

Measuring Behavioral Similarity in *Drosophila*: A Comparative Study of Time-Series Distance Metrics

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ABSTRACT

Comparing time-series data is crucial for tasks such as classification, clustering, anomaly detection, and overall similarity assessment. We investigated various distance-based measures on time-series behavioral data obtained from *Drosophila melanogaster* via the Fly Bowl setup and the JAABA model. This dataset captures 11 distinct behaviors across experimental sessions, stored as score weights or as binary arrays. Our Python-based workflow overcame MATLAB-based data-loading challenges, enabling multi-experiment processing.

We implemented and evaluated five approaches—Hamming Distance, Interval Overlap, Hidden Markov Model (HMM), Dynamic Time Warping (DTW), and Euclidean Distance—to capture both synchronous and sequence-based similarities. We measured these algorithms using the ratio of inter-group to intra-group distances: a higher ratio indicates better group separation. Small-dataset results suggest HMMs achieve the strongest separation, whereas DTW has the least discriminative power. Future work involves scaling to larger datasets, refining behavior weighting, exploring SFA-based distances, and fixing data normalization issues.

1. INTRODUCTION

Time-series analysis underpins classification, clustering, and anomaly detection in diverse fields, including biology, finance, neurobiology. In the biological context, capturing multi-dimensional behaviors of *Drosophila melanogaster* over time provides deep insights into genetic and environmental influences.

The Fly Bowl setup, paired with the JAABA annotator, yields time-series data of 11 behavioral channels. Values are stored either as score weights (with smaller numbers indicating higher likelihood of a behavior) or as post-processed binary arrays. Since the original data pipeline was MATLAB-based, we developed a new Python interface to load multiple experiments and produce standardized arrays or interval representations suitable for similarity assessment.

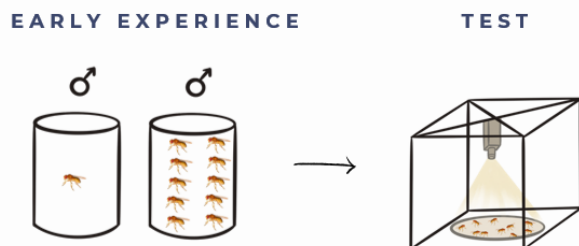


Figure 1: *Drosophila* behavior data collection

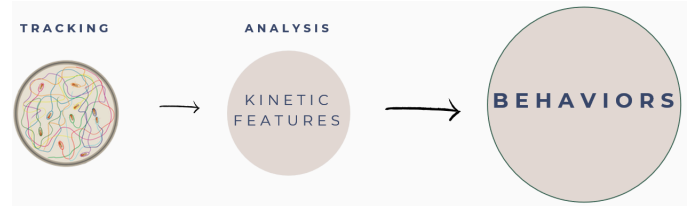


Figure 2: *Drosophila* behavior data collection

2. METHODS

2.1 Data Description and Preprocessing

Each experiment contains a time-series of 11 behaviors for multiple flies.

- Score Weights: A numeric time-series per behavior, one vector per fly per behavior.
- Binary (Post Processed): A binary time-series per behavior, one vector per fly per behavior. Multiple behaviors can be active simultaneously in any given frame.

For analysis, we ensured each fly's data is in a consistent Python structure (NumPy arrays or interval lists). We also built a GUI to batch-load many experiments at once.

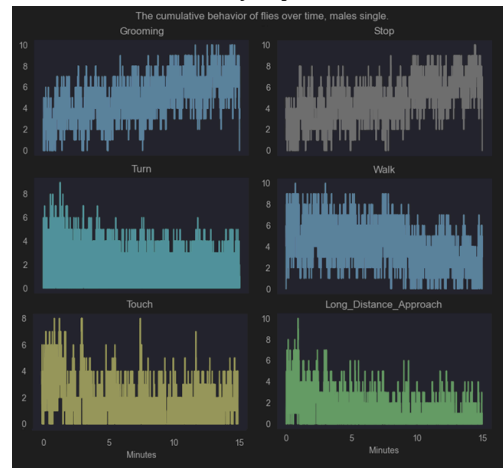


Figure 3: Trends in the data (especially Grooming) which emphasizes the time importance of the time-series nature of the data.

