

Supplementary Material for “A Continuous-Time Semi-Markov Model for Animal Movement in a Dynamic Environment”

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A.1 Likelihood details

This section of supplementary material contains much of the same material of as Section 2.1 and 3.1, but we have added a few additional details for interested readers.

The heart of the CTSMC model is the emigration rate function

$$\lambda_{ij}(t|P_t) = \lim_{h \rightarrow 0} [g_{t+h} = j|P_t]/h, \quad (1)$$

where P_t is the path of the animal up to time t , i.e., $P_t = \{t, (\tau_0, g_0), \dots, (\tau_m, g_m) : \tau_m < t\}$, where τ_m and g_m is the m th transition time and location. We also use a continuous time index for τ and g as well to indicate the continuous-time step function version of the discrete time m index (see Section 2 of the main text). Herein, we use the notation ‘ $[A|B]$ ’ to represent the probability density (distribution) function of A given B . Therefore, $[g_{t+h} = j|P_t]$ is the probability that $g_{t+h} = j$ given the path up to time t . The total rate of emigration from cell i at time t is the accumulation of the emigration rate $\lambda_{ij}(t|P_t)$ over the set of neighboring cells, \mathcal{C}_i ,

$$\Lambda_i(t|P_t) = \sum_{j \in \mathcal{C}_i} \lambda_{ij}(t|P_t). \quad (2)$$

Thus,

$$\text{Prob}(g_{t+h} \neq i|P_t) \approx \Lambda_i(t|P_t) \times h,$$

for small h values. Using the total rate of emigration from a cell i at time t , we can obtain the distribution of the time of the next move, τ_m given the animal moved to cell $g_{m-1} = i$ at time τ_{m-1} . Using standard results from temporal point process methodology, see Section 3.1.6 of Hooten et al. (2017), where the emigration rate function is mathematically equivalent to a point process intensity function, the density function of next movement time is,

$$[\tau_m|P_{\tau_m}] = \Lambda_i(\tau_m|P_{\tau_m}) \exp \left\{ - \int_{\tau_{m-1}}^{\tau_m} \Lambda_i(u|P_u) du \right\}. \quad (3)$$

There is one complication that needs to be addressed at the end of the telemetry device deployment, the censoring of the last observation. If the individual is followed from time $\tau_0 = 0$ to time $T \geq \tau_M$, the last cell movement, then the time between τ_M and T also needs to be accommodated. So, let τ_{M+1} be the unobserved ‘next’ transition occurring after the animal is no longer being observed at time T . The quantity necessary to accommodate the censoring is,

$$\begin{aligned} [\tau_{M+1} > T|P_{\tau_{M+1}}] &= 1 - \int_{\tau_M}^T [\tau|P_\tau] d\tau \\ &= \exp \left\{ - \int_{\tau_M}^T \Lambda_i(u|P_u) du \right\} \end{aligned} \quad (4)$$

(Hooten et al. 2017). For the remainder of the model development we will set $\tau_{M+1} = T$, the end of the observation window for the telemetry deployment.

Now, if one conditions on the fact that the next move will be at time τ_m , then the cell to which the move is made, is a categorical variable over \mathcal{C}_i ,

$$[g_m = j | \tau_m, P_{\tau_m}] = \frac{\lambda_{ij}(\tau_m | P_{\tau_m})}{\Lambda_i(\tau_m | P_{\tau_m})} \quad (5)$$

(Norris 1998). If we now assume that the emigration hazard function, $\lambda_{ij}(t | P_t)$, is also a function of a parameter vector, say $\boldsymbol{\theta}$ then, given an observed path P , the likelihood is,

$$\begin{aligned} \mathcal{L}(\boldsymbol{\theta} | P) &= \left\{ \prod_{m=1}^M [g_m | \tau_m, P_{\tau_m}] \times [\tau_m | P_{\tau_m}] \right\} \times [\tau_{M+1} > T | P_{\tau_{M+1}}] \\ &= \prod_{m=1}^M \frac{\lambda_{g_{m-1}, g_m}(\tau_m | P_{\tau_m})}{\Lambda_{g_{m-1}}(\tau_m | P_{\tau_m})} \times \Lambda_{g_{m-1}}(\tau_m | P_{\tau_m}) \exp \left\{ - \int_{\tau_{m-1}}^{\tau_m} \Lambda_{g_{m-1}}(u | P_u) du \right\} \\ &\quad \times \exp \left\{ - \int_{\tau_M}^T \Lambda_{g_M}(u | P_u) du \right\} \\ &= \left\{ \prod_{m=1}^M \lambda_{g_{m-1}, g_m}(\tau_m | P_{\tau_m}) \right\} \times \exp \left\{ - \int_0^T \sum_{j \in \mathcal{C}_{g_u}} \lambda_{g_u, j}(u | P_u) du \right\} \end{aligned} \quad (6)$$

A.2 Additional results for the fur seal analysis

In this section we provide some additional figures and tables for those readers interested in the full results of the fur seal analysis. Figure A.1 illustrates the imputation draws for all of the pups. Figure A.2 illustrates the posterior model probabilities for all animals and all imputations. Table A.1 gives the posterior model probabilities for each animal averaged over imputations.

Table A.1: Posterior model probabilities (PMP) for the CTSMC movement analysis. All models included the ‘Base’ model for movement, where The base model contains effects for: $\log r_t$, previous_{ijt} , north_{ij} , east_{ij} , plus an intercept and interaction term $\log r_t \times \text{previous}_{ijt}$. Model numbers correspond to rows and associated models in Table 1 from the main text.

ID	Model							
	1	2	3	4	5	6	7	8
330		0.14			0.86			
335	0.04	0.34	0.05		0.57			
349		1.00						
351		0.92			0.08			
355		0.99			0.01			
362		0.99			0.01			
367		0.77			0.23			
377		1.00						
380		0.50			0.45	0.05		
381		1.00						
385		1.00						
388		1.00						
394		1.00						
405		0.03			0.96			0.01
408		0.05			0.95			

Table A.2: Estimates for base movement rate function parameter $\tilde{\beta}_{1,ij}$ which defines the distribution of the residence time in each cell in the absence of habitat drivers of movement. The $\tilde{\beta}_{1,ij}$ is a function of the previous movement direction of the animal, previous_{ij} . If $\text{previous}_{ij} = -1$ movement is in the opposite direction as the past movement, while the reverse is true for $\text{previous}_{ij} = 1$. Values of $\text{previous}_{ij} = \pm 0.5$ indicate diagonal movements relative to the previous movement depending on the sign. Values of $\tilde{\beta}_{1,ij} > 0$ indicate residence times that are more regular relative to an exponential distribution (CTMC assumption), while $\tilde{\beta}_{1,ij} < 0$ indicates residence times that tend to be clustered, i.e., several short stays followed by a long stay.

ID	previous_{ij}	$\tilde{\beta}_{1,ij}$	CI
330	-1.0	-0.83	[-0.93, -0.72]
	-0.5	-0.30	[-0.39, -0.21]
	0.5	0.74	[0.57, 0.92]
	1.0	1.26	[1.03, 1.5]
335	-1.0	-0.97	[-1.03, -0.9]
	-0.5	-0.35	[-0.42, -0.29]
	0.5	0.88	[0.73, 1.02]
349	1.0	1.49	[1.3, 1.68]
	-1.0	-0.96	[-1.03, -0.89]
	-0.5	-0.42	[-0.49, -0.36]
351	0.5	0.65	[0.51, 0.8]
	1.0	1.19	[1, 1.39]
	-1.0	-0.81	[-0.9, -0.73]
355	-0.5	-0.31	[-0.38, -0.25]
	0.5	0.69	[0.55, 0.83]
	1.0	1.19	[1, 1.38]
362	-1.0	-1.00	[-1.07, -0.94]
	-0.5	-0.38	[-0.45, -0.31]
	0.5	0.87	[0.72, 1.03]
367	1.0	1.49	[1.28, 1.72]
	-1.0	-0.98	[-1.04, -0.91]
	-0.5	-0.37	[-0.42, -0.31]
377	0.5	0.86	[0.72, 1.01]
	1.0	1.47	[1.27, 1.67]
	-1.0	-1.02	[-1.1, -0.94]
380	-0.5	-0.36	[-0.42, -0.29]
	0.5	0.97	[0.83, 1.12]
	1.0	1.64	[1.44, 1.83]
385	-1.0	-0.82	[-0.91, -0.72]
	-0.5	-0.34	[-0.41, -0.26]
	0.5	0.62	[0.48, 0.76]
388	1.0	1.10	[0.91, 1.29]
	-1.0	-0.96	[-1.04, -0.88]
	-0.5	-0.36	[-0.43, -0.29]
394	0.5	0.84	[0.7, 0.98]
	1.0	1.44	[1.25, 1.62]

ID	previous_{ij}	$\tilde{\beta}_{1,ij}$	CI
381	-1.0	-1.04	[-1.11, -0.98]
	-0.5	-0.43	[-0.5, -0.37]
	0.5	0.77	[0.63, 0.91]
385	1.0	1.37	[1.18, 1.56]
	-1.0	-0.84	[-0.93, -0.75]
	-0.5	-0.33	[-0.4, -0.25]
388	0.5	0.70	[0.57, 0.84]
	1.0	1.22	[1.04, 1.4]
	-1.0	-0.96	[-1.02, -0.91]
394	-0.5	-0.38	[-0.44, -0.33]
	0.5	0.78	[0.66, 0.89]
	1.0	1.36	[1.2, 1.51]
405	-1.0	-0.93	[-1.01, -0.86]
	-0.5	-0.37	[-0.44, -0.31]
	0.5	0.75	[0.6, 0.89]
408	1.0	1.31	[1.11, 1.5]
	-1.0	-0.95	[-1.02, -0.88]
	-0.5	-0.38	[-0.44, -0.32]
385	0.5	0.77	[0.64, 0.89]
	1.0	1.34	[1.16, 1.5]
	-1.0	-0.97	[-1.04, -0.9]
388	-0.5	-0.47	[-0.54, -0.4]
	0.5	0.54	[0.4, 0.68]
	1.0	1.04	[0.86, 1.23]

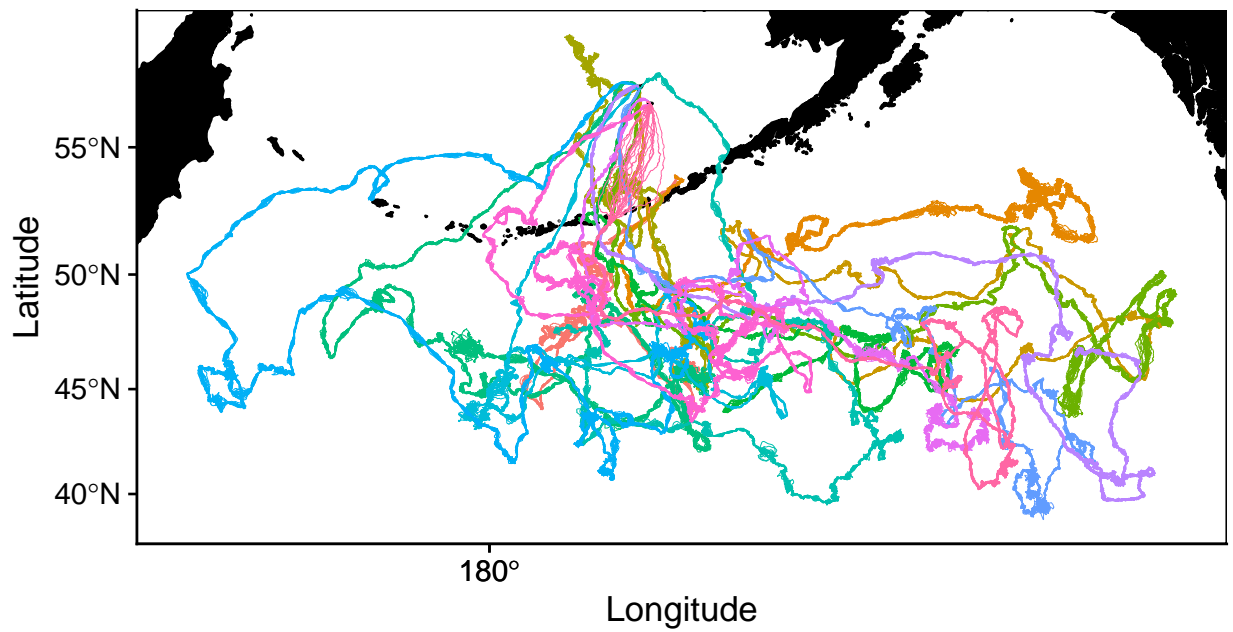


Figure A.1: Imputed paths for analysis by the CTSMC model. Each color represents a different northern fur seal pup. Each imputation contains 20 paths for each individual.

