

Bayesian Analysis of Latent Underdispersion Using Discrete Order Statistics



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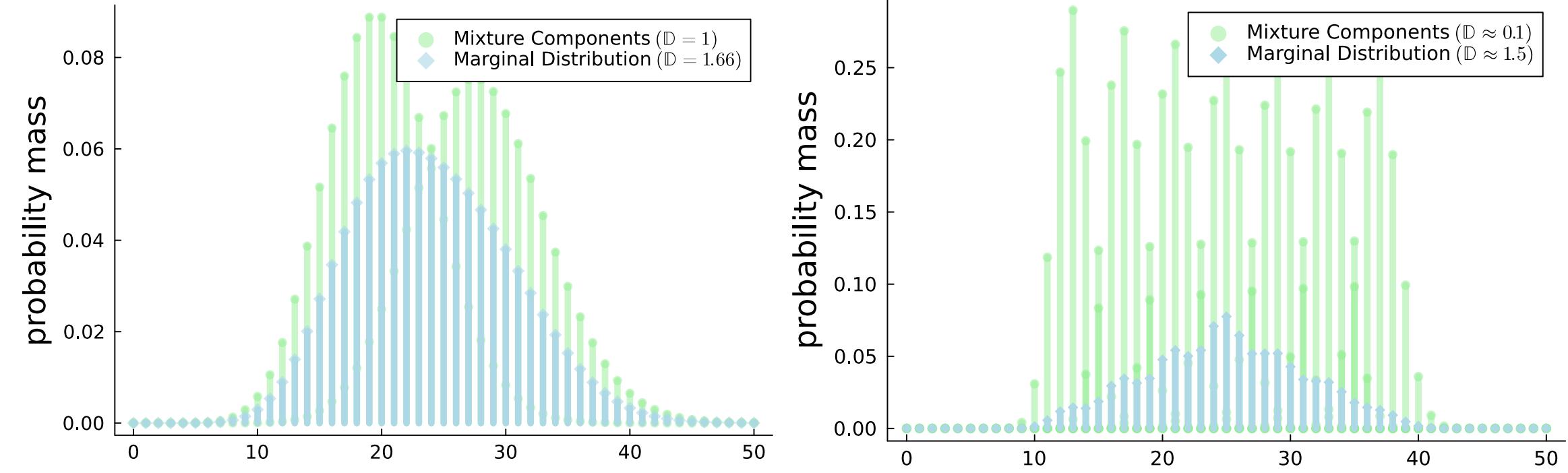
Conditional Underdispersion

Problem: no flexible tools exist to model underdispersed count data in probabilistic modeling frameworks.

Definition: A discrete random variable X is underdispersed with respect to the Poisson distribution if

$$\text{D}[X] = \mathbb{V}[X]/\mathbb{E}[X] < 1$$

Count data which is *marginally* overdispersed may be consistent with a model that is underdispersed *conditionally*, once covariates or latent variables are observed.



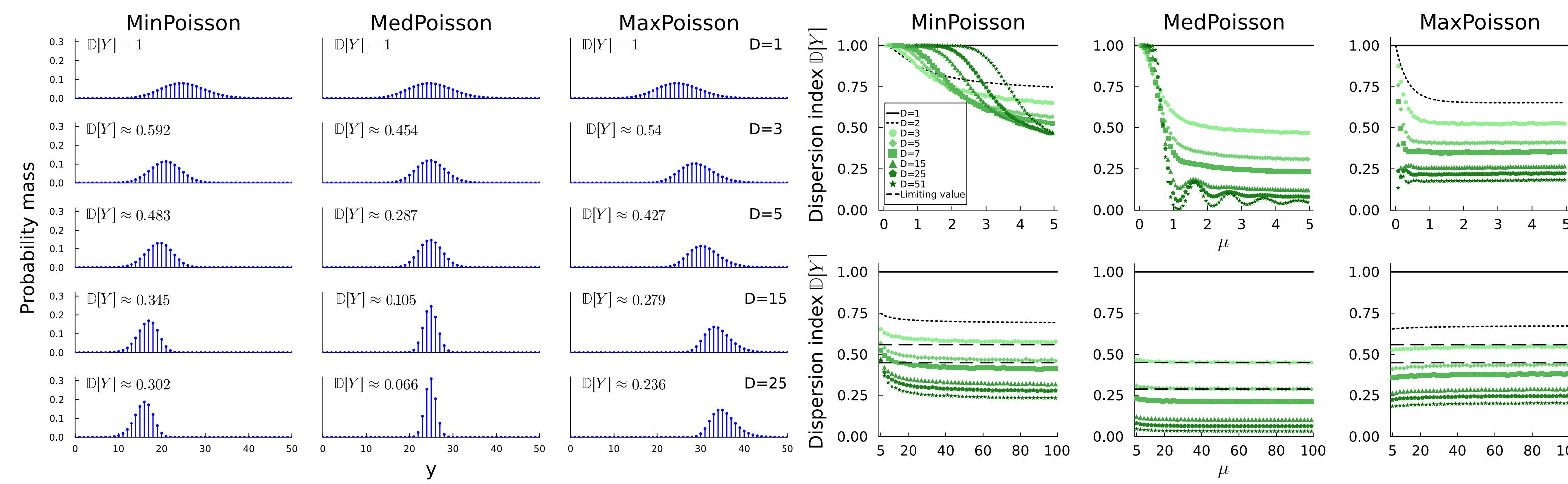
Key Benefit: Modeling conditional underdispersion allows for more precise probabilistic predictions than are possible with a Poisson likelihood.

