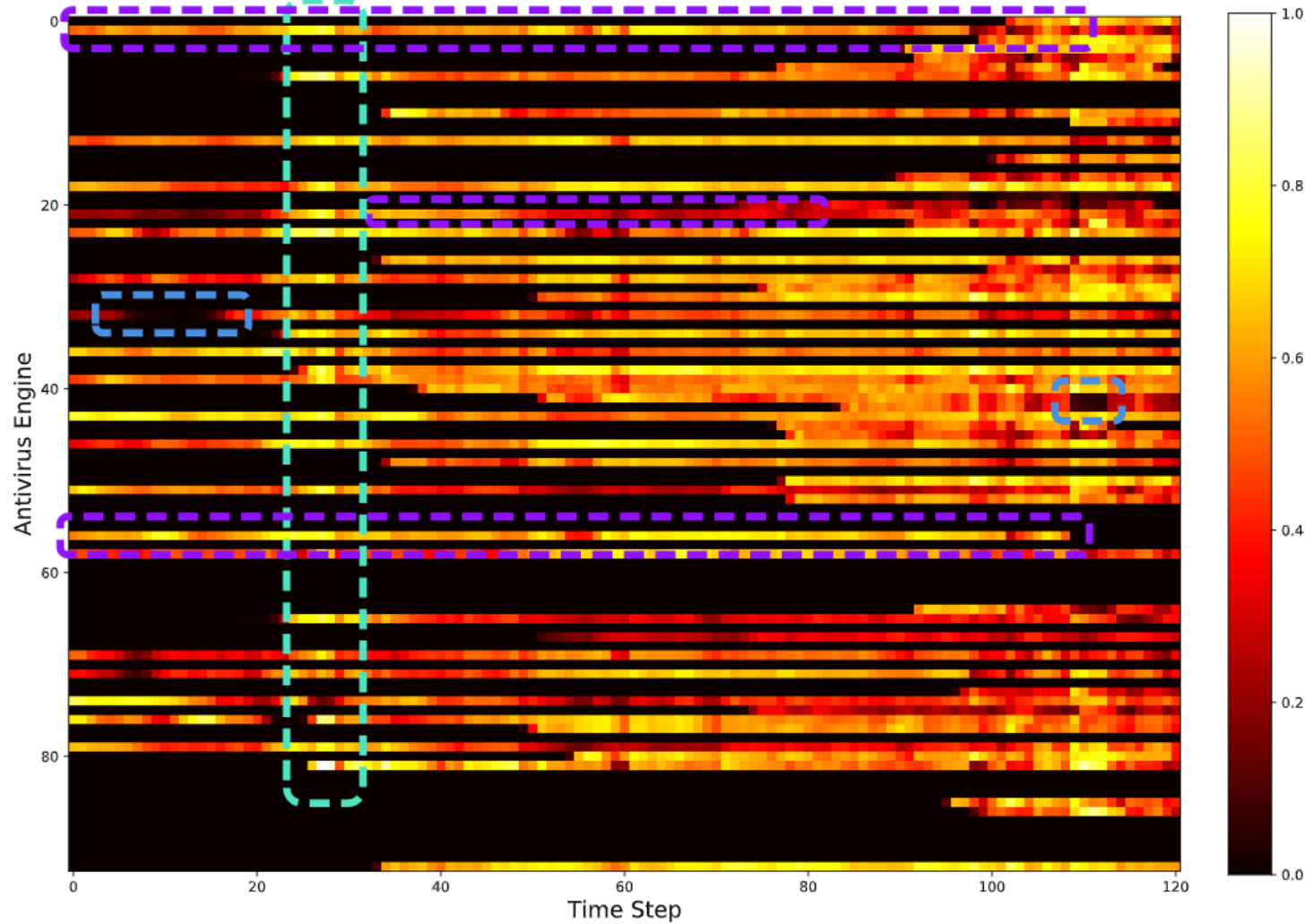
R1SM-T MONTHLY EXPLAINED CLASSIFICATION SYNCHRONICITY



R1SM-T DETECTION TIME-SERIES COMPONENT 1



R1SM-T CLASSIFICATION TIME-SERIES COMPONENT 1



Correlation change over time not present from just detection plots.

Sudden drops in correlation

Global structure change only for classification

CONCLUSIONS

- First-order interactions alone are not sufficient for modeling the complex interactions between AVs
 - We do not fully understand causes of AV correlation
 - Relationships between AVs more volatile than previously thought
- Future AV aggregation approaches should weight voters as both a function of correlation and time