2.2 Similarity Search Algorithms

1. Hamming Distance

- Motivation: Ideal for binary multi-hot vectors (where multiple behaviors may co-occur).
- Mathematics:

$$d_{\text{Hamming}}(x, y) = \sum_{t=1}^T \sum_{b=1}^B \mathbf{1}[x_{t,b} \neq y_{t,b}]$$

where x and y are two time-series (each $T \times B$), $\mathbf{1}[\cdot]$ is an indicator function, and t indexes frames, b indexes behaviors.

2. Interval Overlap

- Motivation: If we convert each behavior's "active times" into intervals (start,end), we want to measure how much these intervals align.
- Mathematics: For each behavior, compute the sum of overlapping intervals between two flies. The "distance" can be:

$$d_{\text{Overlap}} = 1 - \frac{\text{Total Overlap}}{\text{Total Union}}$$

where "Total Overlap" is the summed intersection of intervals, and "Total Union" is the combined duration minus overlap.

3. Hidden Markov Model (HMM)

- Motivation: Behaviors can transition from one state to another over time. HMMs capture these transitions probabilistically. This approach helps to notice differences in patterns.
- Mathematics: Each fly's data is converted into discrete states or multi-hot states. Train an HMM by maximizing the likelihood of state transitions:

$$P(\text{observations} \mid \text{HMM parameters}) \rightarrow \max$$

Compare two HMMs (A and B) by scoring how well model A explains B's data (and vice versa) and combine these likelihoods into a distance measure.

4. Dynamic Time Warping (DTW)

- Motivation: Allows time-series that may be "out of phase" or "stretched" to align.
- Mathematics: Recursively defines a warping path π to minimize cumulative Euclidean cost:

$$d_{\text{DTW}}(x, y) = \min_{\pi} \sum_{(i,j) \in \pi} \|x_i - y_j\|$$

5. Euclidean Distance (Baseline)

- Motivation: Straight-line distance in the $T \times B$ space.
- Mathematics:

$$d_{\text{Eucl}}(x, y) = \sum_{t=1}^T \sum_{b=1}^B (x_{t,b} - y_{t,b})^2$$

2.3 Evaluation Metric

We measure:

- Intra-Group Distance: Average distance among flies within the same group.
- Inter-Group Distance: Average distance among flies from different groups.

We then form the ratio:

$$\text{Ratio} = \frac{\text{Intra-Group Distance}}{\text{Inter-Group Distance}}$$

where a higher ratio suggests better group discrimination.

3. EXPERIMENTAL RESULTS

3.1 Small Dataset Findings

We ran all methods on a small subset and found:

Method	Avg Intra Group	Avg Inter Group	Ratio (Inter/Intra)
Hamming Distance	0.605	0.363	1.665
Interval Overlap	0.564	0.344	1.638
Hidden Markov Model	0.998	0.320	3.120
Dynamic Time Warping	0.502	0.489	1.027
Euclidean	0.619	0.520	1.189

HMMs displayed the highest ratio, indicating clear distinction across groups. But that doesn't tell us anything right now, because due to computational complexity, we tested this on too small a sample of flies. DTW performed poorly, likely because time distortions here do not correspond to meaningful behavior changes.

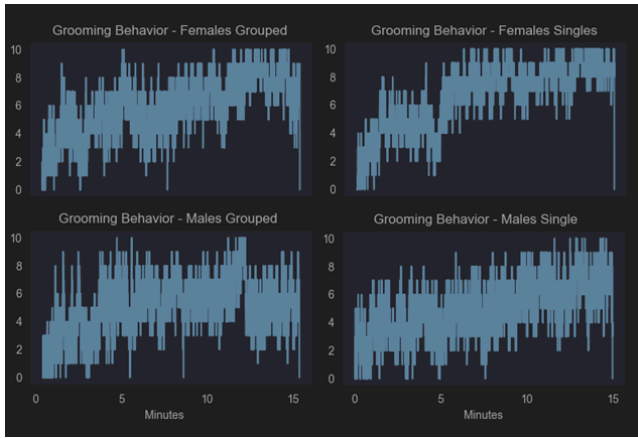


Figure 4: Intergroup similarity, using grooming as an example

3.2 Additional Correlation Checks

We also observed higher correlations within the same group than across different groups, supporting our distance-based findings.

