

A universal probabilistic spike count model reveals ongoing modulation of neural variability

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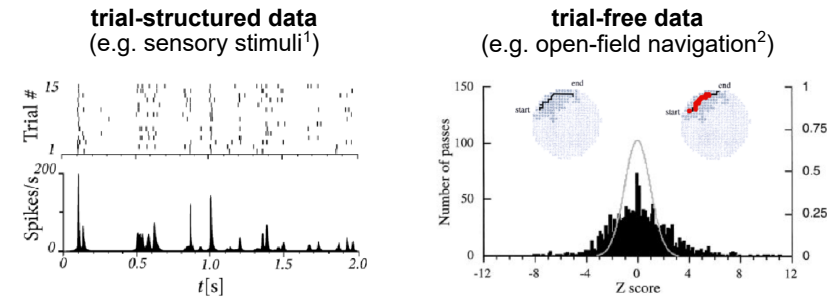
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Problem

Neural responses throughout the brain are variable



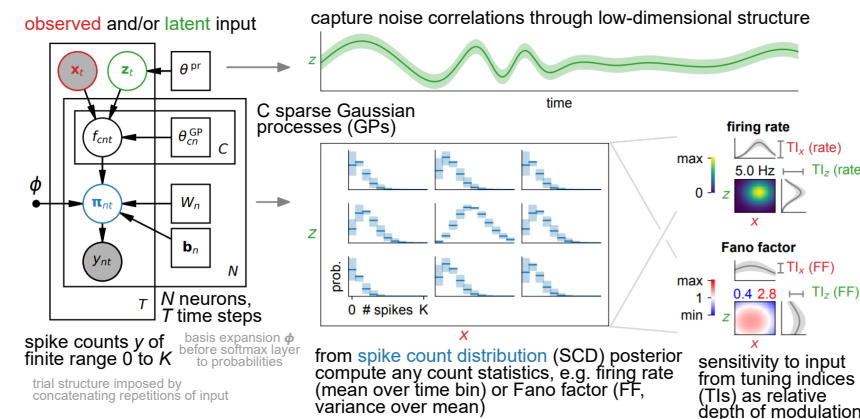
Current approaches:

- cannot flexibly model neural variability with modulation to external covariates
- use different methods for data with and without repeatable trials

model	feature	weak constraints on possible count statistics	decoupled mean and variance	modulation of count statistics by covariates
parametric count likelihood encoding ³		✗	✗	✓
heteroscedastic versions of above ⁴		✗	✓	✓
copula-based countmodels ⁵		✓	✓	✗
Dirichlet priors and histograms ⁶		✓	✓	✗
universal count model (ours)		✓	✓	✓

Solution and approach

We introduce the universal count model (UCM):



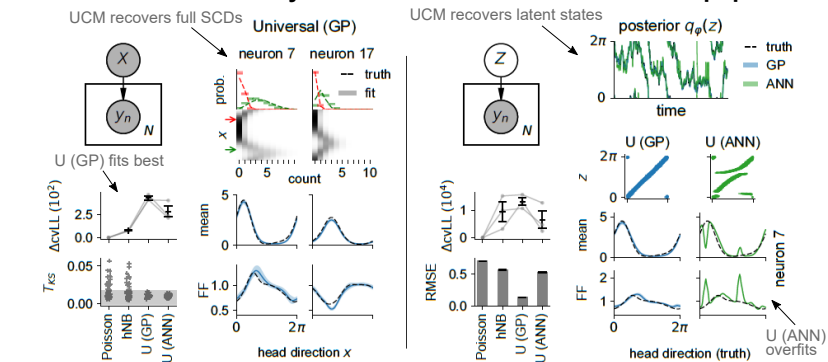
- Bayesian method providing prior over modulated SCDs directly for a finite count range, analogous to Dirichlet priors
- stochastic variational inference for approximate posteriors over latent states and modulated SCDs
- for $C = K$ and sufficiently many latent dimensions, the model is universal in that it can capture any modulated joint SCD

Model fit assessment

- **cross-validated log-likelihood cvLL** (real number) indicates better predictive performance of model for higher values
- **Kolmogorov-Smirnov test statistic T_{KS}** (between 0 and 1) quantifies whether data is statistically distinguishable from model
- **generalized Z-scores ξ** (real number) transformed spike count values using model posterior, samples from the model distribution lead to unit normal distributed scores
- **dispersion metric T_{DS}** (< 0 : under-, > 0 : overdispersed) quantifies if Z-scores are more/less dispersed, i.e. variable, than the model
- **generalized noise correlations r_{ij}** (between -1 and 1) pairwise correlations in generalized Z-scores, can be transformed to Fisher-Z value (real number, more convenient sampling distribution under model)

