**Analysis**

We estimated the methylation response to age and dispersal using a Bayesian generalized linear mixed model (GLMM). The likelihood was beta with a logit link because the data were proportions. The response variable was proportion methylation, the predictor variables were age, dispersal, and their interaction, and bird id was a random intercept.

To compare the number of genes that changed methylation states across treatments, we used a GLMM with a Gamma likelihood and log link, because the data were continuous non-negative. The response variable was the number of genes and the predictor variables were the direction of methylation change during age transitions (no change, gain of methylation, loss of methylation), bird behavior (dispersed or natal), and age transition (hatchling to fledgling or fledgling to adult).

We fit each model using the *brms* package (Bürkner2018) in R (R Core Team 2019) via Hamiltonian Monte Carlo in *rstan* (Stan Development Team 2019). We ran four chains of 2000 iterations each. The first 1000 iterations were discarded as warmup in each chain. We used posterior predictive checks (Conn et al. 2018) to test model performance and checked chains for convergence by ensuring that r-hats were < 1.1. Prior values for all parameters were chosen using prior predictive checks to ensure that prior predictions from the model generated reasonable upper and lower bounds of the outcome variable. For the model of methylation response, priors *N*(0, 2) for the intercept, *N*(0, 1) for the betas, and Cauchy(0, 1) for the standard deviation. For the number of genes model, priors were *N*(0, 6) for the intercept, *N*(0, 1) for the betas, and Cauchy(0, 1). All data and accompanying code are available at <https://github.com/jswesner/liebl_birds>.

**Results**

D and N were had similar methylation in the hatchling stage. The proportion of methylated genes averaged 0.8 +/- 0.03 (mean and sd of the posterior distribution) in D while N averaged 0.81 +/- 0.03 (Table X). In contrast, at the fledgling stage D averaged 0.76 +/- 0.03 compared to 0.84 +/- 0.03 for N (Figure X). This corresponded to a mean difference of 0.08 +/- 0.04 (95% CrI: -0.04 to 0.17), with a 97% probability that N had higher methylation than D. By the adult stage, this difference disappeared, with D averaging 0.77 +/- 0.03 compared to 0.74 +/- 0.03 for N.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| Table X. Summaries of the posterior distribution of results from the generalized linear mixed model. | | | | | |
| age | dispersed | mean | sd | low95 | high95 |
| H | D | 0.8 | 0.03 | 0.73 | 0.85 |
| H | N | 0.81 | 0.03 | 0.75 | 0.87 |
| F | D | 0.76 | 0.03 | 0.68 | 0.82 |
| F | N | 0.84 | 0.03 | 0.78 | 0.89 |
| A | D | 0.83 | 0.03 | 0.77 | 0.88 |
| A | N | 0.8 | 0.03 | 0.74 | 0.86 |