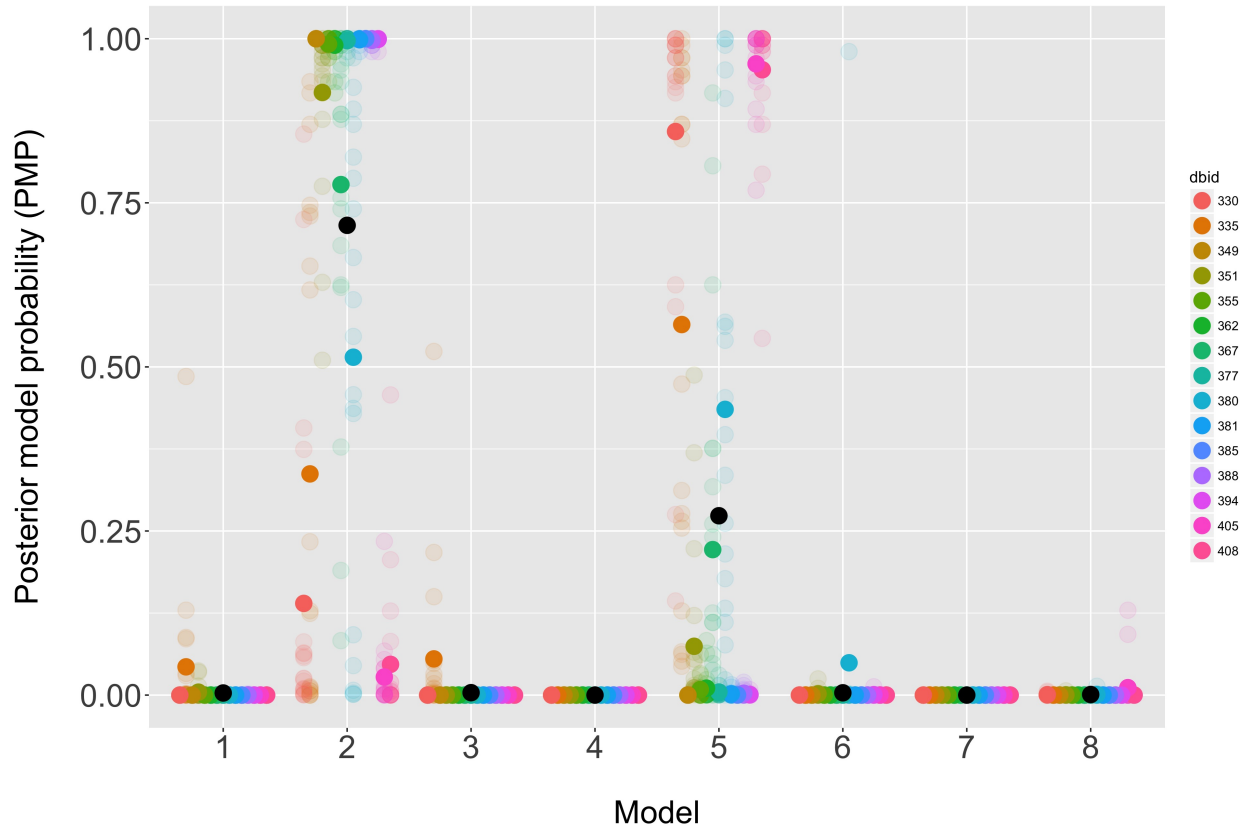


Figure A.2: Posterior model probability (PMP) estimates for 15 northern fur seal pup CTSMC analyses. Solid color dots represent individual PMP estimates for those models with nonzero PMP for any animal. The transparent dots of the same color represent the PMP values for each process imputation. The black dots represent a population-level PMP estimate based on the mean PMP from each animal.

A.3 CTMC analysis of animal ‘355’

In order to assess any improvement of the semi-Markov model over the Markov version of the movement process, we reanalyzed the data from animal 355 with the CTMC model of Hanks, Hooten, and Alldredge (2015). By necessity, the covariates must be adjusted to accommodate the constant rate function between moves. So, to this end, we chose to keep the oceanographic covariates constant at the level first encountered when the animal enters the cell. In addition, for the time varying coefficients, the times when the animal first entered the cell were used, rather than the continuous time of since deployment. Finally, the base model of the CTMC version is just an intercept, the effect of time since the last move is removed, such that the base rate for residency is an exponential distribution. The following table gives the results for the posterior model probabilities for all 16 models, 8 CTSMC from the original analysis plus 8 more CTMC versions. All models are ranked by their posterior model probabilities to all decimal places possible. So even though the PMP for all models below the first 2 are equal to 0.00 to 2 decimal places, all CTSMC models scored higher PMP than all CTMC models when considering all decimal places numerically possible.

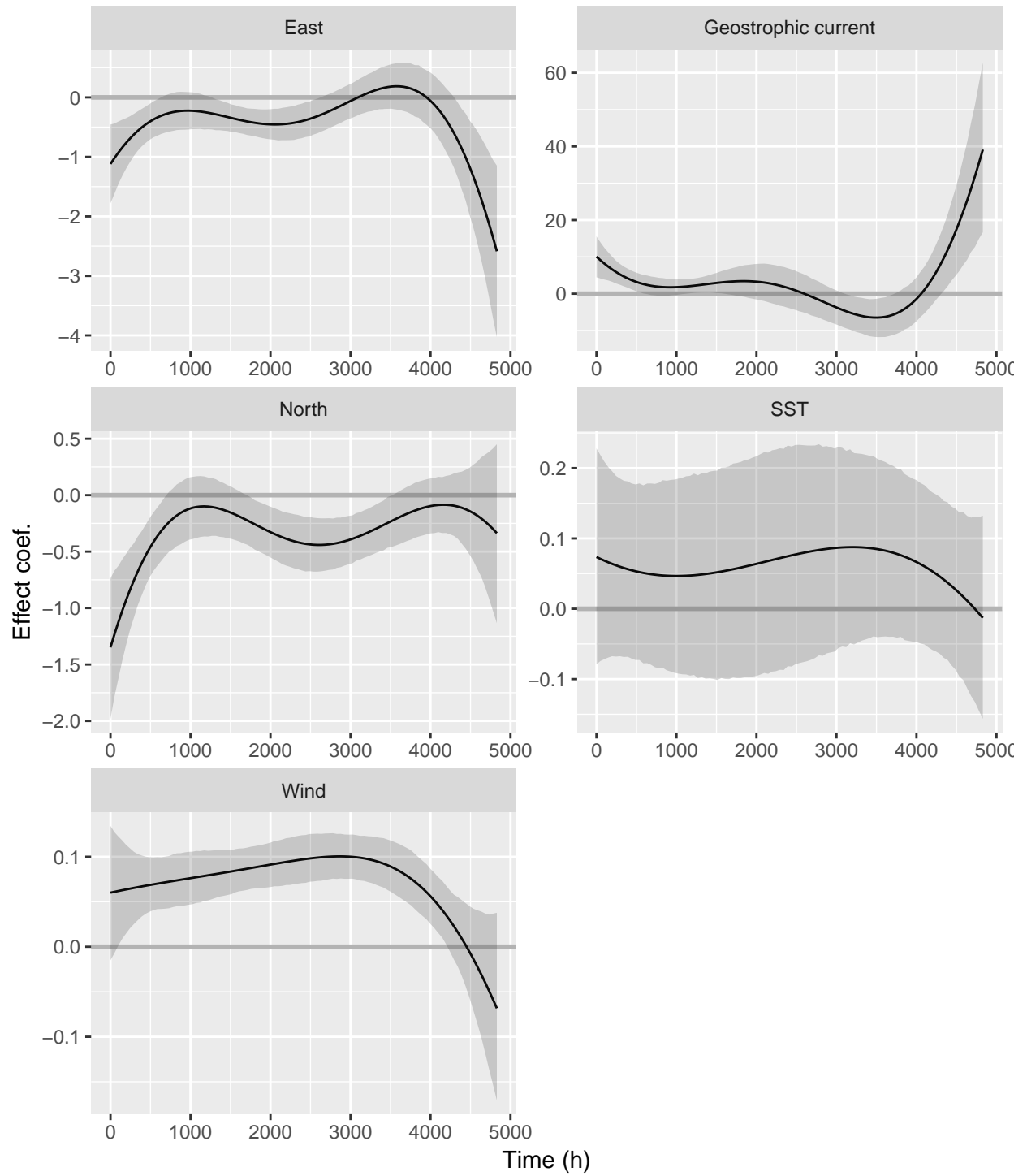
Table A.3: Model selection results of CTMC versus CTSMC analysis for animal 355. The first column gives the model class, Markov (CTMC) vs. semi-Markov (CTSMC; this paper). All covariates are labeled with a time index, but in Markov models the covariates only change when the animal enters a new cell, whereas, for semi-Markov the covariates change on the schedules described in the main paper (whether the animal moves or not). In addition, the base model in the Markov version is not a function of the log of the time since last movement.

Class	Model	PMP
semi-Markov	wind_{ijt}	0.99
	$\text{wind}_{ijt} + \text{curr}_{ijt}$	0.01
	$\text{wind}_{ijt} + \text{sst}_{it}$	0.00
	$\text{wind}_{ijt} + \text{curr}_{ijt} + \text{sst}_{it}$	0.00
	base only	0.00
	curr_{ijt}	0.00
	sst_{it}	0.00
	$\text{curr}_{ijt} + \text{sst}_{it}$	0.00
Markov	$\text{wind}_{ijt} + \text{curr}_{ijt}$	0.00
	wind_{ijt}	0.00
	$\text{wind}_{ijt} + \text{curr}_{ijt} + \text{sst}_{it}$	0.00
	$\text{wind}_{ijt} + \text{sst}_{it}$	0.00
	base only	0.00
	curr_{ijt}	0.00
	sst_{it}	0.00
	$\text{curr}_{ijt} + \text{sst}_{it}$	0.00

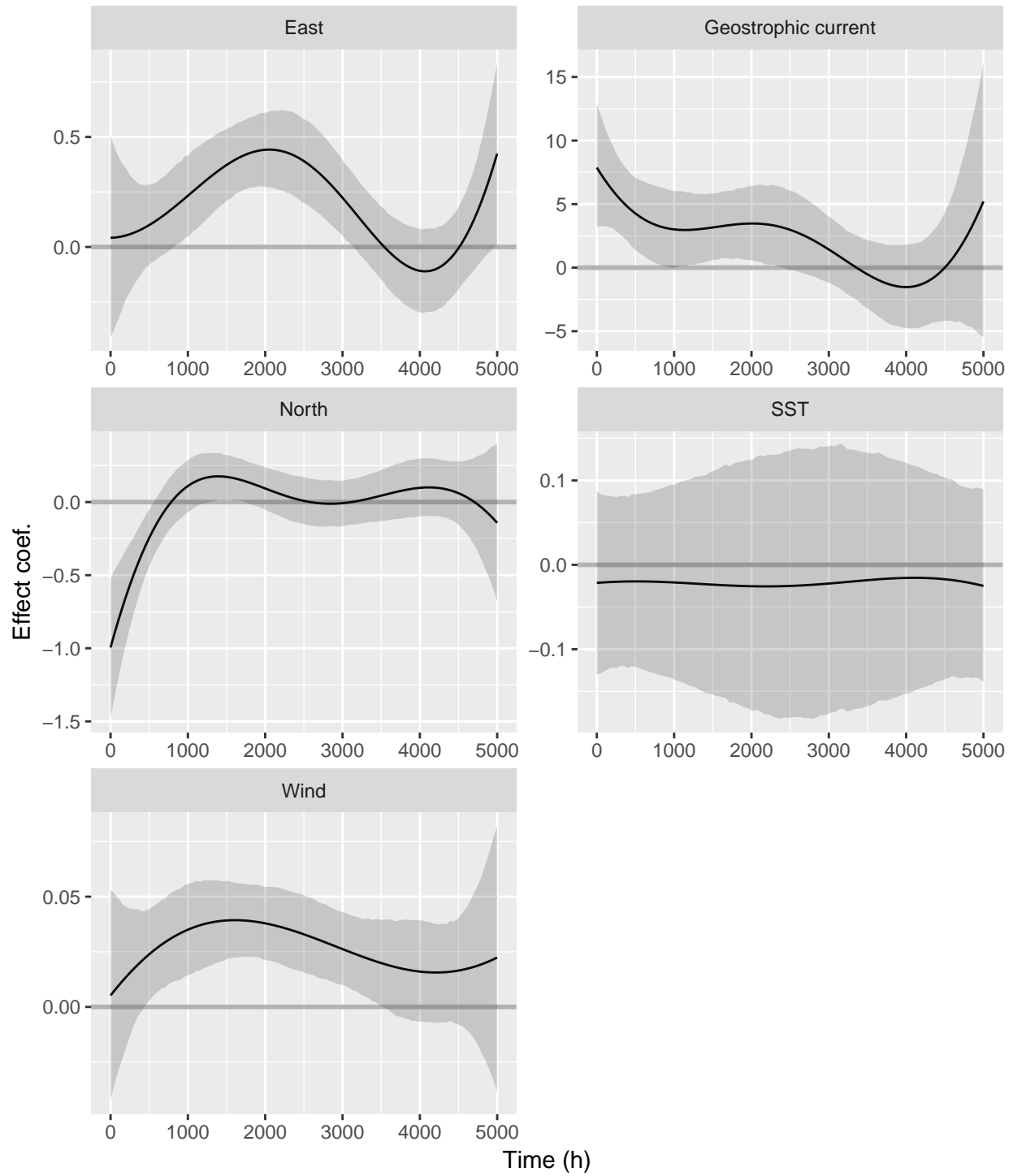
A.4 Individual Results for Saturated Model

This group of plots presents the coefficient estimates for each individual animal. Only the saturated model ($\sim \log(\text{residence}) * \text{previous} + \text{B:north} + \text{B:east} + \text{B:wind} + \text{B:curr} + \text{B:sst}$) is shown.