Validation on synthetic data

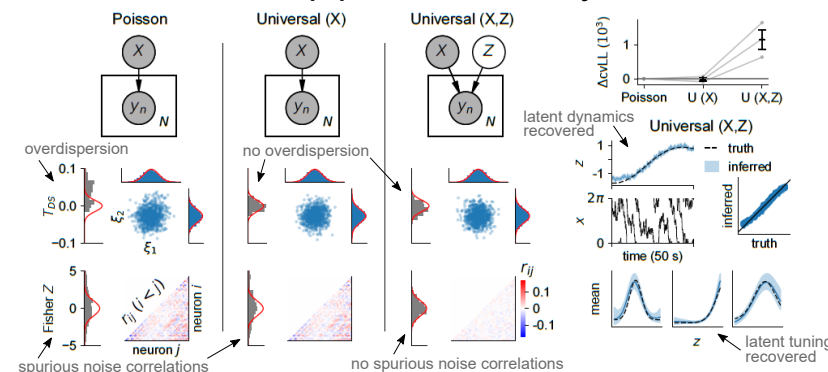
Heteroscedastic Conway-Maxwell-Poisson "head direction" population



Poisson and heteroscedastic negative binomial (hNB) baselines, UCM (U) has a non-Bayesian version with artificial neural networks (ANN) replacing the GP

UCM recovers heteroscedastic count process data for both observed and latent input settings, while baseline models fail to capture count statistics

Poisson "head direction" population modulated by a latent state



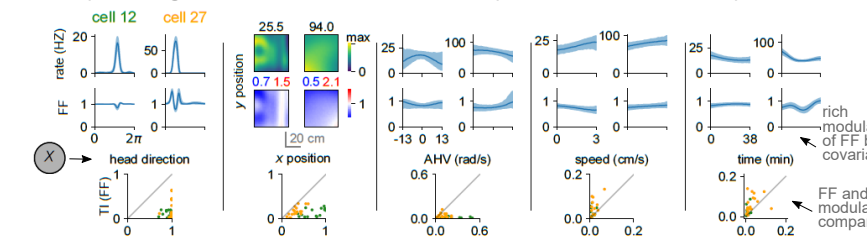
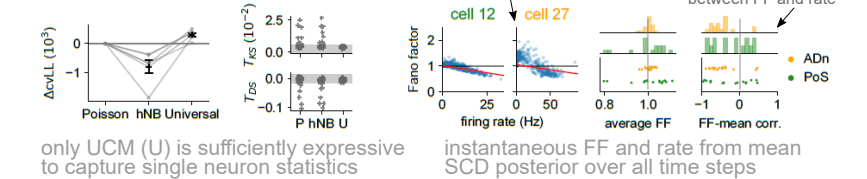
observed state causes apparent overdispersion as well as noise correlations as seen in the Poisson reference model

Observed input UCM captures empirical single neuron count statistics, while latent-observed UCM additionally recovers unobserved shared modulator

Head direction cell population

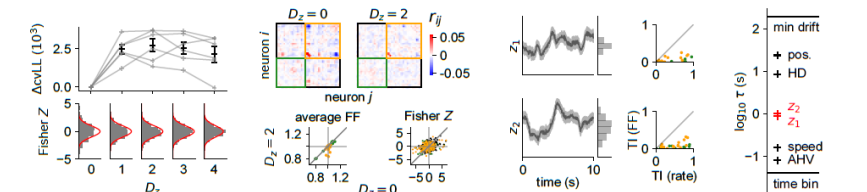
Data recorded from anterodorsal thalamic nucleus (ADn) and postsubiculum (PoS) in the mouse brain⁵, binned at 40 ms.

Observed input



UCM captures single neuron count statistics while baseline methods fail, revealing both super- and sub-Poissonian variability ($FF > 1$ and < 1), decoupled rate and FF, and cases where FF modulation exceeds that of the rate

Latent-observed input Euclidean latent dimensions are added on top of the regression model above, jointly inferring latent states with the rest



Two-dimensional latent trajectories with a timescale of ~ 1 s explain noise correlations best, primarily modulating rates and reducing apparent variability

Conclusion

We introduced the UCM, a Bayesian method inferring modulated joint SCDs from spike count data. Compared to current methods, UCM removes strong constraints on count statistics while not requiring trials. Applied to mouse head direction cells:

- Cells can show both over- and underdispersion (latter common at higher rates)
- FF and mean counts can be decoupled
- FF modulation can be comparable or even exceed that of the rate.
- 2D latent states with a timescale of ~ 1 s explain away noise correlations

References

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