Sensorimotor Habituation in Drosophila Larvae

Population-Level Modeling and Individual Phenotyping Validation

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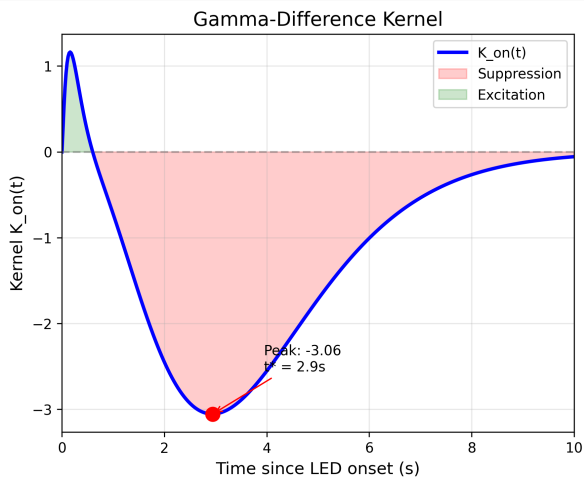
Executive Summary – Original Study

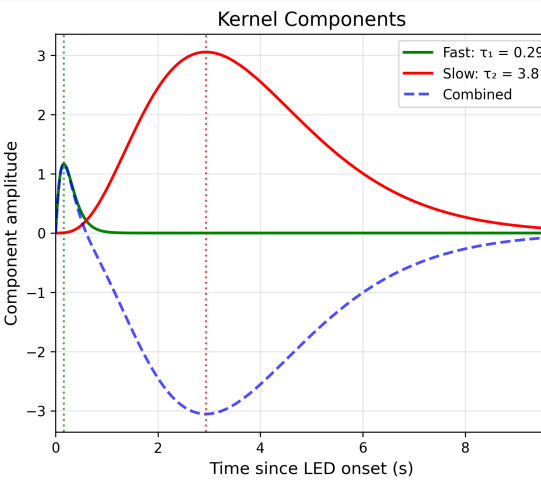
Population-Level Sensorimotor Habituation Model

- Larval reorientation behavior follows a **gamma-difference kernel** with two timescales
- Fast excitatory component with $\tau_1 \approx 0.3$ seconds drives the initial response
- Slow inhibitory component with $\tau_2 \approx 4$ seconds produces delayed suppression
- Model validated across 14 experiments with 701 tracks

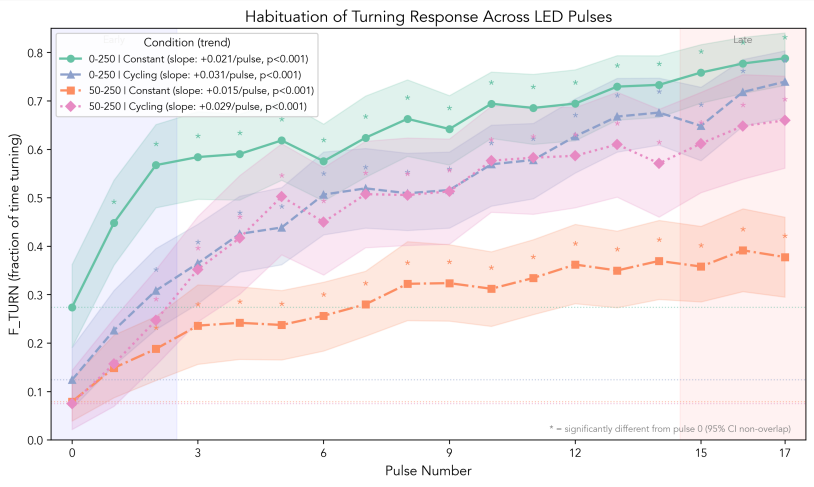
Key Result The gamma-difference kernel accurately predicts population-level reorientation dynamics.