Poisson Order Statistics are Underdispersed

We introduce discrete order statistics as a modular building block for probabilistic modeling. In particular, we build models with likelihoods of the form:

$$Y = Z_{(j,D)} \text{ for } j \in \{1, \dots, D\}, \text{ where } Z_d \stackrel{\text{iid}}{\sim} \text{Poisson } (\mu)$$

This family of likelihoods gives rise to underdispersed count distributions.



D , the number of latent Poissons, controls the index of dispersion $\text{D}[X]$.

As D grows larger, $\text{D}[X]$ decreases as long as μ is sufficiently large.

Data Augmentation Connects Inference to the Poisson

We derive efficient MCMC-based inference for models with Poisson order statistic likelihoods via a data augmentation scheme with updates of the following form

$$Z_1, \dots, Z_D \sim P(Z_1, \dots, Z_D \mid \mu, Y) \quad (1)$$

$$\mu \sim P(\mu \mid Z_*, Y), \text{ where } Z_* = \sum_{d=1}^D Z_d \quad (2)$$

With the appropriate prior on μ , sampling from (2) is standard. Sampling from (1) is cumbersome due to the positive probability of exact ties.

Algorithm 4.1 Sampling from $P(Z_1, \dots, Z_D \mid \theta, Z^{(j,D)} = Y) \propto \mathbb{1}(Y = Z^{(j,D)}) \prod_{d=1}^D f_\theta(Z_d)$

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1: Input: observation  $Y \in \mathbb{N}_0$ , order  $D \in \mathbb{N}$ , rank  $j \in [D]$ , parent distribution  $f_\theta$ 
2: Initialize:  $n^{(<Y)} = n^{(=Y)} = n^{(>Y)} = 0$ 
3: for  $d = 1 \dots D - 1$  do
4:    $p_d^{(<Y)} \leftarrow P(Z_d < Y \mid \theta, n^{(<Y)}, n^{(=Y)}, n^{(>Y)}, Z^{(j,D)} = Y)$ 
5:    $p_d^{(=Y)} \leftarrow P(Z_d = Y \mid \theta, n^{(<Y)}, n^{(=Y)}, n^{(>Y)}, Z^{(j,D)} = Y)$ 
6:    $p_d^{(>Y)} \leftarrow P(Z_d > Y \mid \theta, n^{(<Y)}, n^{(=Y)}, n^{(>Y)}, Z^{(j,D)} = Y)$ 
7:    $c_d \sim \text{Cat}(p_d^{(<Y)}, p_d^{(=Y)}, p_d^{(>Y)})$  where  $c_d \in \{<Y, =Y, >Y\}$ 
8:    $n^{(<Y)} \leftarrow n^{(<Y)} + 1$ 
9:   if  $n^{(<Y)} \geq 1$  and  $n^{(<Y)} = n_{\max}^{(<Y)} = j - 1$  then
10:     $Z_{d+1}, \dots, Z_D \stackrel{\text{iid}}{\sim} \text{trunc}f_\theta_{[Y, \infty)}$ 
11:    break
12:  end if
13:  if  $n^{(<Y)} \geq 1$  and  $n^{(>Y)} = n_{\max}^{(>Y)} = D - j$  then
14:     $Z_{d+1}, \dots, Z_D \stackrel{\text{iid}}{\sim} \text{trunc}f_\theta_{[0, Y]}$ 
15:    break
16:  end if
17:  if  $n^{(<Y)} = n_{\text{succ}}^{(<Y)} = \max(j - n^{(<Y)}, D - n^{(>Y)} - j + 1)$  then
18:     $Z_{d+1}, \dots, Z_D \stackrel{\text{iid}}{\sim} f_\theta$ 
19:    break
20:  end if
21: end for
22:  $n^{(<Y)} = \max(n^{(<Y)}, 1)$ 
23:  $Z_1, \dots, Z_{n^{(<Y)}} \stackrel{\text{iid}}{\sim} \text{trunc}f_\theta_{[0, Y-1]}$ 
24:  $Z_{n^{(<Y)}+1}, \dots, Z_{n^{(<Y)}+n^{(=Y)}} \stackrel{\text{iid}}{\sim} f_\theta$ 
25:  $Z_{n^{(<Y)}+n^{(=Y)}+1}, \dots, Z_D \stackrel{\text{iid}}{\sim} \text{trunc}f_\theta_{[Y+1, \infty)}$ 
26: Output:  $\{Z_1, \dots, Z_D\}$ 

