**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**

*Methylation response*

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.

*Change in methylation*

Across the 122,970 tested genes, most did not change methylation status across age transitions and remained similar between behavior types (Figure X2). Among the remaining genes, the number that either gained or lost methylation were higher in dispersers than in natal birds, particularly during the hatchling to fledgling transition (Table X2). For example, during this transition, dispersers had ~16,900 more genes that became methylated than did natal birds and had ~17,200 more genes that lost methylation (Table X2). The probability that these differences were greater than zero between dispersers and natal was > 97% for hatchling to fledgling comparisons. For birds transitioning between the fledgling to adult stage, the differences in the number of genes that changed methylation state was smaller and more variable. Dispersers had ~9,000 more genes that became methylated during this transition, but both behavior types lost a similar amount of methylation.

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| Table X. Summaries of the posterior distribution of the proportion of genes that were methylated from a 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 |

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| Table X2. Differences in gene methylation during age transitions among natal and dispersing birds. Values represent the mean, standard deviation, and credible intervals of the differences number of genes in each category between dispersers and natal birds from the posterior distribution of a Bayesian GLMM. prob\_diff is the probability that a difference is greater than zero. | | | | | |
| key | mean | sd | low95 | high95 | prob\_diff |
| HF\_no | -15760 | 31770 | -82101 | 45513 | 0.29 |
| HF\_gain | 17621 | 10413 | -988 | 39123 | 0.97 |
| HF\_lose | 18159 | 10381 | 788 | 41550 | 0.98 |
| FA\_no | -6688 | 33486 | -72368 | 63995 | 0.39 |
| FA\_gain | 9395 | 7490 | -4366 | 25633 | 0.92 |
| FA\_lose | -2589 | 8175 | -18434 | 14735 | 0.34 |

**Figure X.** Mean proportion of methylated genes at each age for dispersing and natal birds. Boxplots represent summaries of the posterior distribution, lines connect estimated values in each stage across 1000 iterations of the posterior distribution, and data points are the raw data.

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**Figure X2.** Mean number of methylated genes that either did not change, gained, or lost methylation during the transition from hatchling to fledgling or from fledgling to adult. Boxplots represent summaries of the posterior distribution for each dispersing and natal birds and data points are the raw data.

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