Kernel Structure

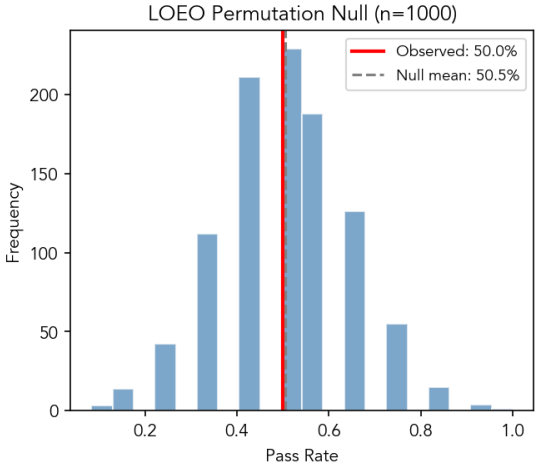




Habituation Dynamics



Leave-One-Experiment-Out Validation

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LOEO PERMUTATION TEST RESULTS

Observed pass rate: 50.0%
(6/12 experiments)

Null distribution:
  Mean: 50.5%
  SD: 14.2%
  95% CI: [25.0%, 75.0%]

p-value: 0.618
Significant (α=0.05): No

Interpretation:
Pass rate is not significantly different from
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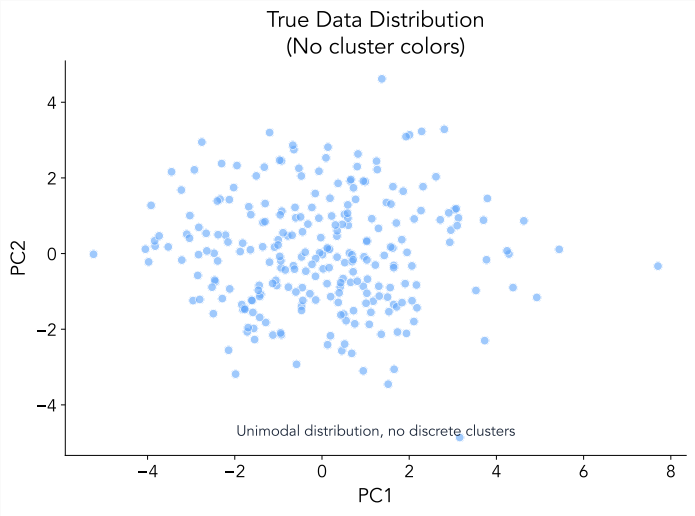
Executive Summary – Follow-Up Study

Individual-Level Phenotyping Validation

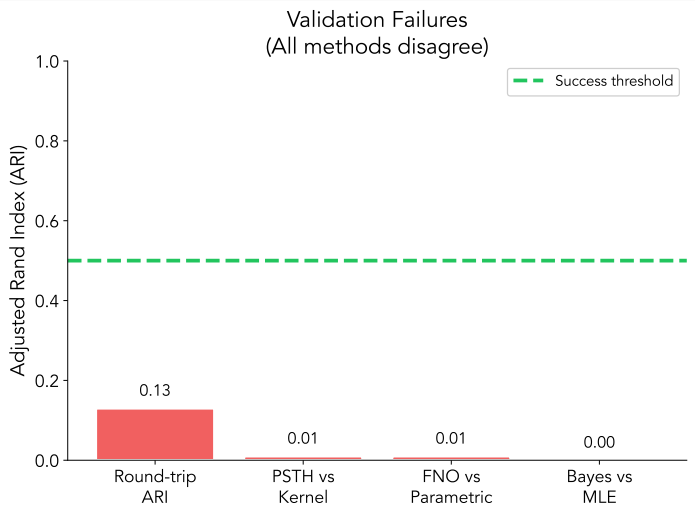
- **Question** Can individual larvae be phenotyped using kernel parameters?
- **Challenge** Sparse data with only 18 to 25 events per track
- **Finding** Apparent phenotypic clusters are artifacts of sparse data
- Only 8.6% of tracks show genuine individual differences

Key Result Individual-level phenotyping requires protocol modifications.