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Using this algorithm, we can exactly sample from (1) for any discrete order statistic Y , including, for example, negative binomial order statistics.

Choosing which Order Statistic

While all Poisson order statistics can be used to model underdispersion, there are differences:

Maximum: computationally efficient, especially under **sparsity**. ($Y = 0 \implies Z_1, \dots, Z_D = 0$)

Median: approximately mean-parameterized by latent μ , but more expensive computationally.

Minimum: computationally efficient, but not under sparsity.

Tailored Models for Applications

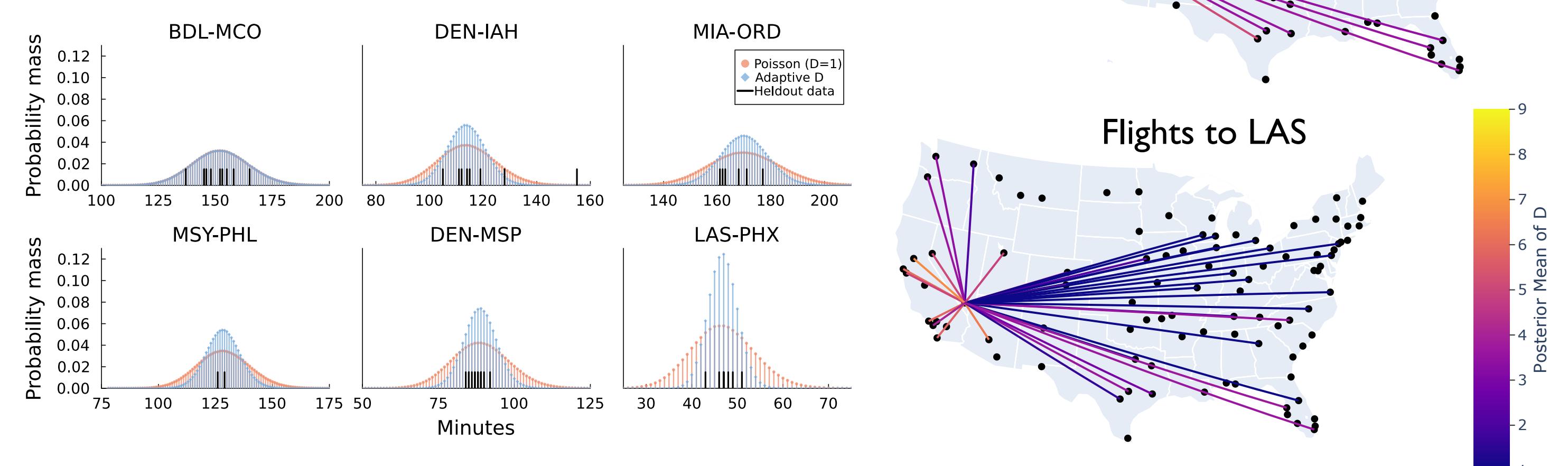
Predicting Flight Times

We model the number of minutes Y_f of flight f with origin $o[f]$, destination $d[f]$, and route $r[f] = (o[f], d[f])$ as

$$Y_f \sim \text{MedPoisson} \left(a_{o[f]} + b_{d[f]} + \text{dist}_{r[f]} \mu_{r[f]}, 2D_{r[f]} + 1 \right)$$

$$D_r \sim \text{Binomial} \left(\frac{D_{\max} - 1}{2}, p \right)$$

Some Example Posterior Predictive Distributions



A flexible dispersion parameter D gives varied uncertainty and learned latent structure.