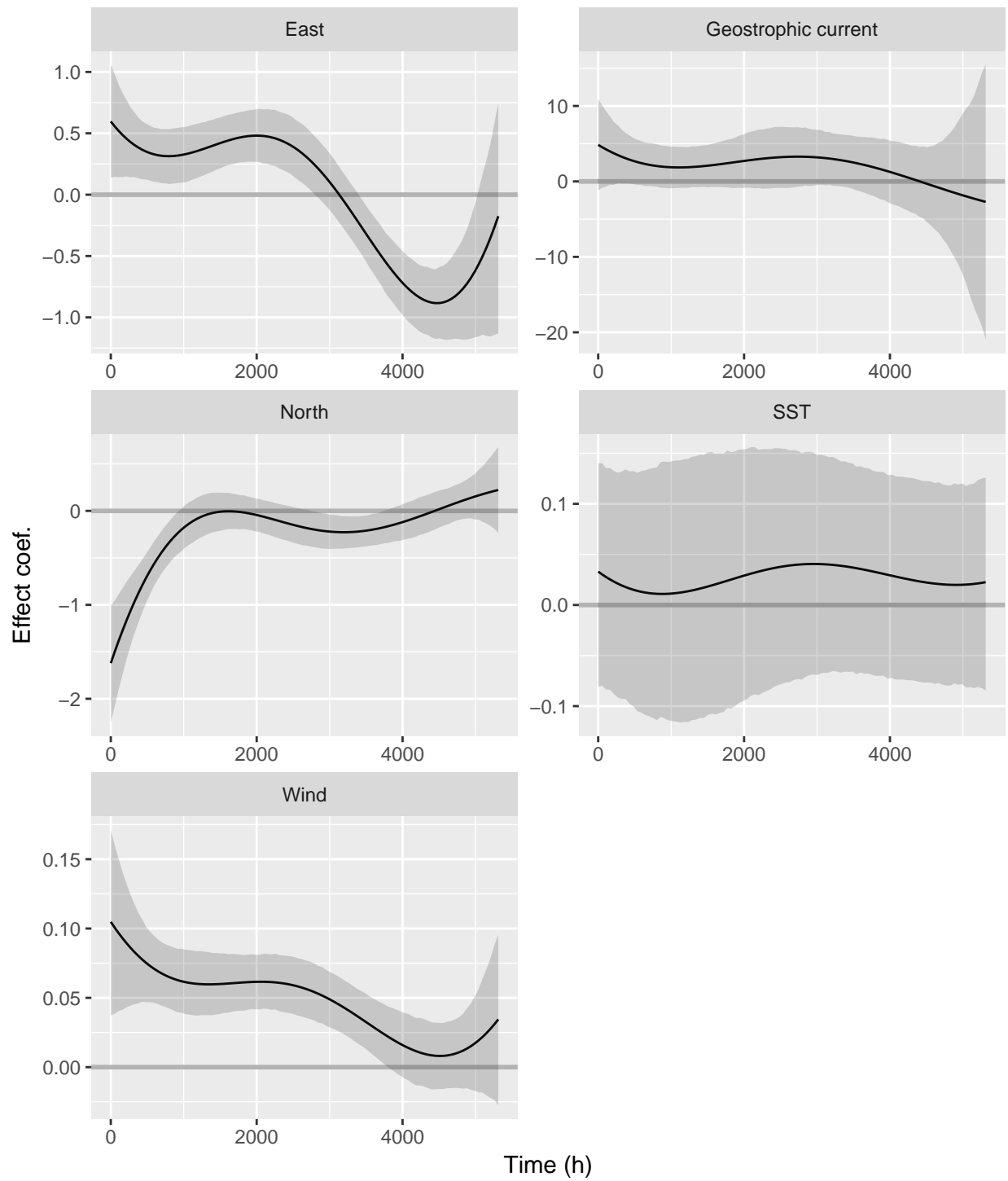
Animal ID: 330



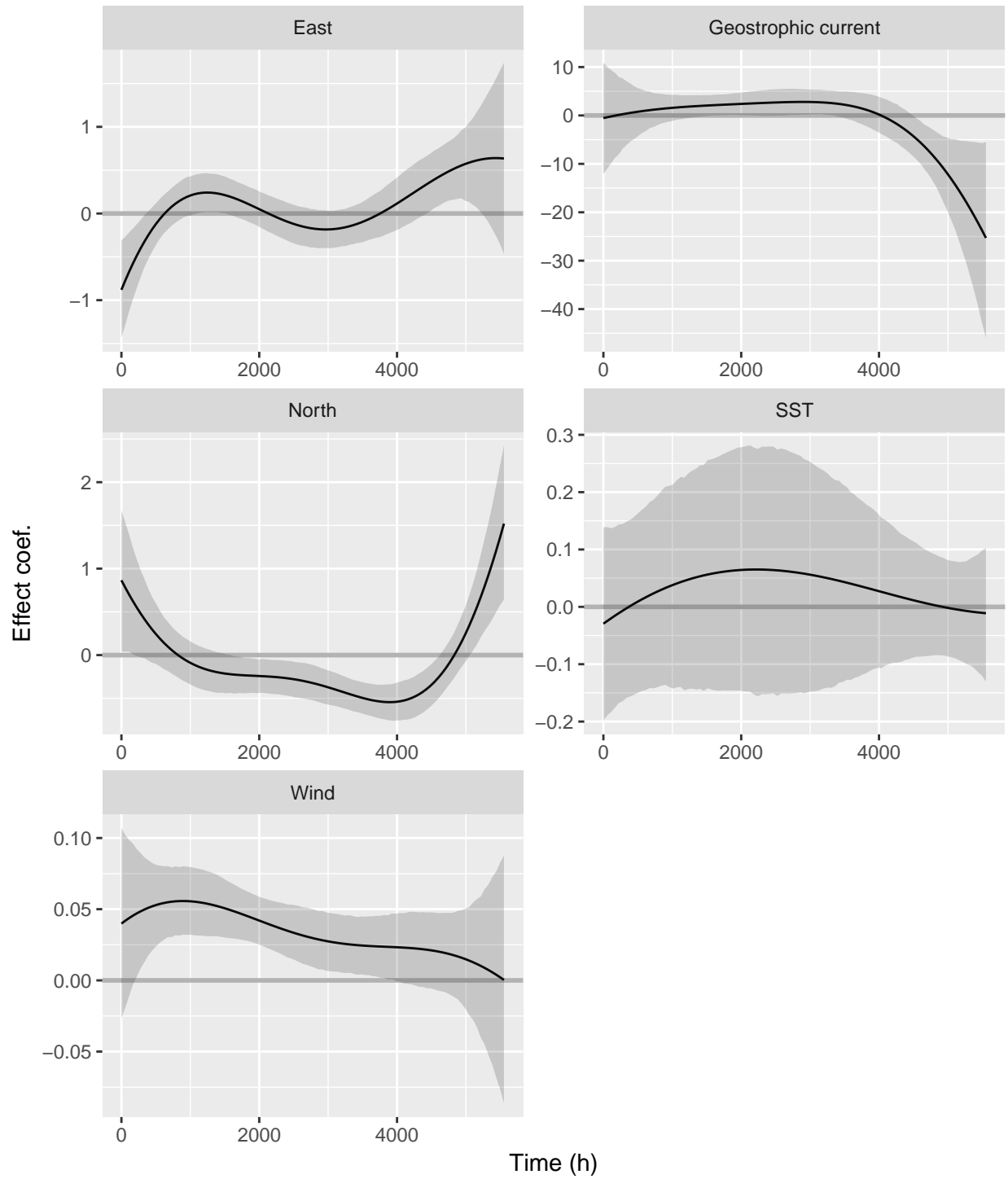
Animal ID: 335



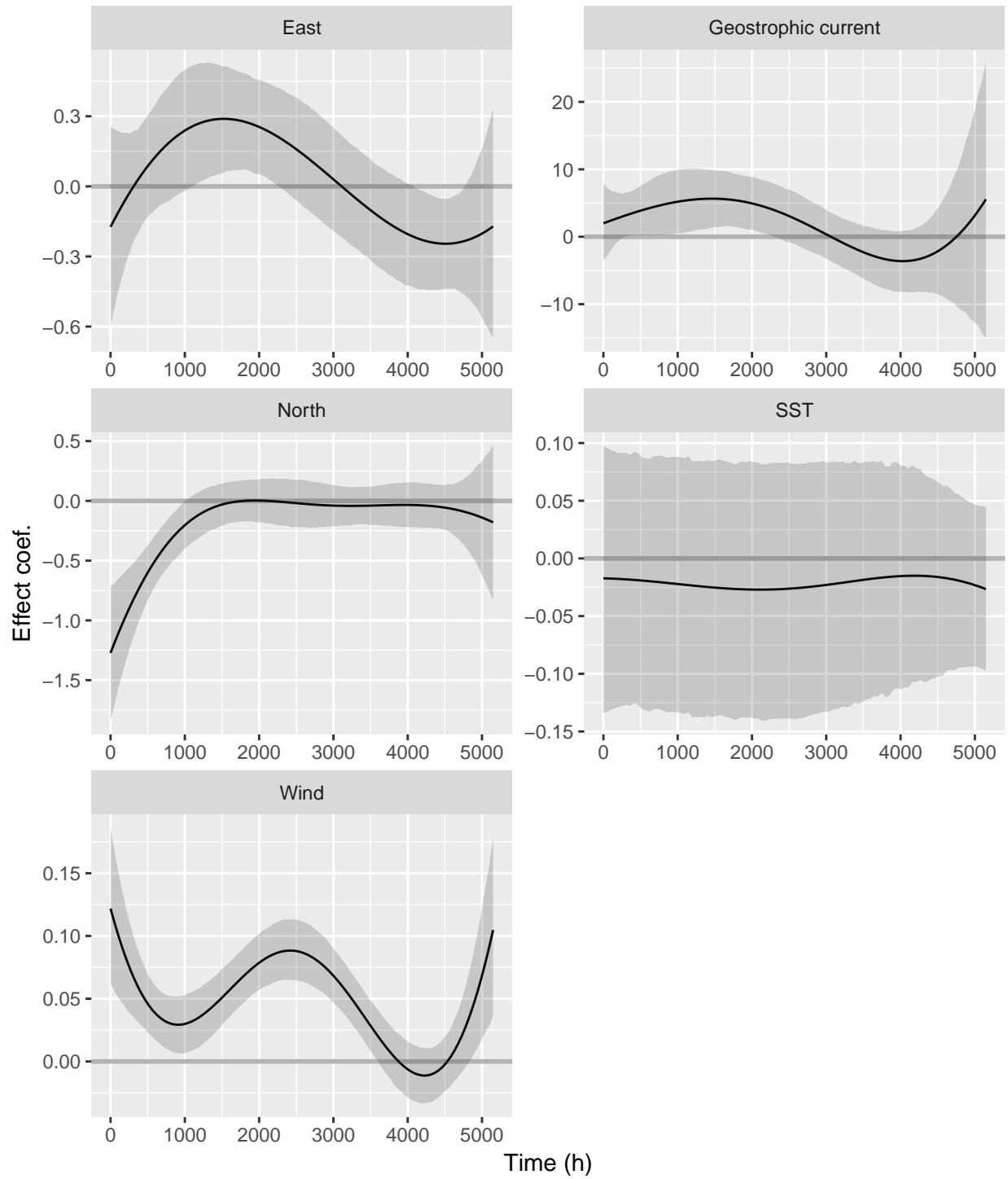
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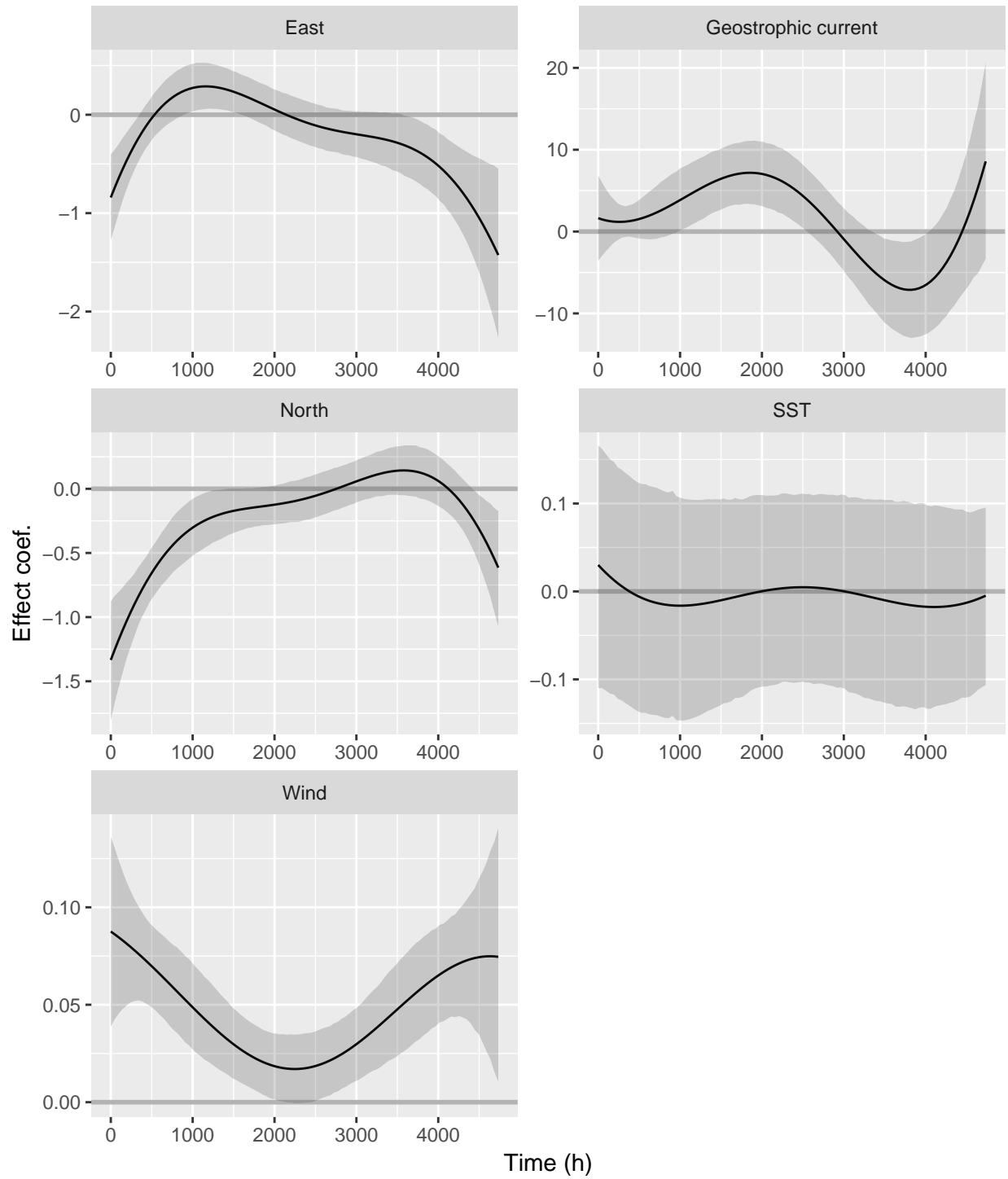
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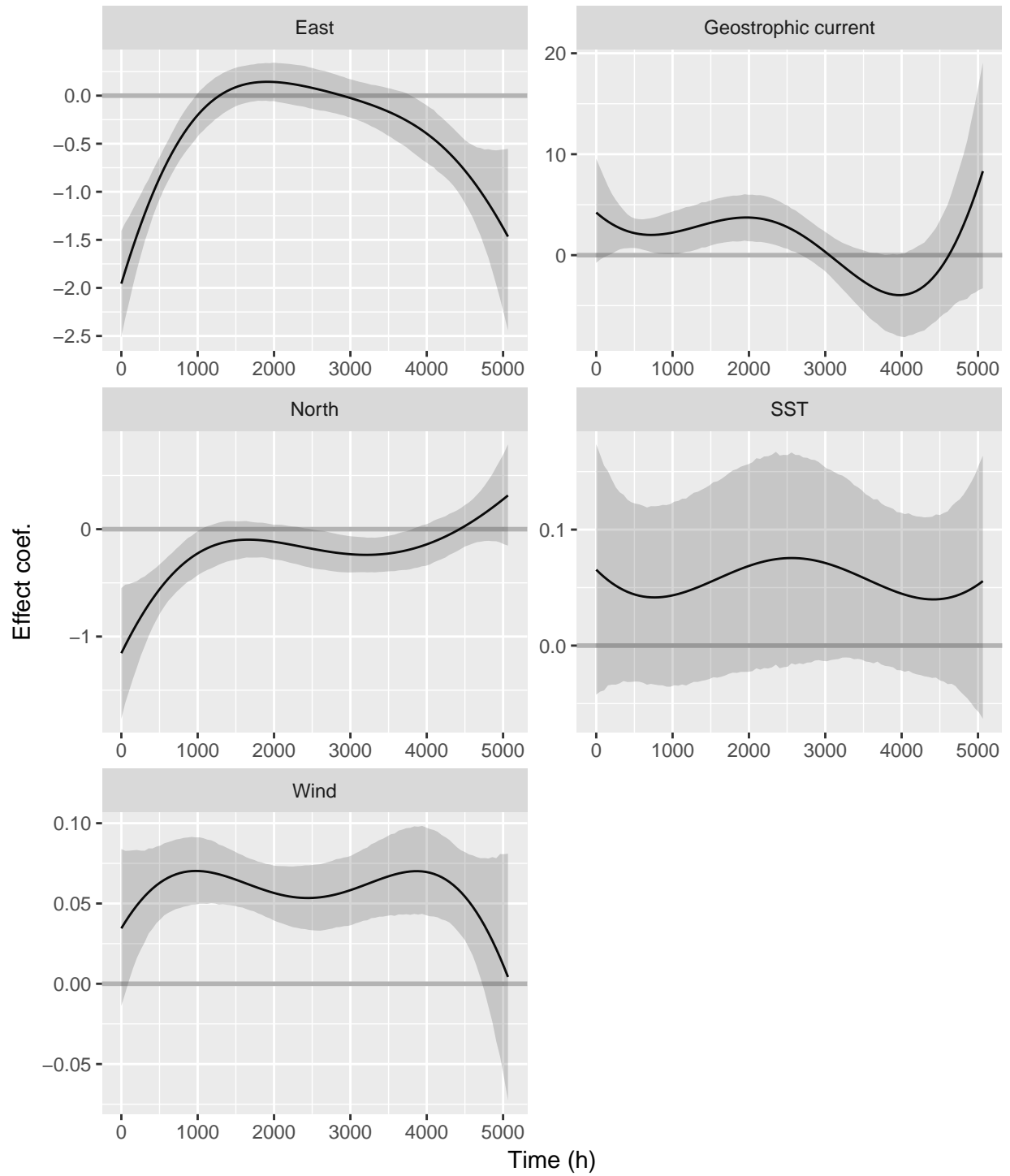