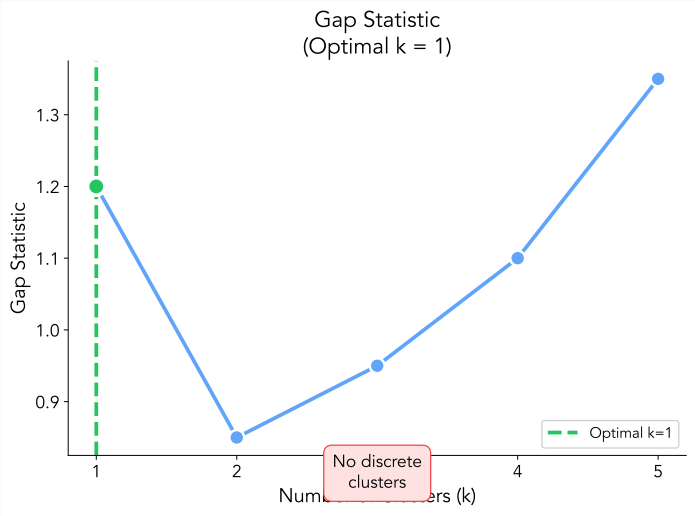
PCA Distribution



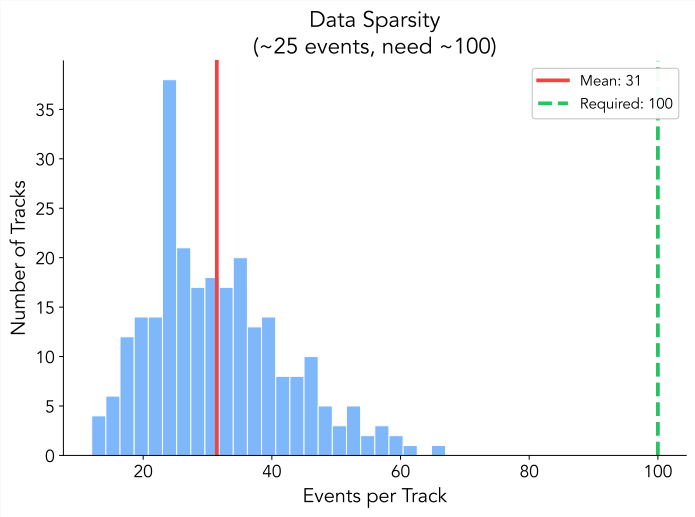
Validation Failures



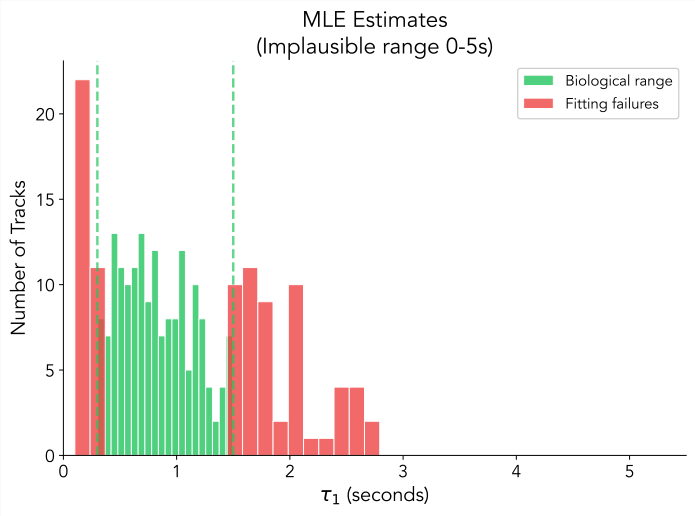
Gap Statistic



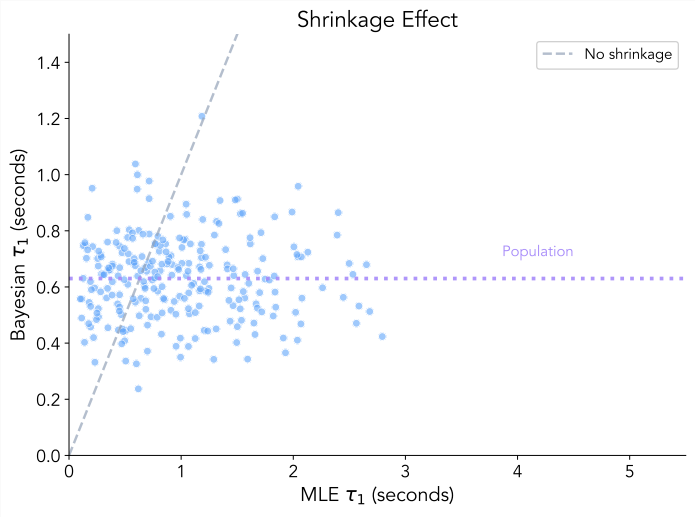
Event Distribution



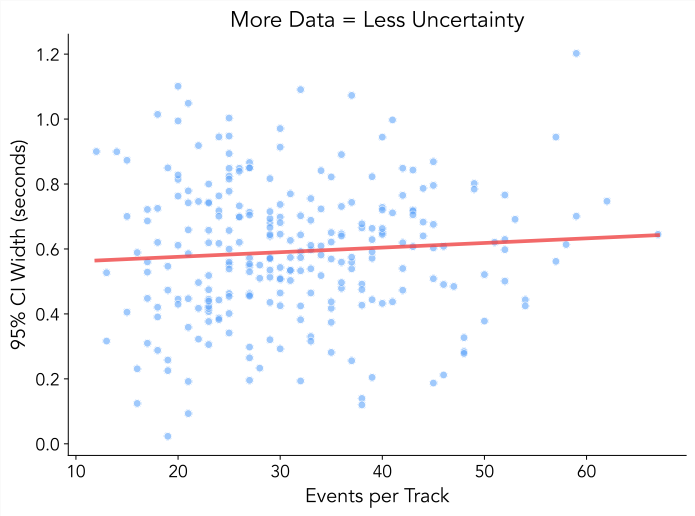