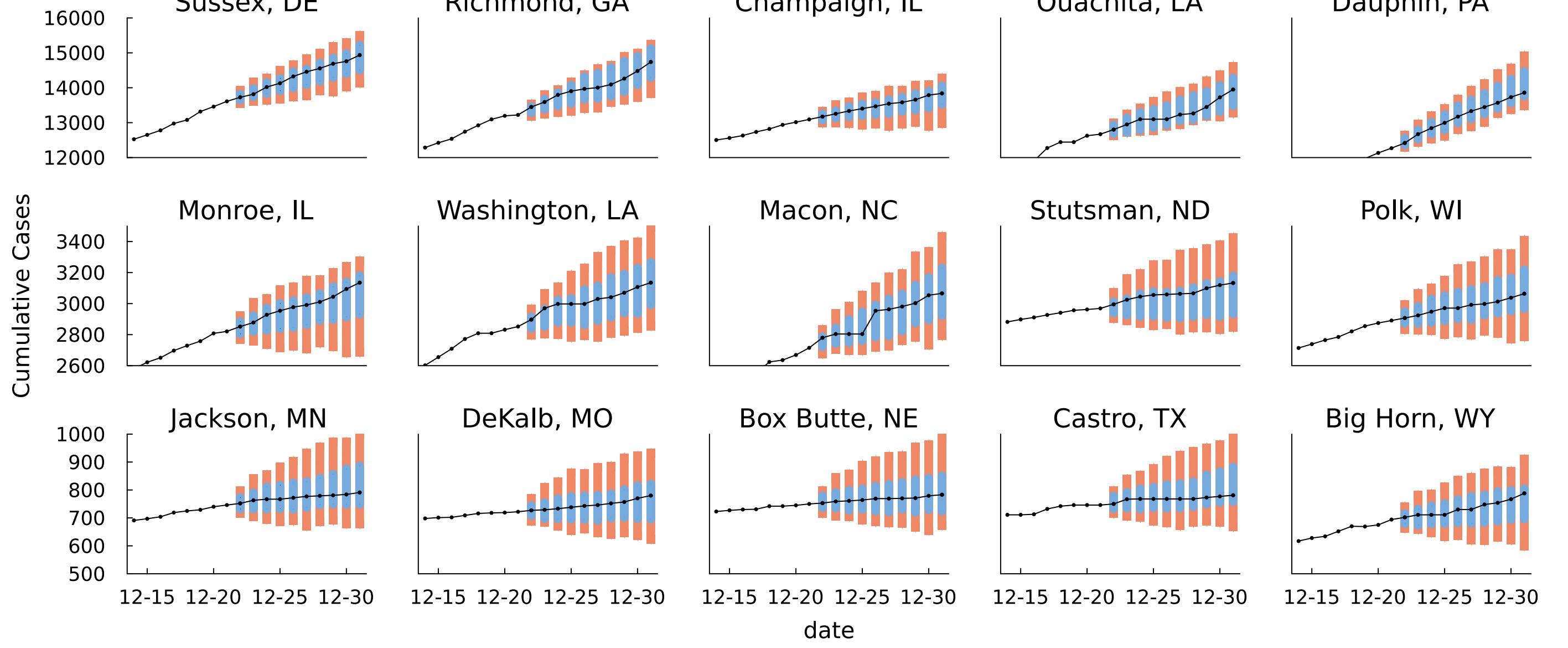
COVID-19 Forecasting

We model the cumulative COVID-19 cases Y_{ct} in each county c at time t as

$$Y_{ct} \sim \text{MedPoisson} \left(Y_{ct-1} + \log(\text{pop}_c) \left(\epsilon + \alpha \sum_{k=1}^K \theta_{ck} \phi_{kt} \right), 2D_{ct} + 1 \right)$$

$$D_{ct} \sim \text{Binomial} \left(\frac{D_{\max} - 1}{2}, \sigma \left(\sum_{q=1}^Q \beta_{cq} \tau_{qt} \right) \right)$$

Some Example Posterior Predictive 95% Credible Intervals



The underdispersed likelihood avoids artificially wide predictive intervals.

