**Analysis**

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

We fit the model using the *brms* package (Bürkner2018) via Hamiltonian Monte Carlo in *rstan* (Stan Development Team 2019). We ran four chains of 2000 iterations each. The first 1000 iterations 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. 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 0.21 +/- 0.3 (mean and sd of the posterior distribution) in D while N averaged 0.19 +/- 0.3 (Table X). In contrast, at the fledgling stage D averaged 0.25 +/- 0.3 compared to 0.16 +/- 0.3 for N (Figure X). This corresponded to a mean difference of 0.08 +/- 0.04 (95% CrI: -0.002 to 0.17), with a 97% probability that D had higher methylation than N. By the adult stage, this difference disappeared, with D averaging 0.17 +/- 0.03 compared to 0.2 +/- 0.03 for N.

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| Table X. Summaries of the posterior distribution of results from the generalized linear mixed model. | | | | | |
| age | dispersed | mean | sd | low95 | high95 |
| H | D | 0.21 | 0.03 | 0.16 | 0.26 |
| H | N | 0.19 | 0.03 | 0.13 | 0.25 |
| F | D | 0.25 | 0.03 | 0.18 | 0.32 |
| F | N | 0.16 | 0.03 | 0.11 | 0.22 |
| A | D | 0.17 | 0.03 | 0.12 | 0.23 |
| A | N | 0.2 | 0.03 | 0.14 | 0.26 |