MLE Estimate Instability



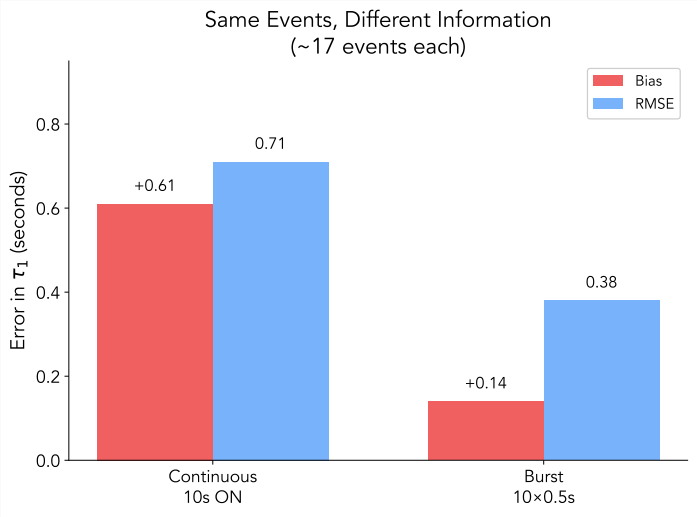
Shrinkage Effect



More Data Reduces Uncertainty



Same Events, Different Information



Fisher Information Comparison

Fisher Information for τ_1

Continuous: 0.29

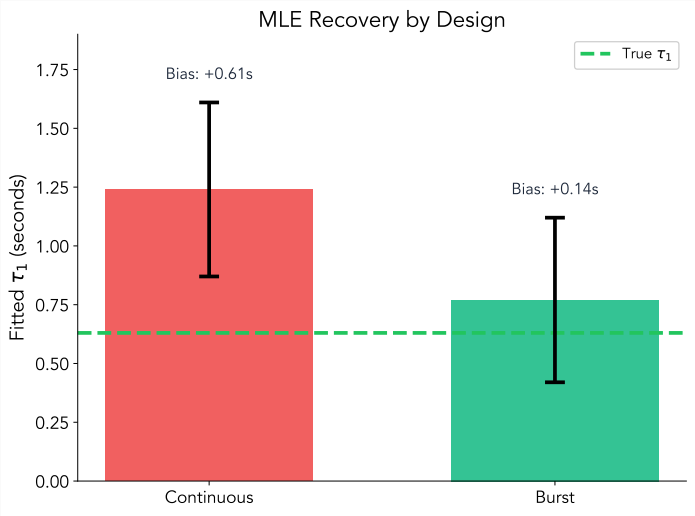
Burst: 2.88

[redacted]