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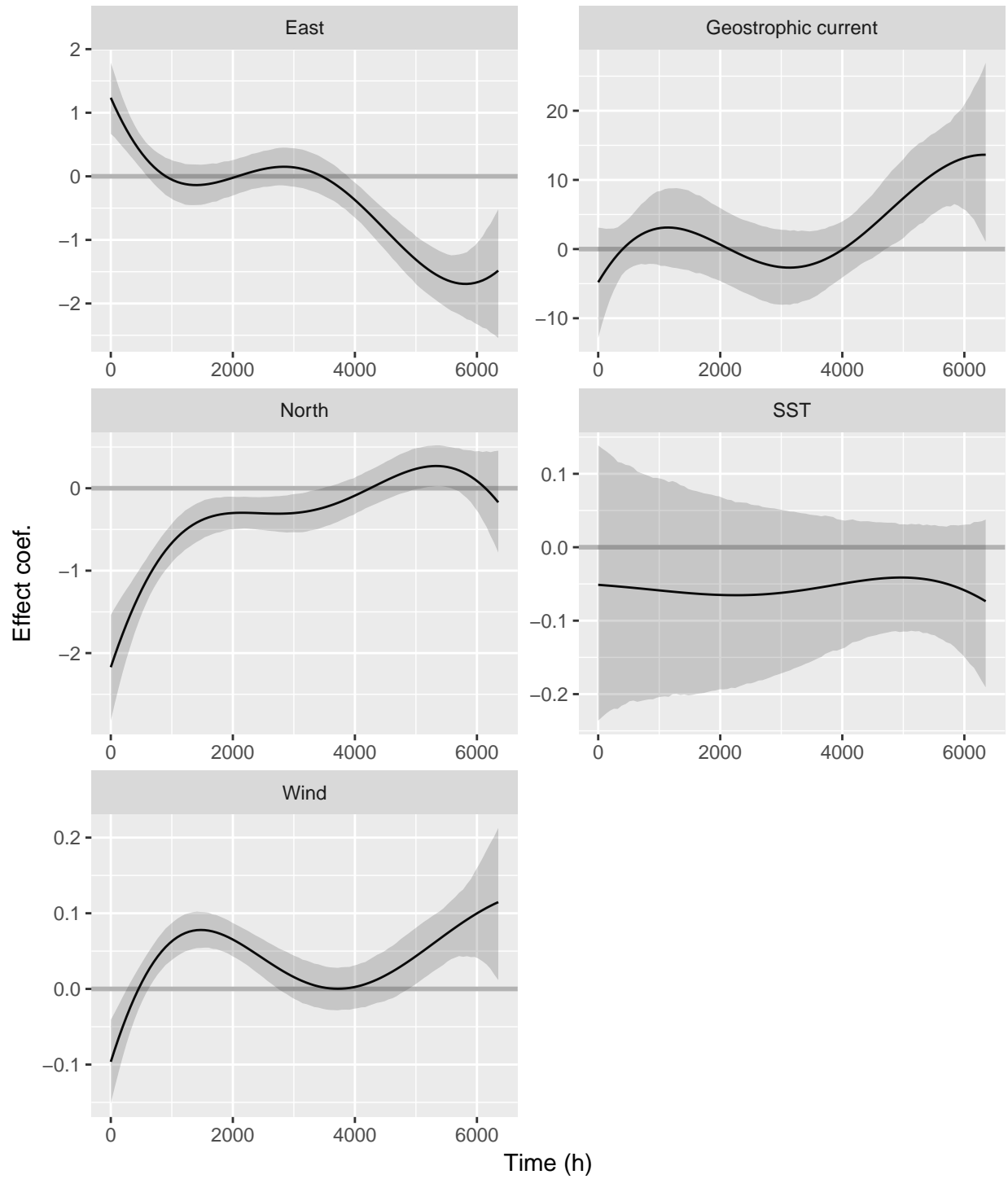
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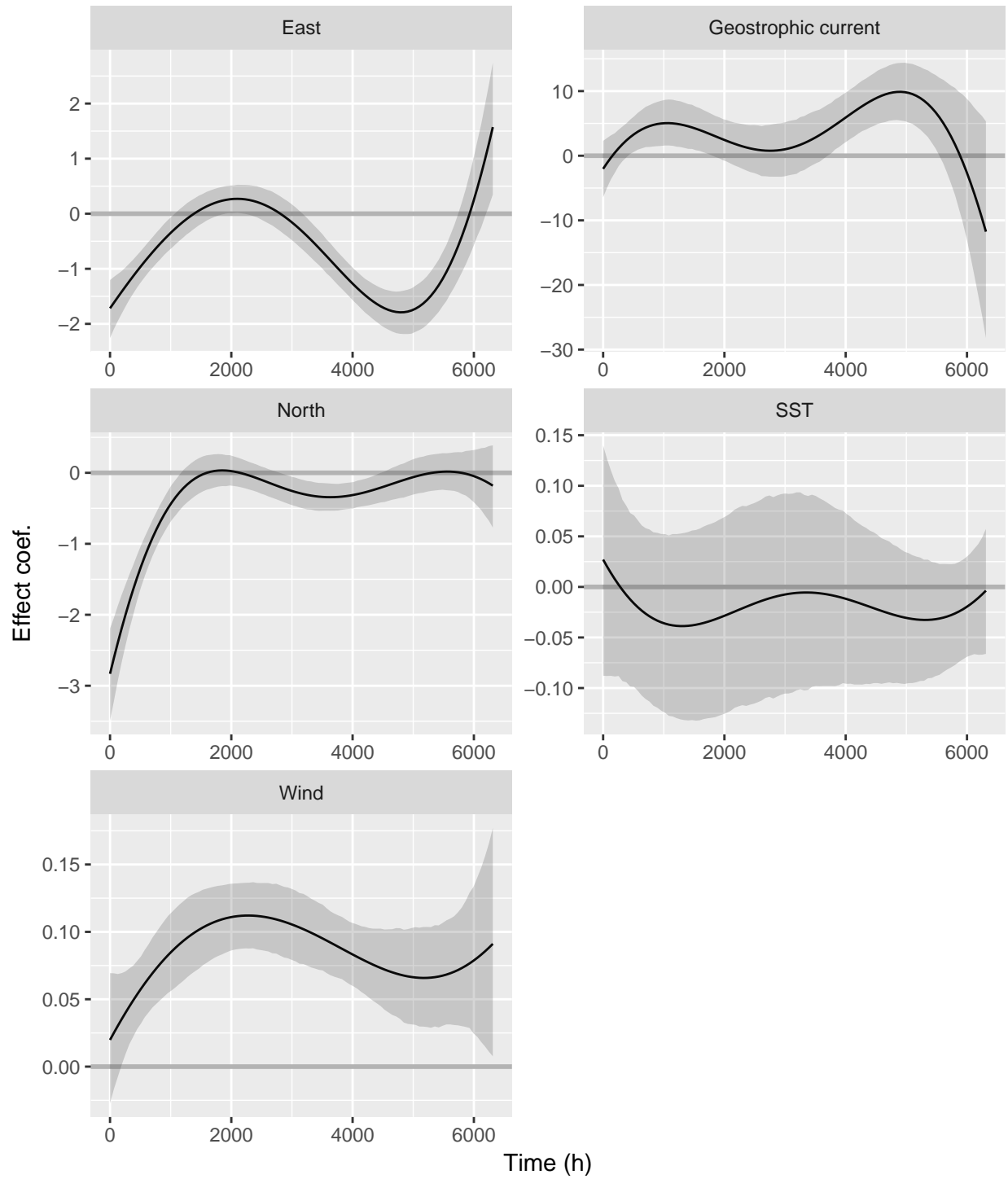
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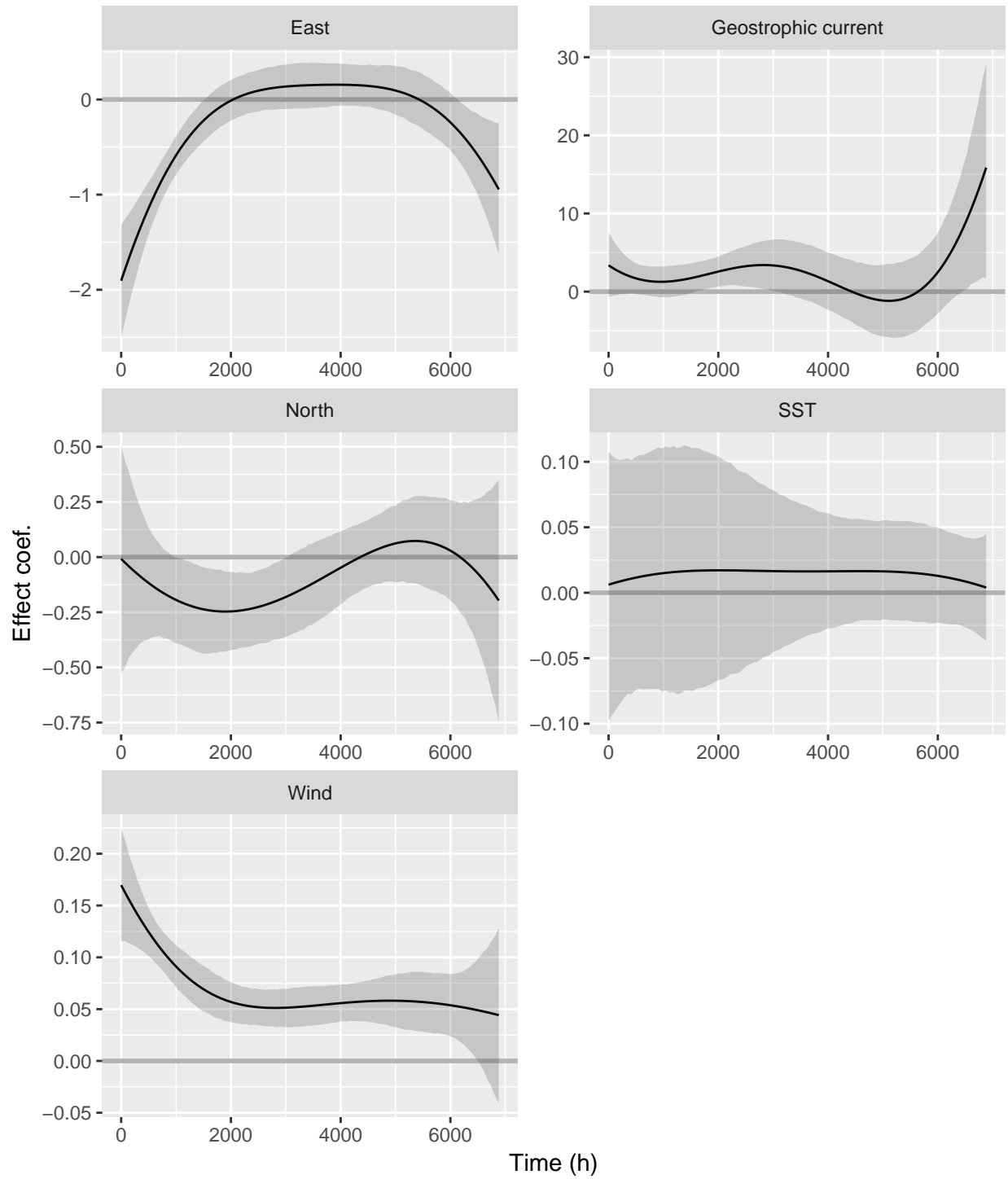
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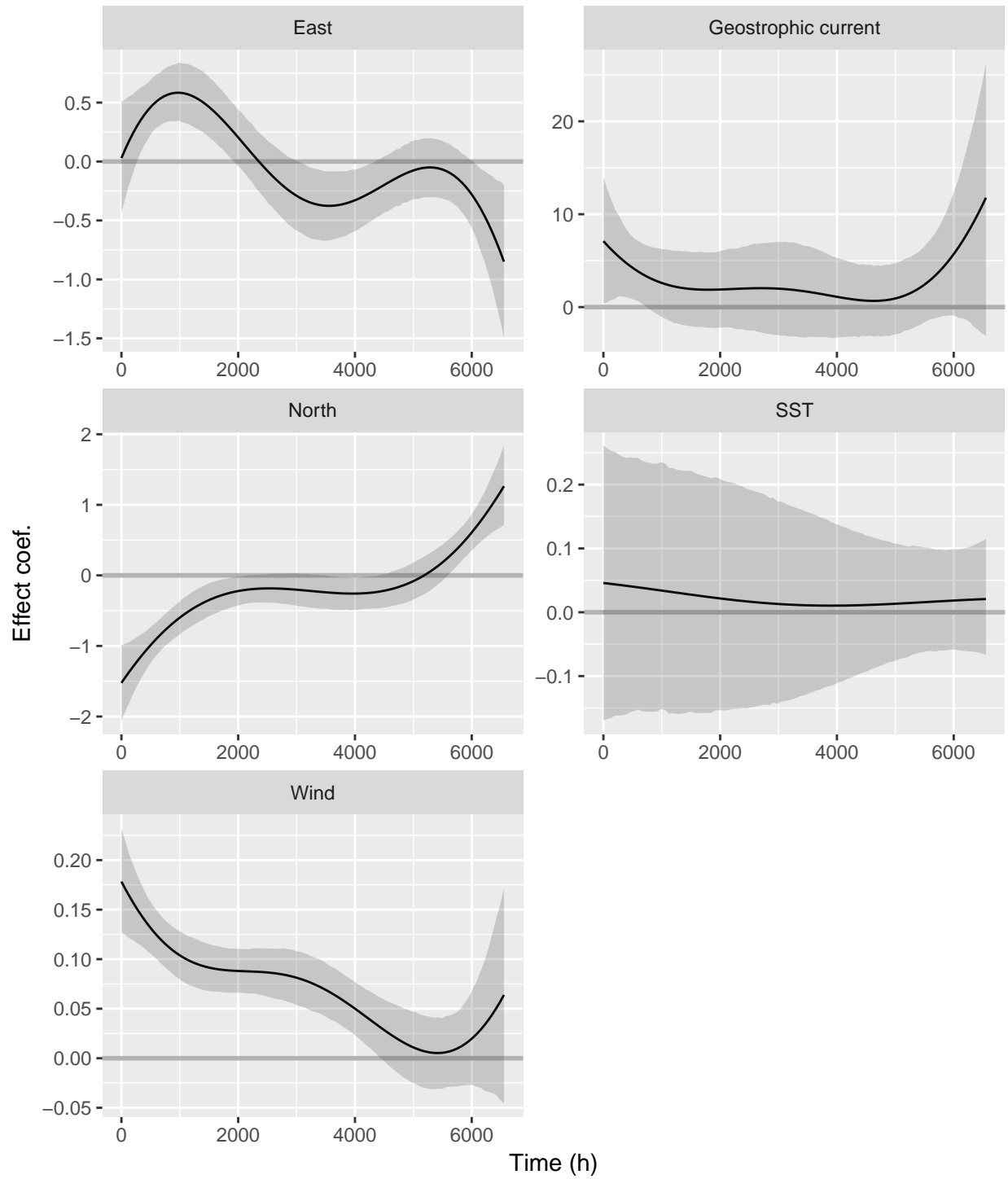