Modeling Abundance of Finnish Birds

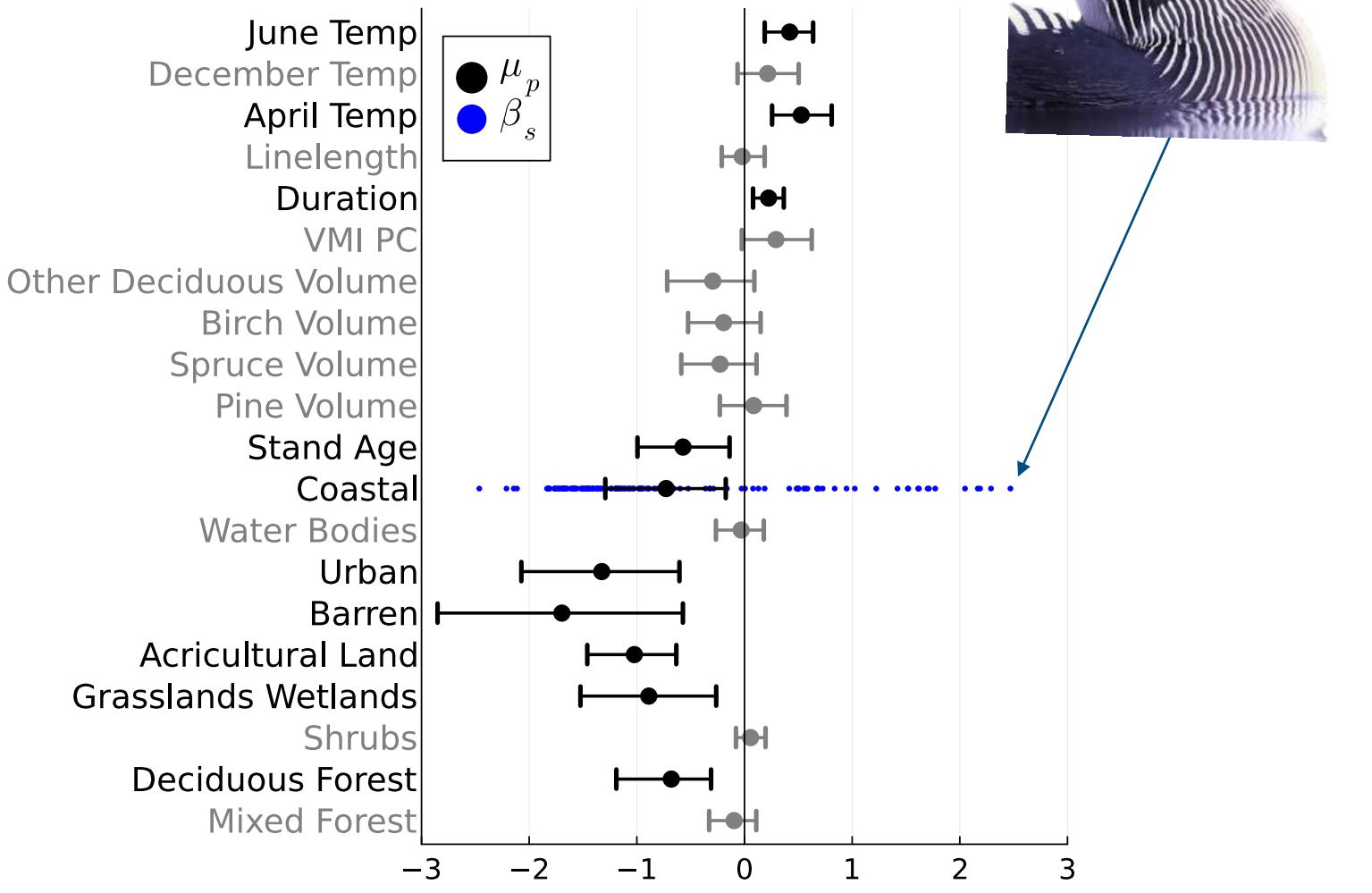
We model the number of birds Y_{ns} at sampling site n of species s , where each sampling site has covariate vector X_{ns} as

$$Y_{ns} \sim \text{MaxPoisson} \left(\sum_{k=1}^K \theta_{nk} \phi_{ks}, D_{ns} + 1 \right)$$

$$D_{ns} \sim \text{Binomial} \left(D_{\max} - 1, \sigma(X_{ns}^T \beta_s) \right)$$