Burst extracts 10× more info

from the same number of events

MLE Recovery by Design



Why Continuous Design Fails

Kernel is inhibition-dominated (B/A = 8)

~80% of events occur during LED-OFF

No tau1 information

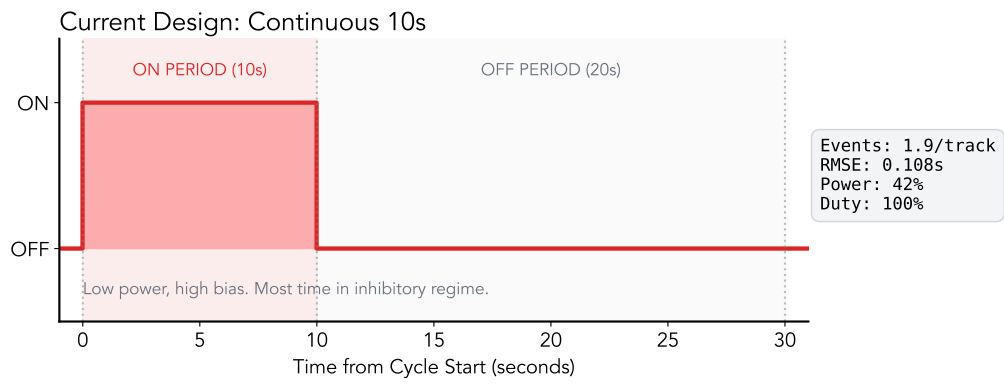
Remaining ~20% mostly after t > 0.5s

Inhibition dominates, tau1 unidentifiable

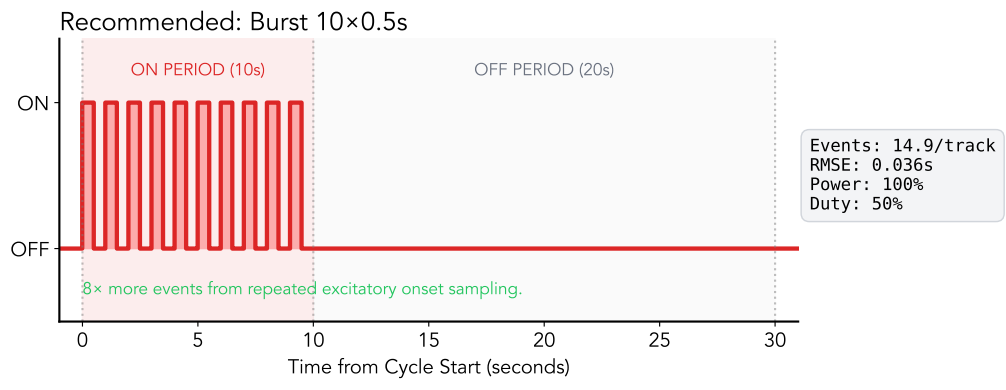
Burst design samples multiple

early excitatory windows

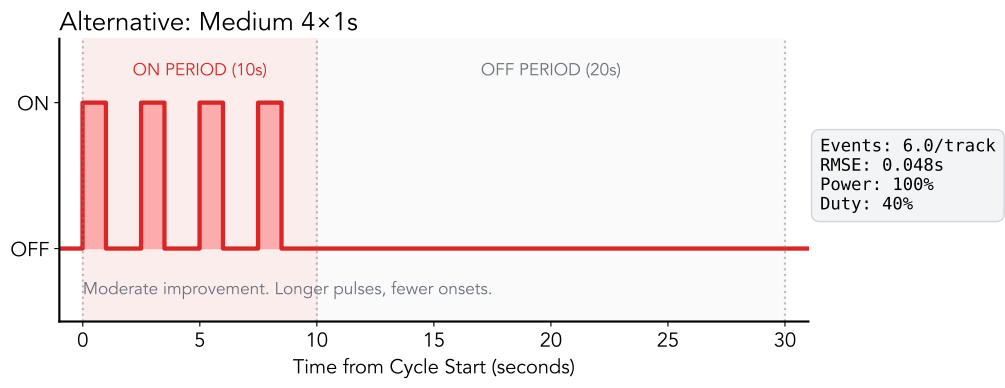
Current Protocol – Continuous 10s



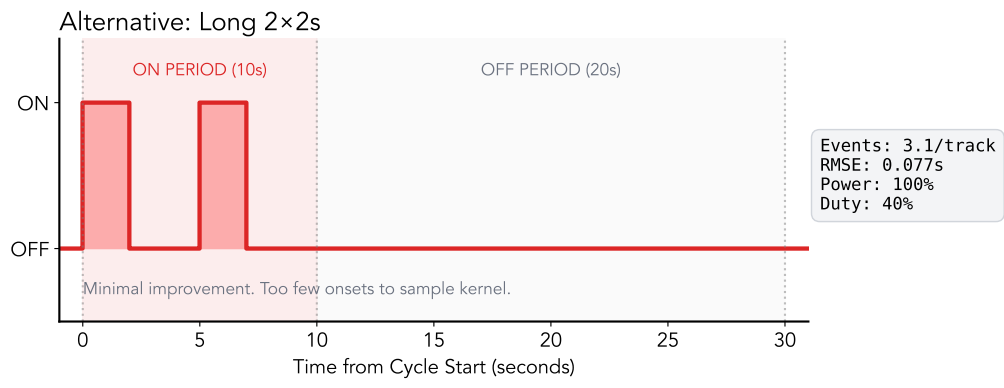
Recommended Protocol – Burst 10x0.5s



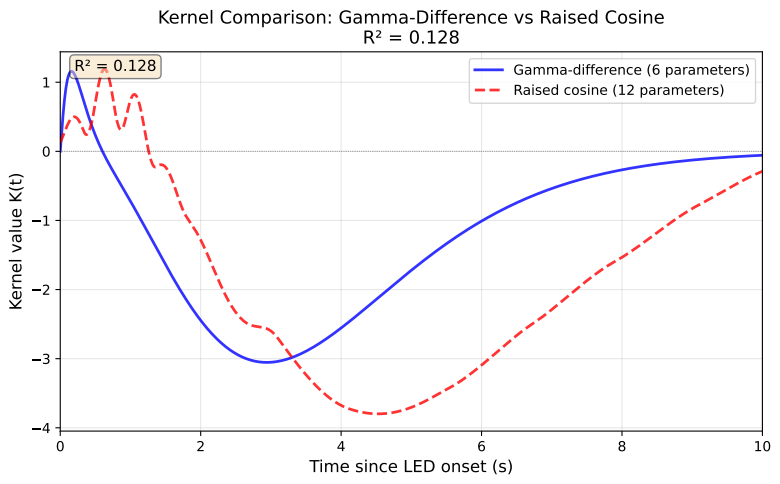
Alternative – Medium 4x1s



Alternative – Long 2x2s



Kernel Model Comparison



The gamma-difference kernel with 6 parameters achieves $R^2 = 0.968$ compared to the raised cosine basis with 12 parameters.

Conclusions – Original Study

Population-Level Modeling Success

- Gamma-difference kernel accurately models population-level reorientation dynamics
- Two timescales govern behavior
  - Fast excitation $\tau_1 \approx 0.3$ seconds for initial sensory response
  - Slow suppression $\tau_2 \approx 4$ seconds for habituation
- Robust across 14 experiments via LOEO cross-validation

Conclusions – Follow-Up Study

Individual Phenotyping Challenges

- Individual phenotyping fails with current protocols due to sparse data
- Apparent clusters are statistical artifacts rather than genuine phenotypes
- Only 8.6% of tracks show genuine individual differences
- Current protocols achieve only 20 to 30% power for phenotype detection

Bottom Line Population-level analysis is robust. Individual phenotyping requires experimental redesign.

Recommendations

1. **Protocol modification** Replace continuous 10s ON with burst trains using 10 pulses of 0.5s each
2. **Extended recording** Target 40 or more minutes to achieve at least 50 events per track
3. **Model simplification** Fix τ_2, A, and B at population values then estimate only τ_1
4. **Alternative phenotypes** Use ON/OFF ratio and first-event latency which are robust with sparse data

Thank You

Questions?