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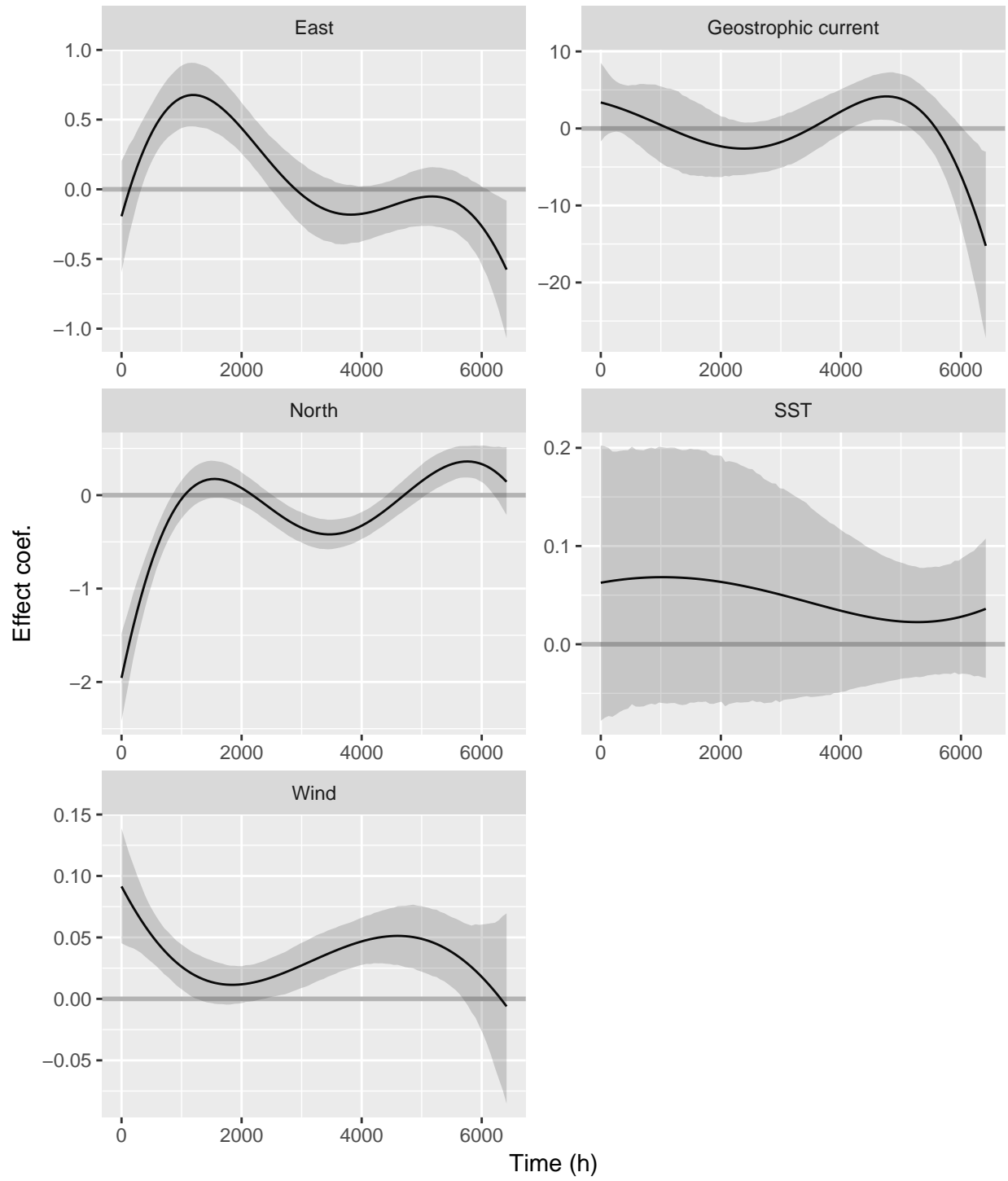
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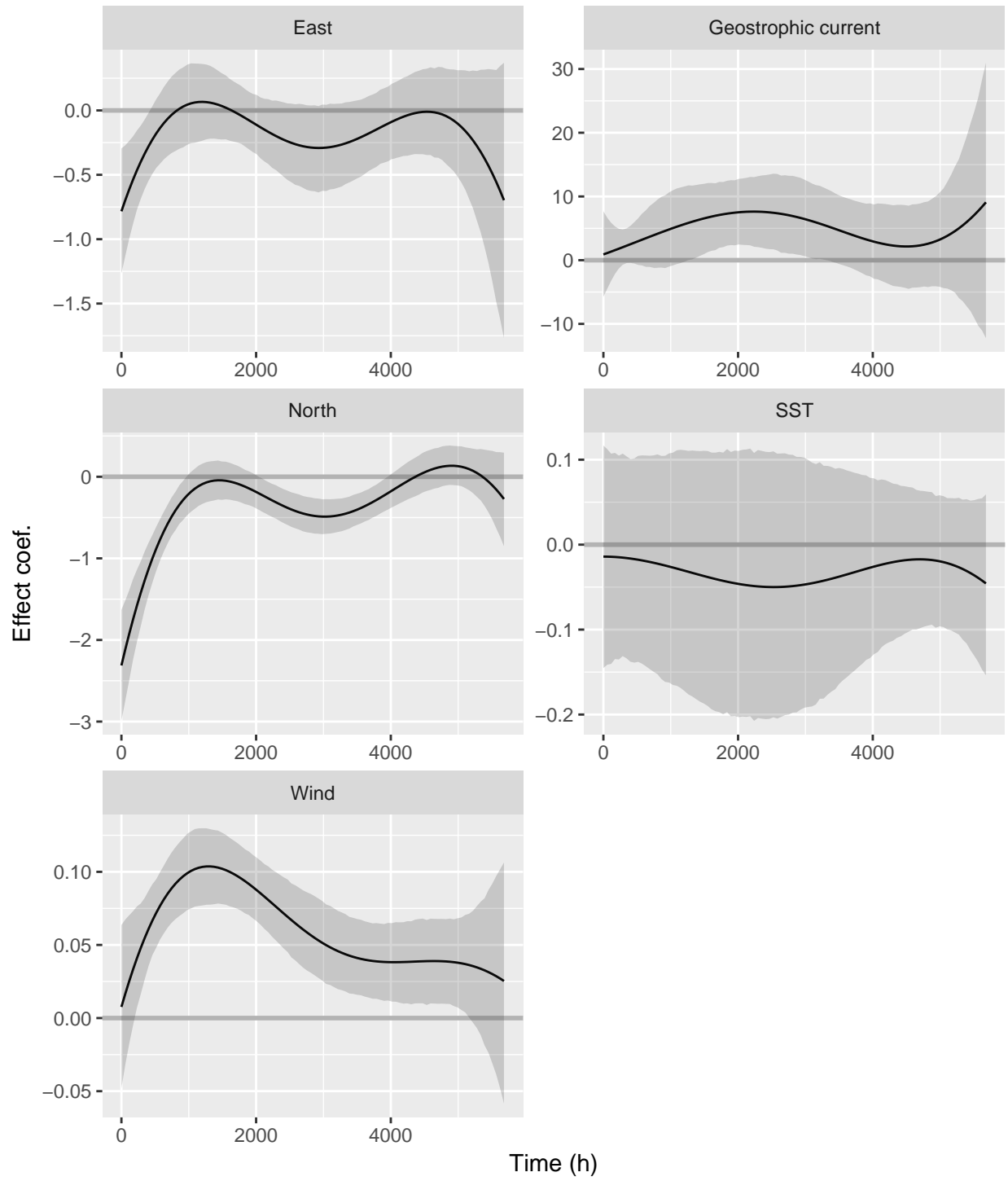
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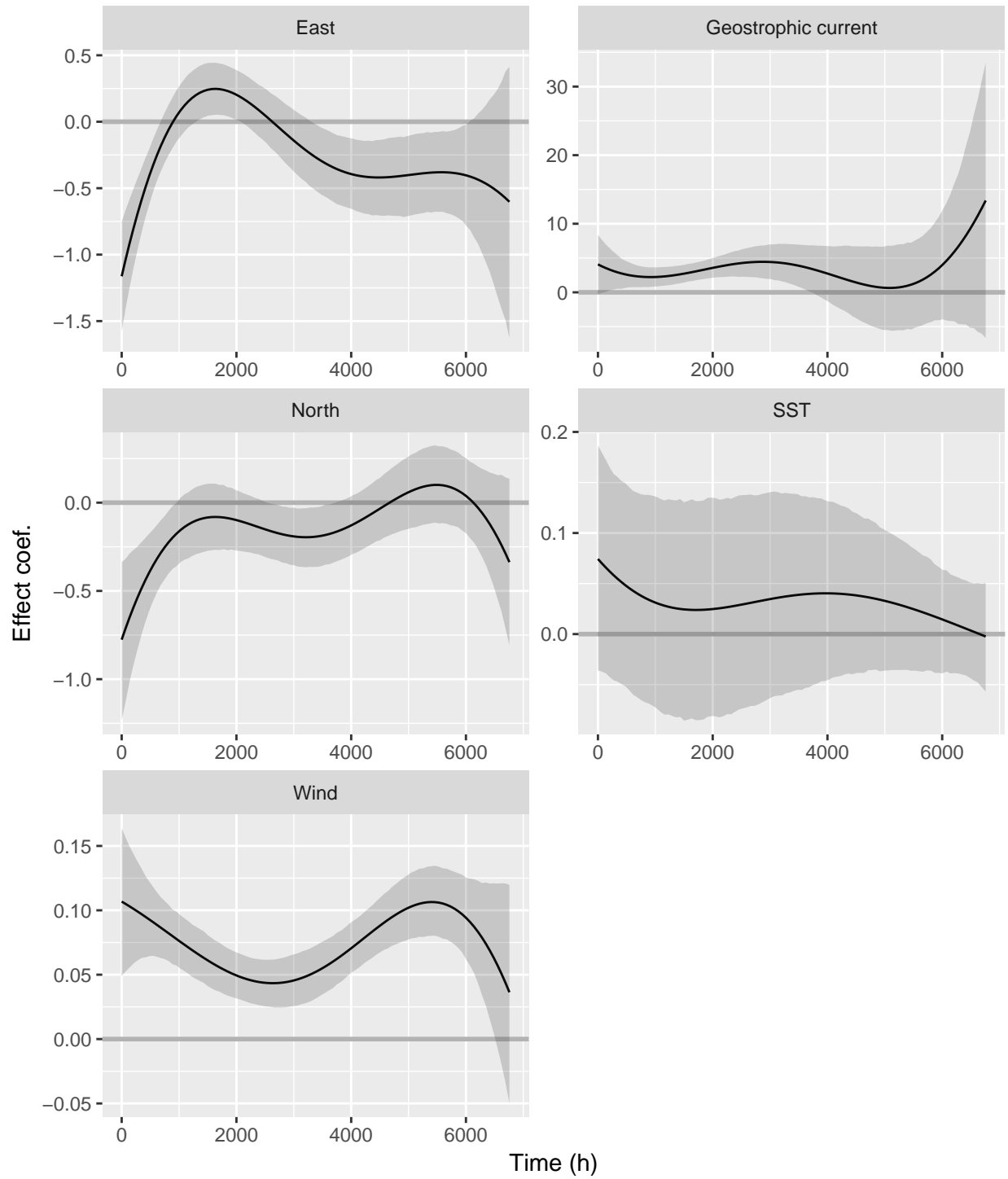
Animal ID: 388