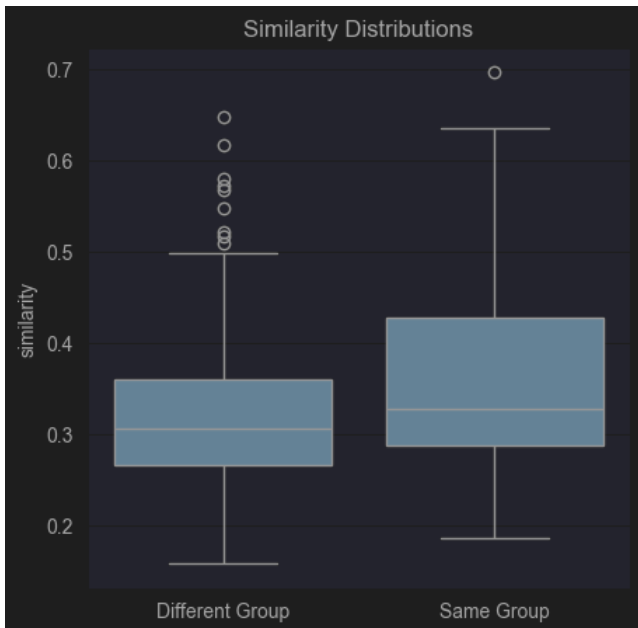


Figure 5: Similarity is measured using Pearson correlation.

Also we checked the Logistic Regression Model. The logistic regression model provides a quantitative relationship between similarity and group membership:

Coefficient $\beta=2.0023$: Higher similarity strongly increases the probability of flies being classified in the same group.

4. DISCUSSION

1. **Scaling:** We intend to run on larger datasets using high-performance computing to confirm these preliminary outcomes.
2. **Refining Behavior Weights:** Not all 11 behaviors are equally informative. Distinct weighting or selective subsets may enhance group discrimination.
3. **Exploring Other Algorithms:** Symbolic Fourier Approximation (SFA) may capture subtle shape variations in the time-series.
4. **Custom Similarity Measures:** Another error minimization or regression-based approaches could directly optimize for group separation.
5. **Normalization Issues:** The incorrect *scoreNorm* parameter in the dataset complicates the interpretation of score weights. We plan to correct and reevaluate.

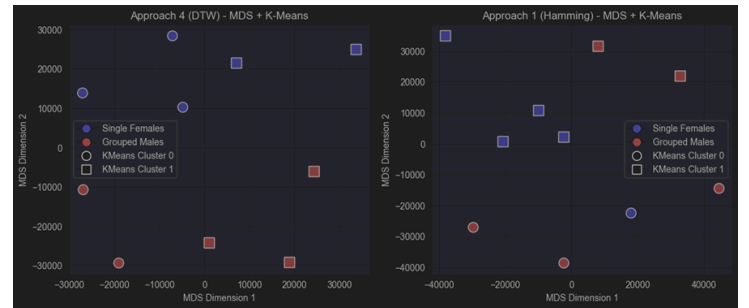


Figure 6: Our sample was very small, so the results have little significance.

5. CONCLUSION

We compared Hamming Distance, Interval Overlap, HMM-based distances, DTW, and Euclidean Distance on *Drosophila* multi-behavior time-series. HMM stands out for discriminative power on the small test set. Future work involves comprehensive testing on larger datasets, refining weighting, implementing advanced distance measures like SFA, and resolving the data normalization problem.

References

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