$$\beta_s \sim N(\mu_s, \sigma_s^2) \quad \mu_s \sim N(0, 1)$$

Interpreting Coefficients of Dispersion



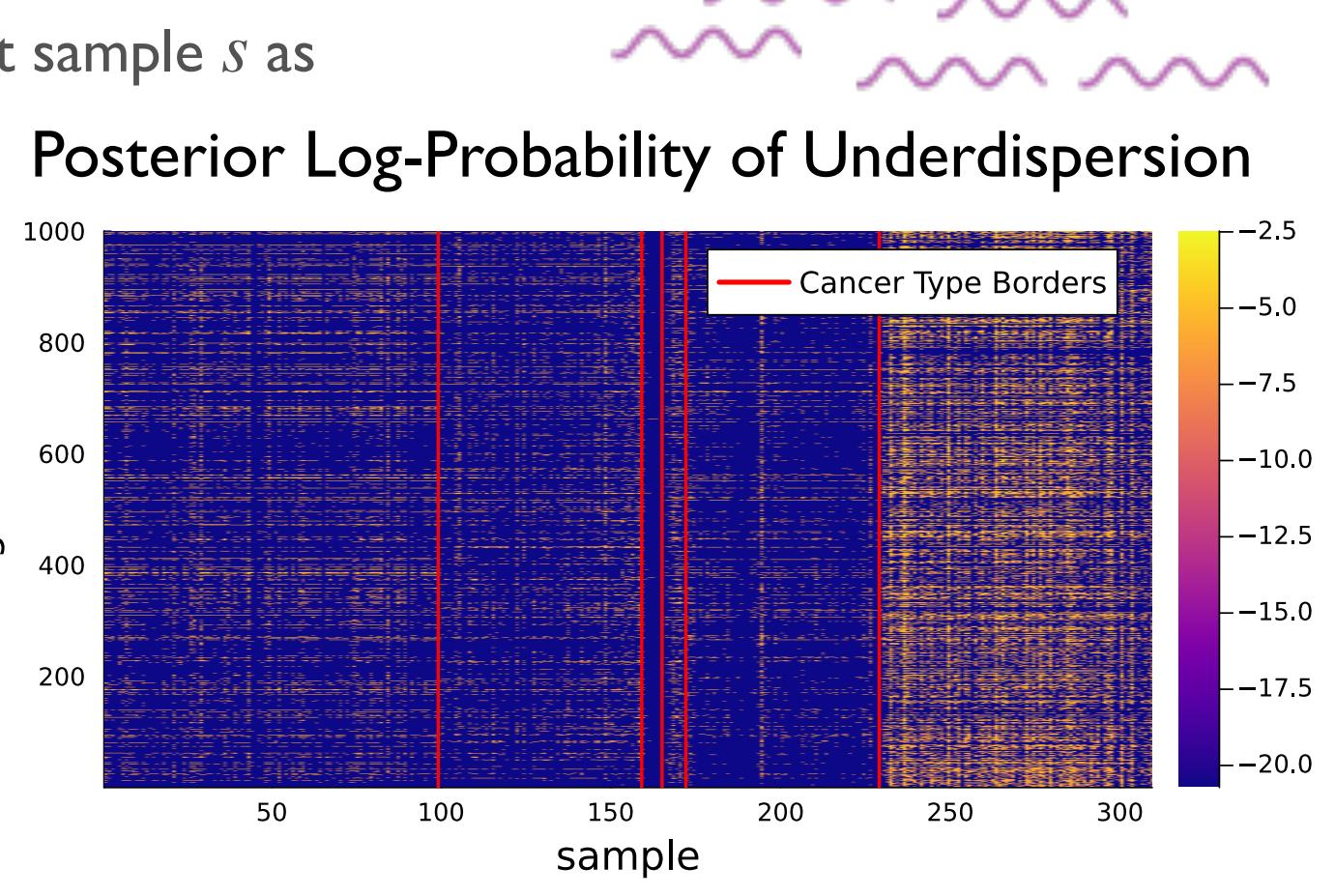
Our model yields more precise predictions for waterbirds in coastal areas.

Investigating Dispersion in RNA-Seq Data

We model the RNA-sequencing count Y_{gs} for gene g at sample s as

$$Y_{gs} \sim \text{MedNB} \left(\sum_{k=1}^K \theta_{gk} \phi_{ks}, p_g, 2D_{gs} + 1 \right)$$

$$D_{gs} \sim \text{Binomial} \left(\frac{D_{\max} - 1}{2}, \sigma \left(c_g + \sum_{q=1}^Q \beta_{gq} \tau_{sq} \right) \right)$$



We find little evidence of underdispersion in RNA sequencing data, but there are different patterns across cancer types.

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