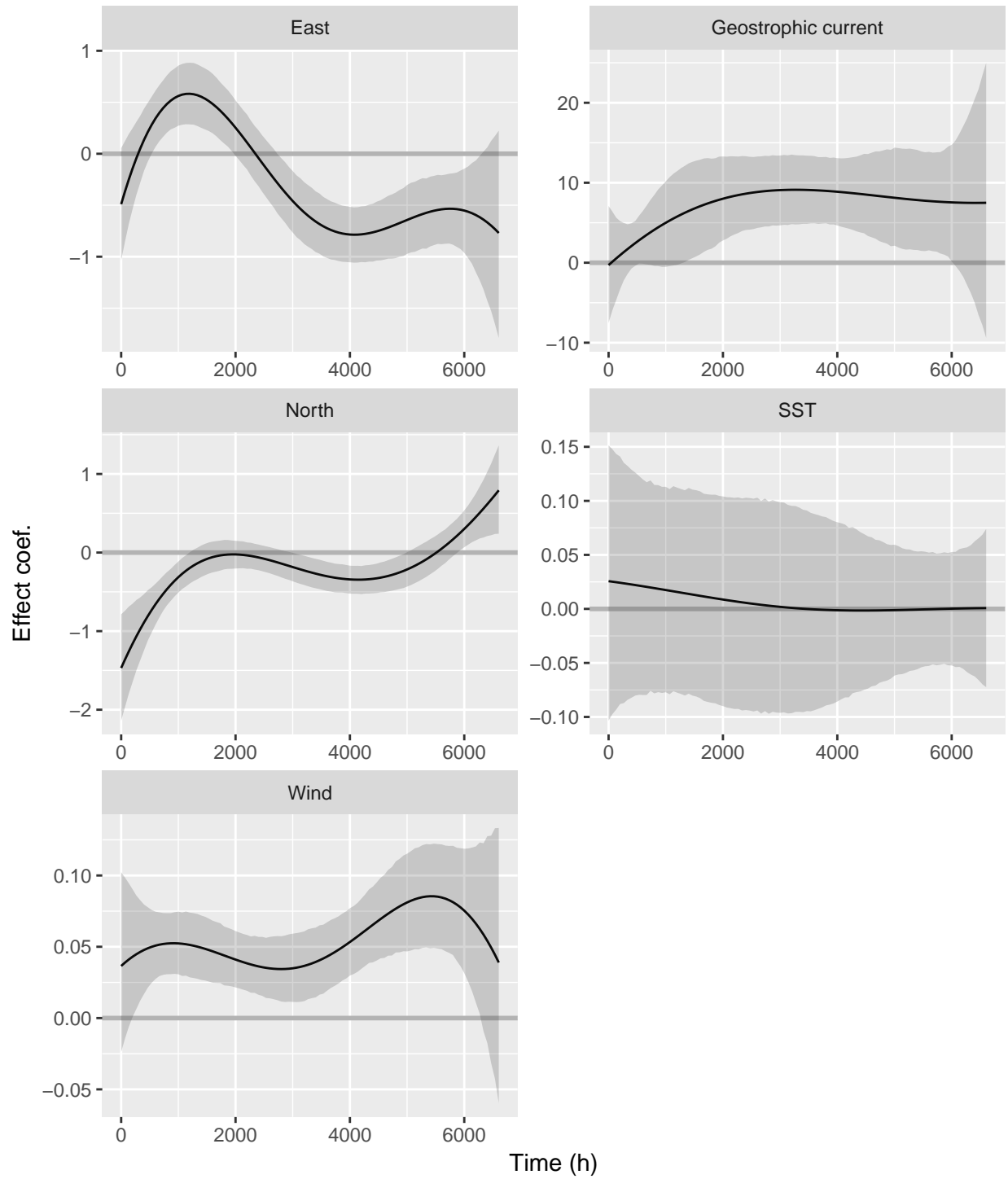
Animal ID: 394



Animal ID: 405

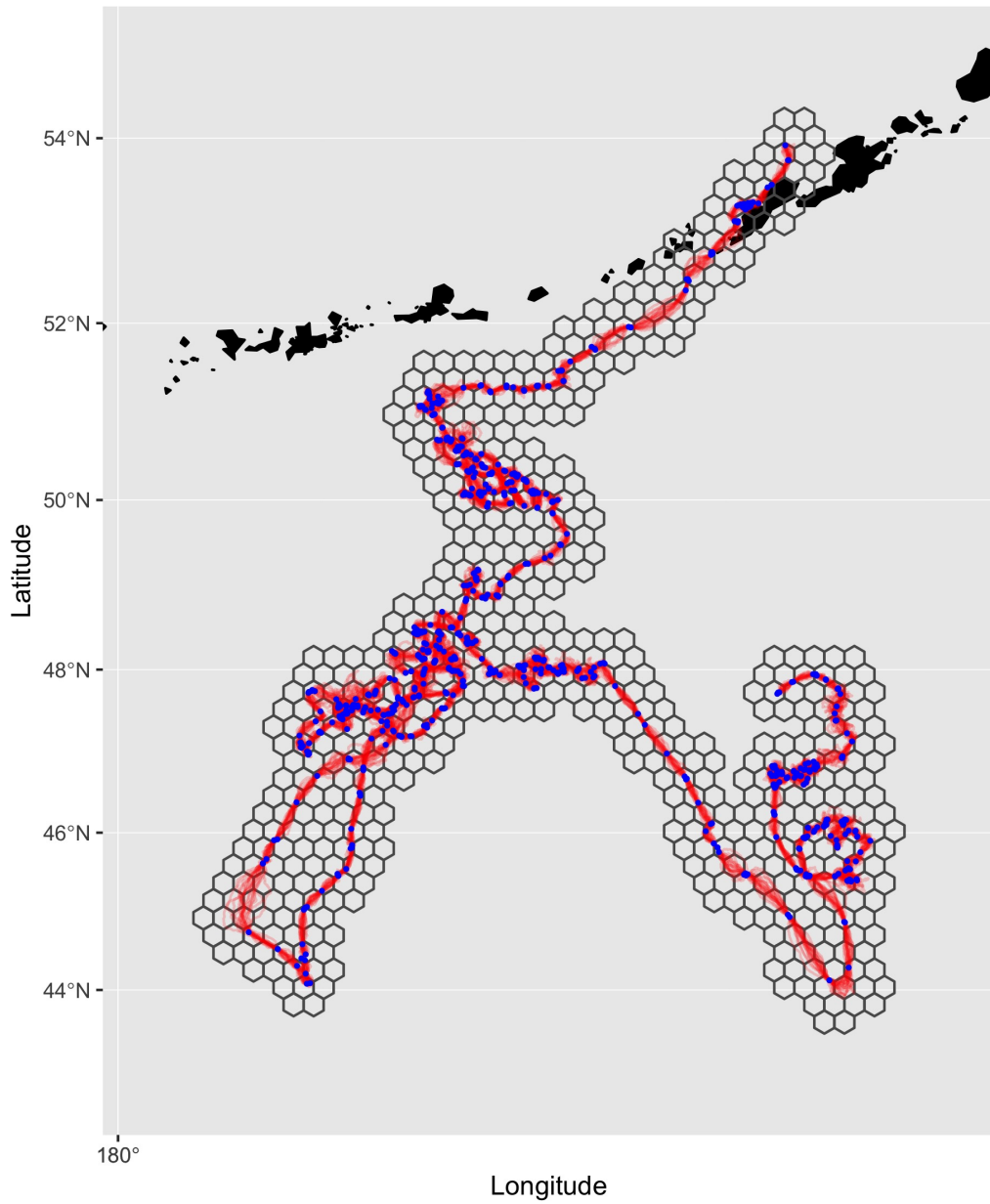


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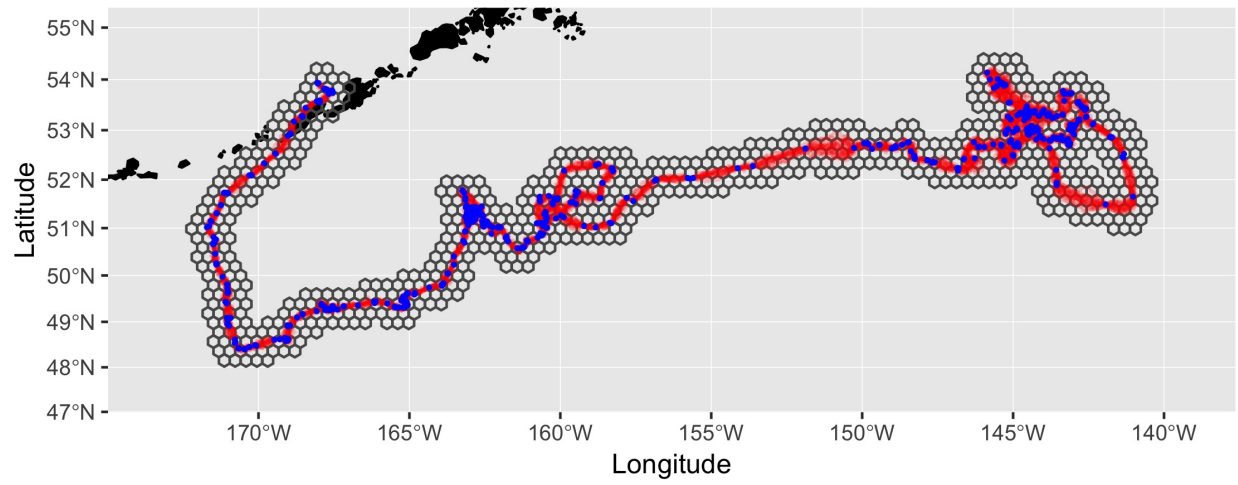


A.5 Individual data plots for each animal

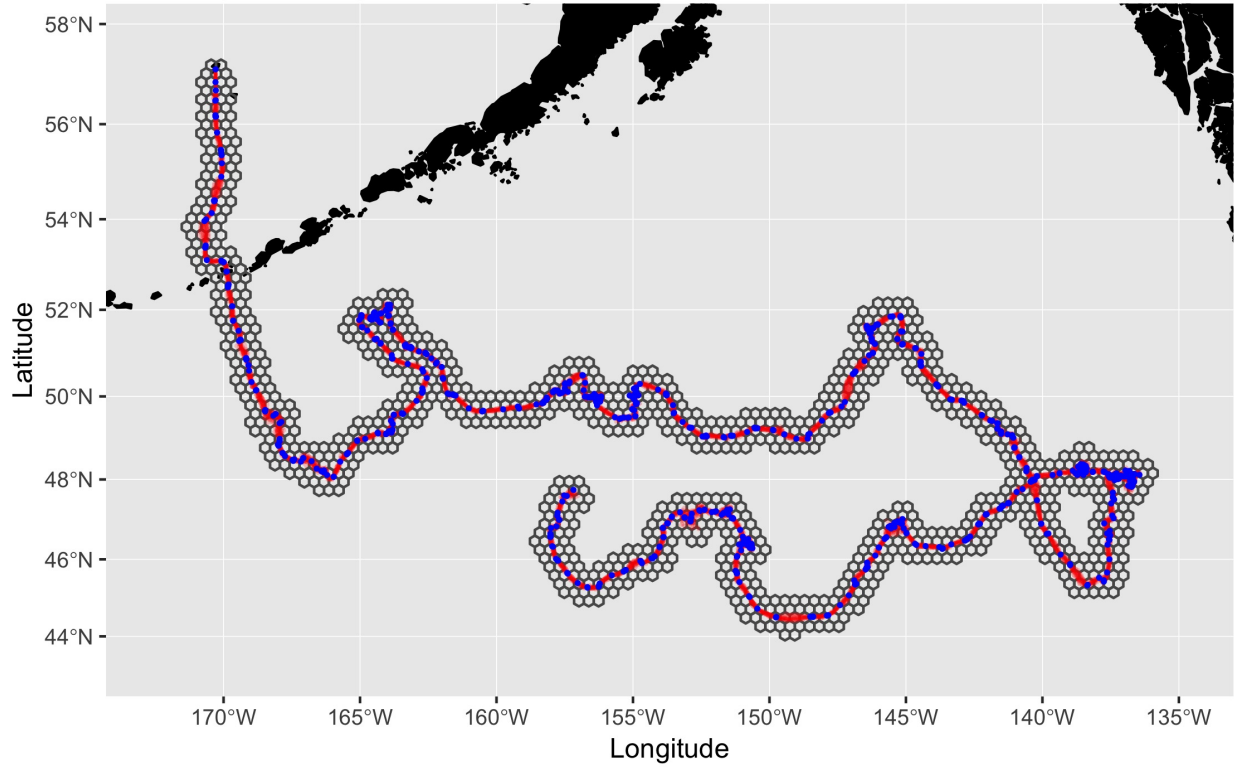
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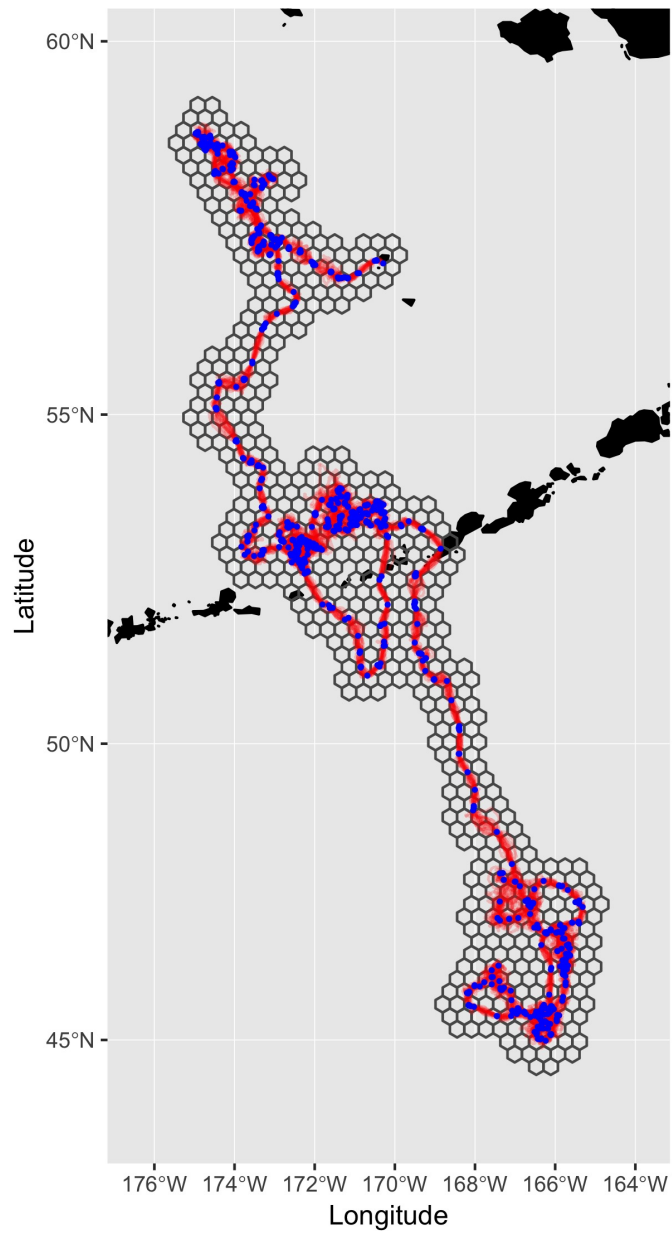
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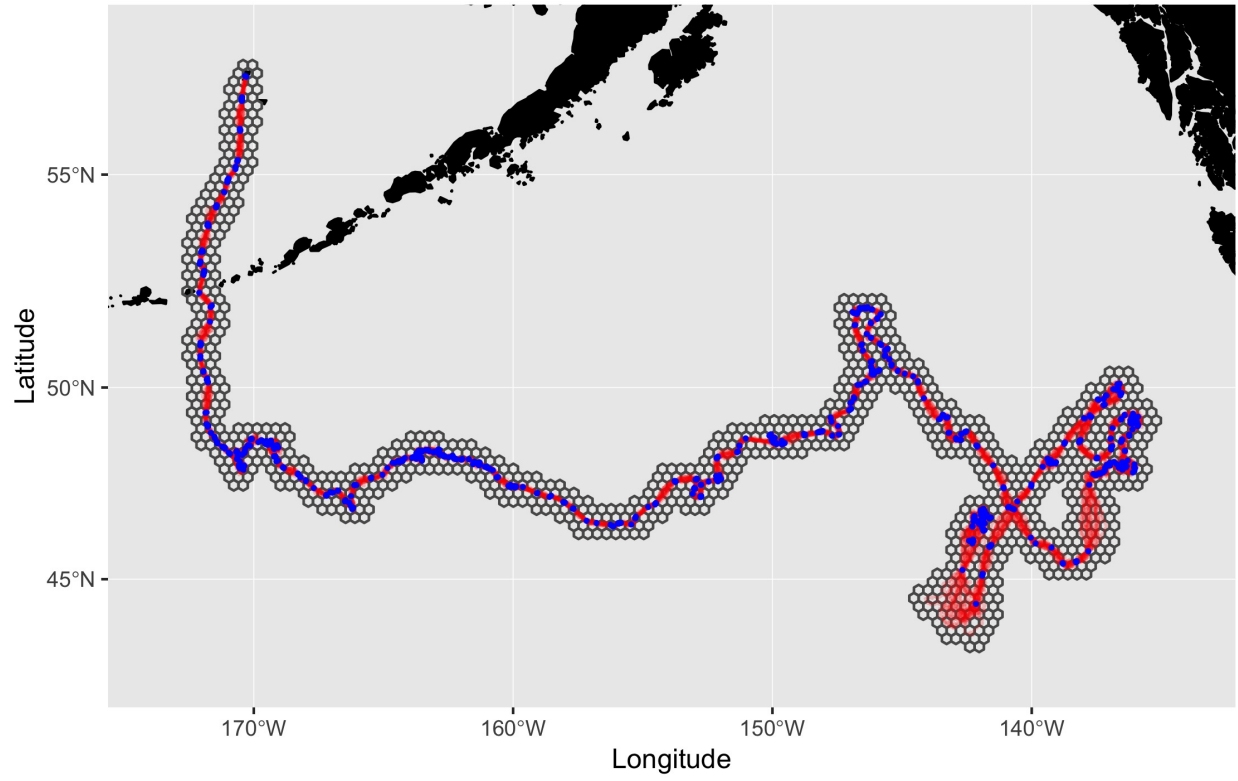
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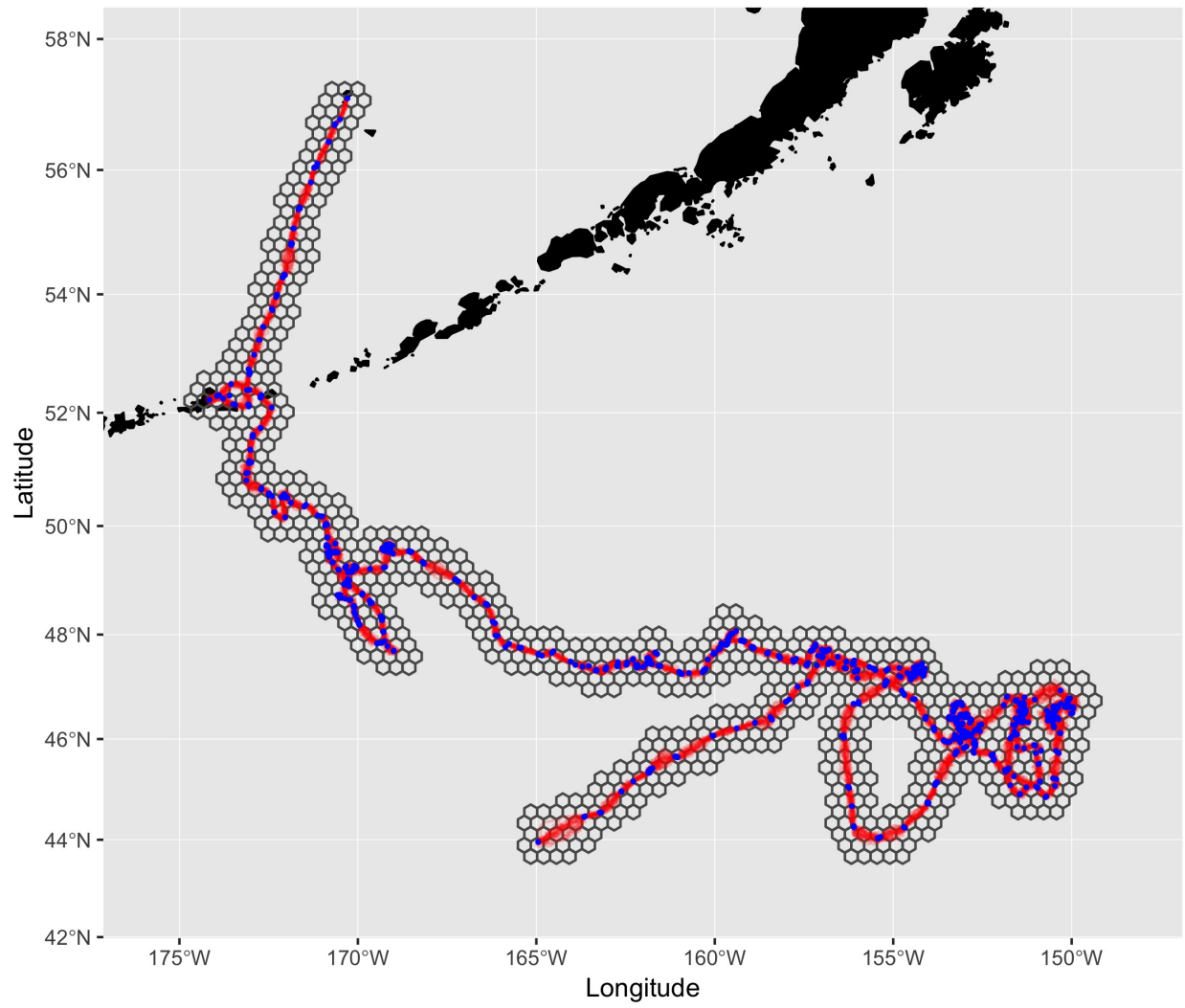
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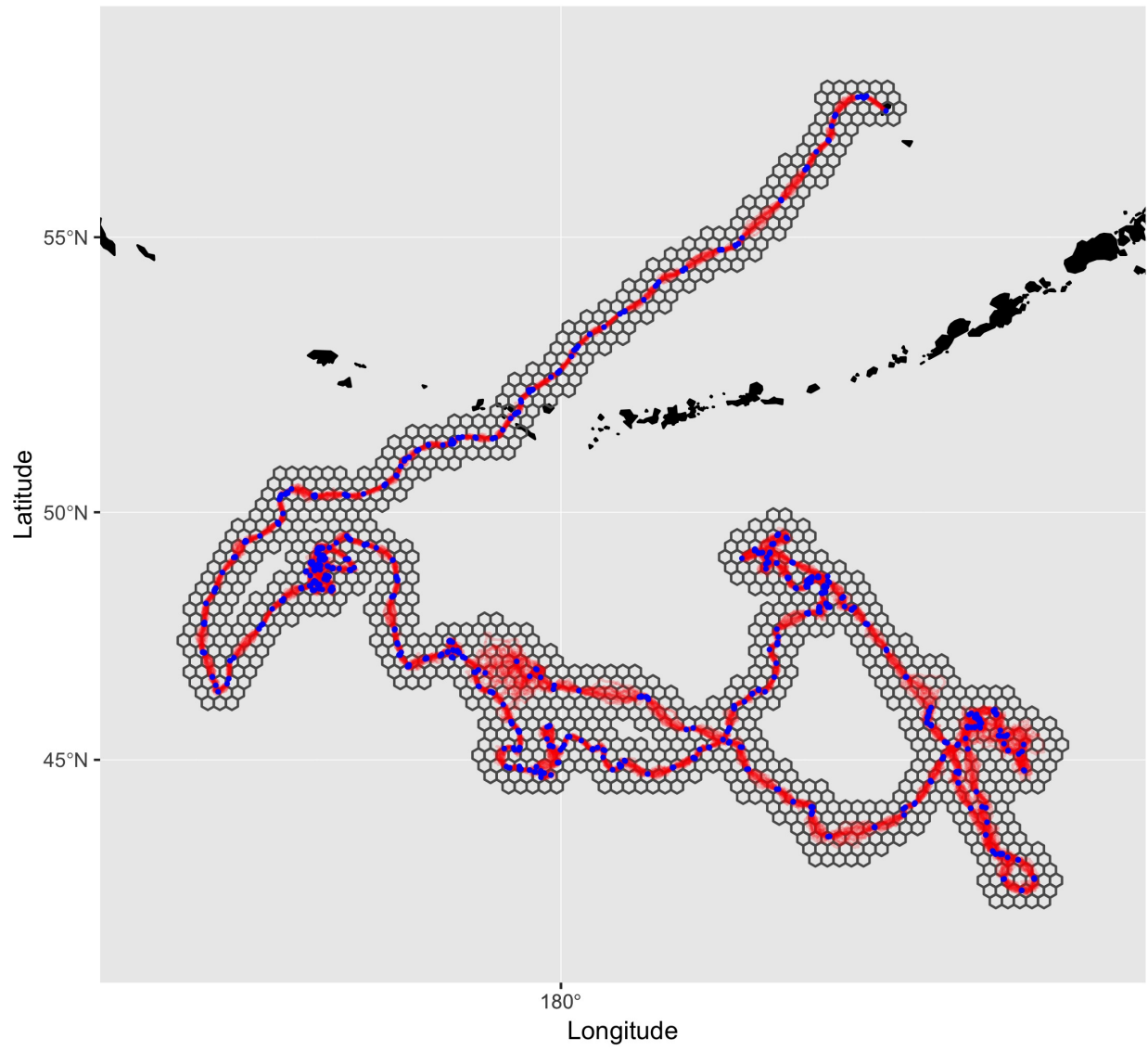
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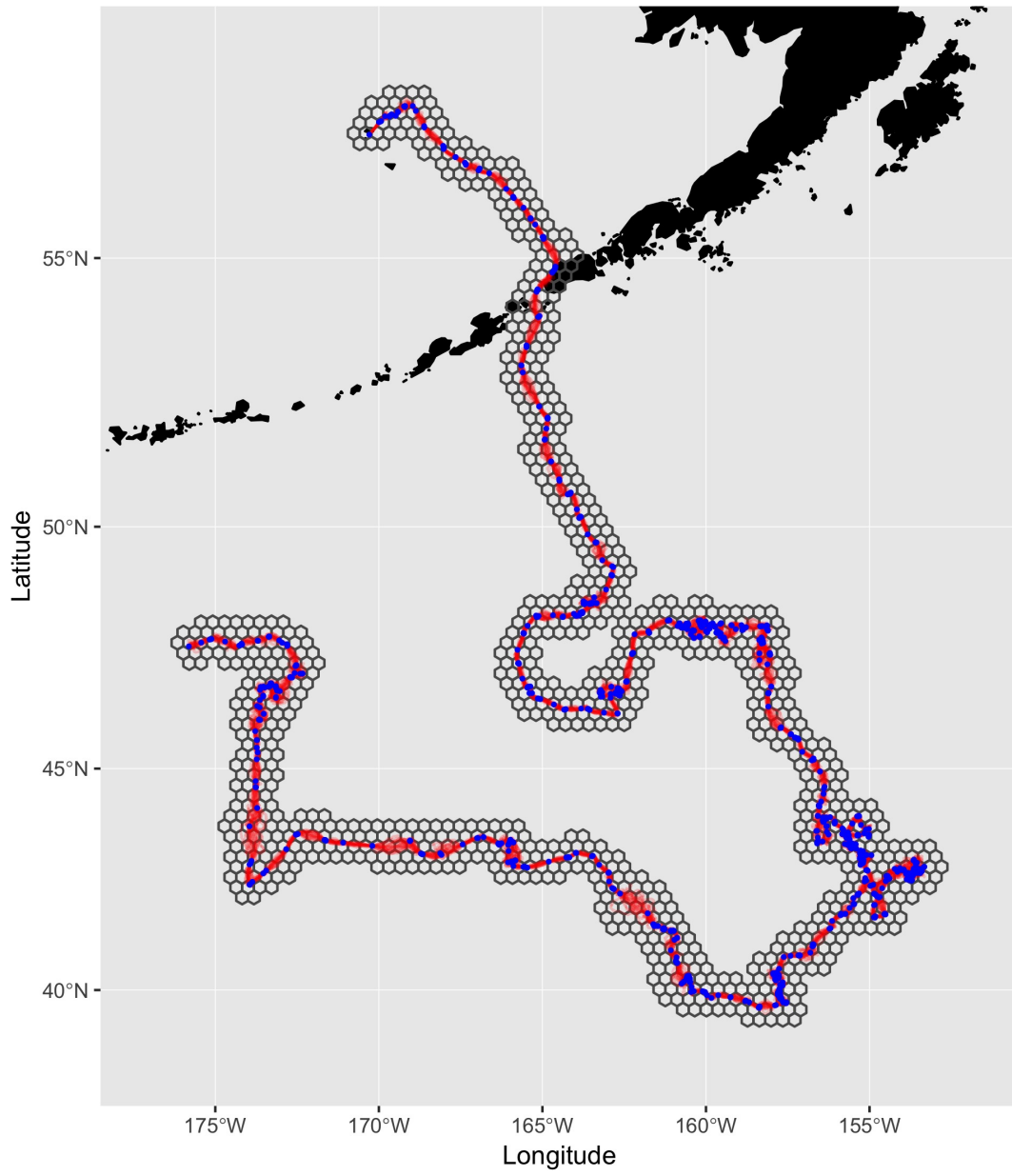
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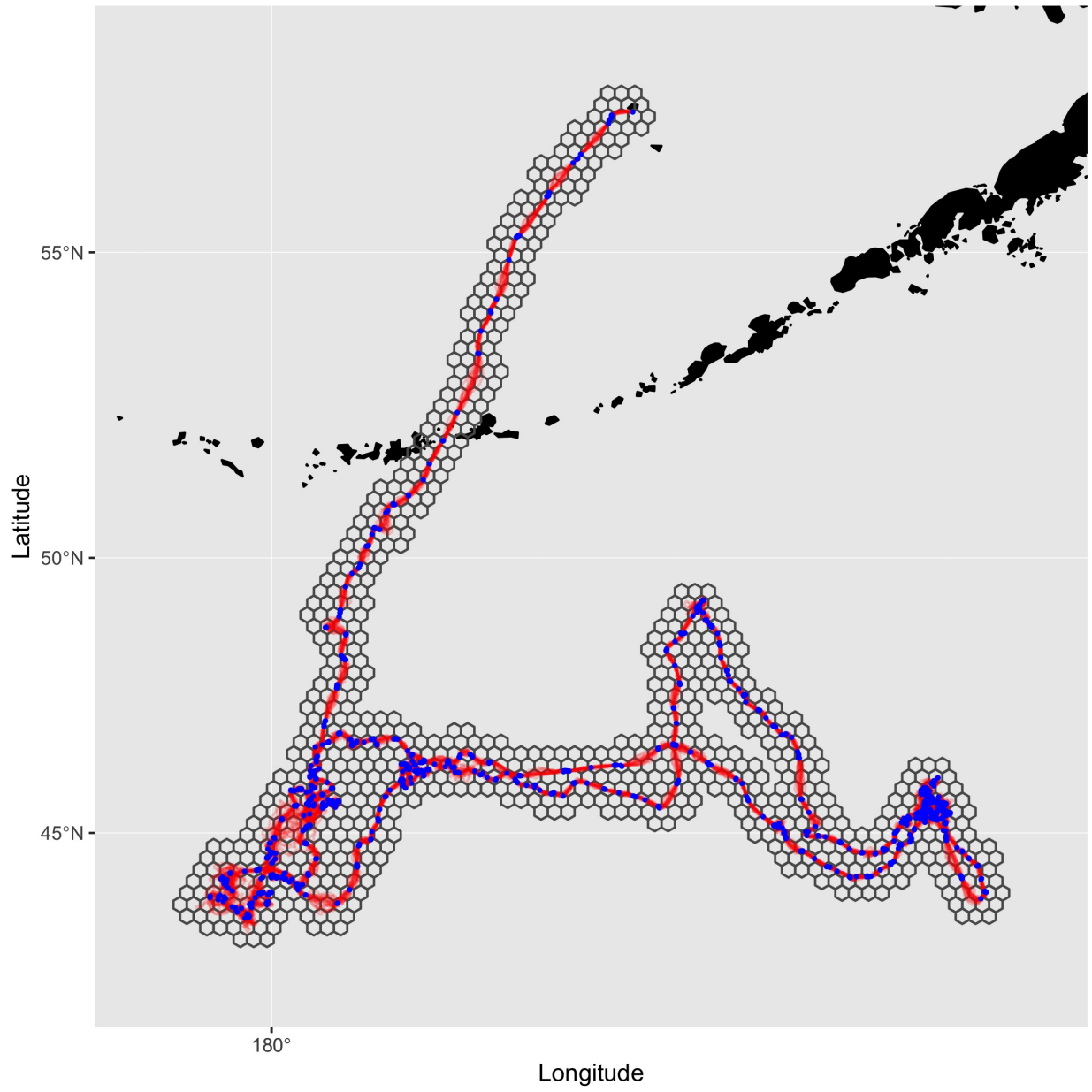
Animal ID: 367



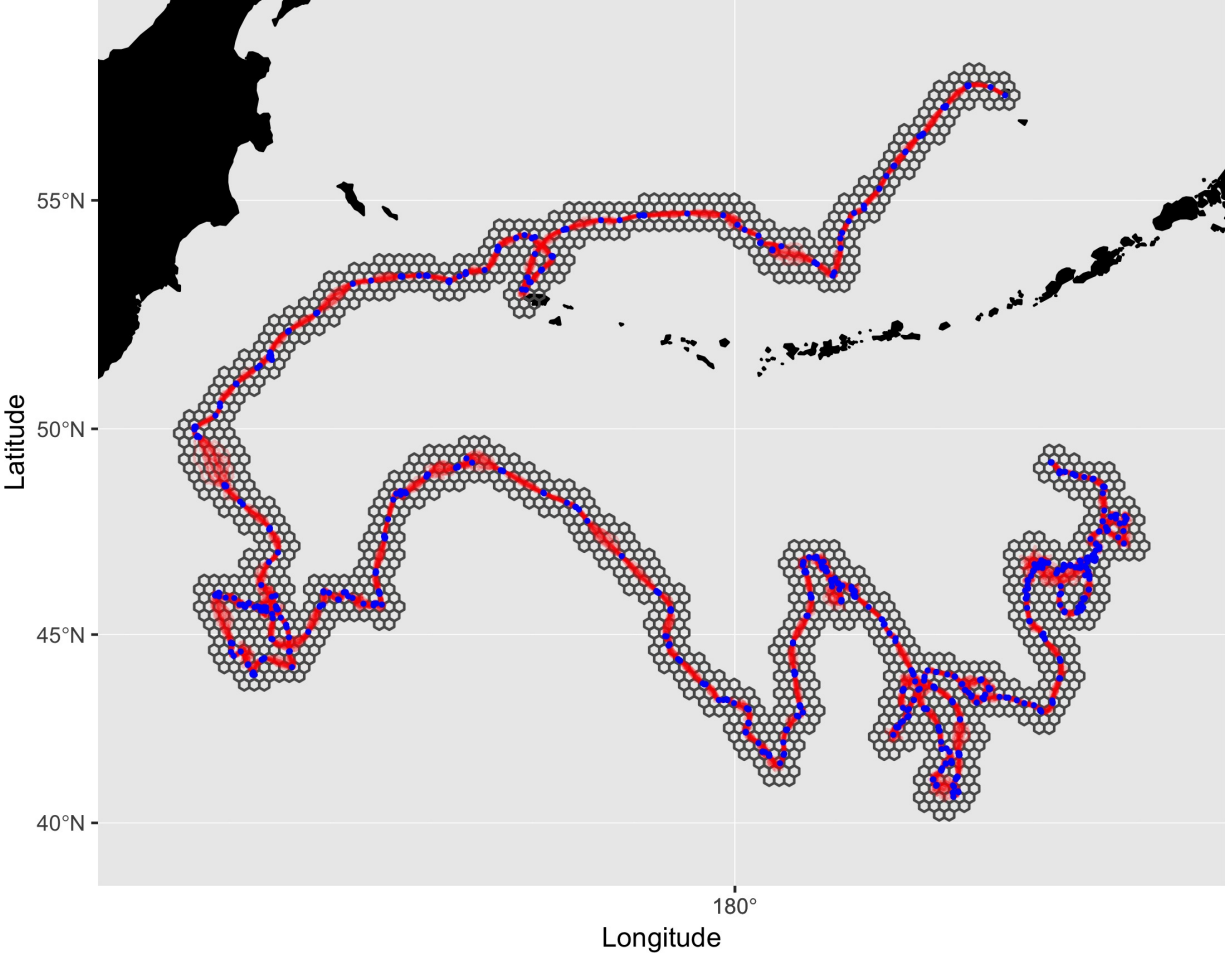
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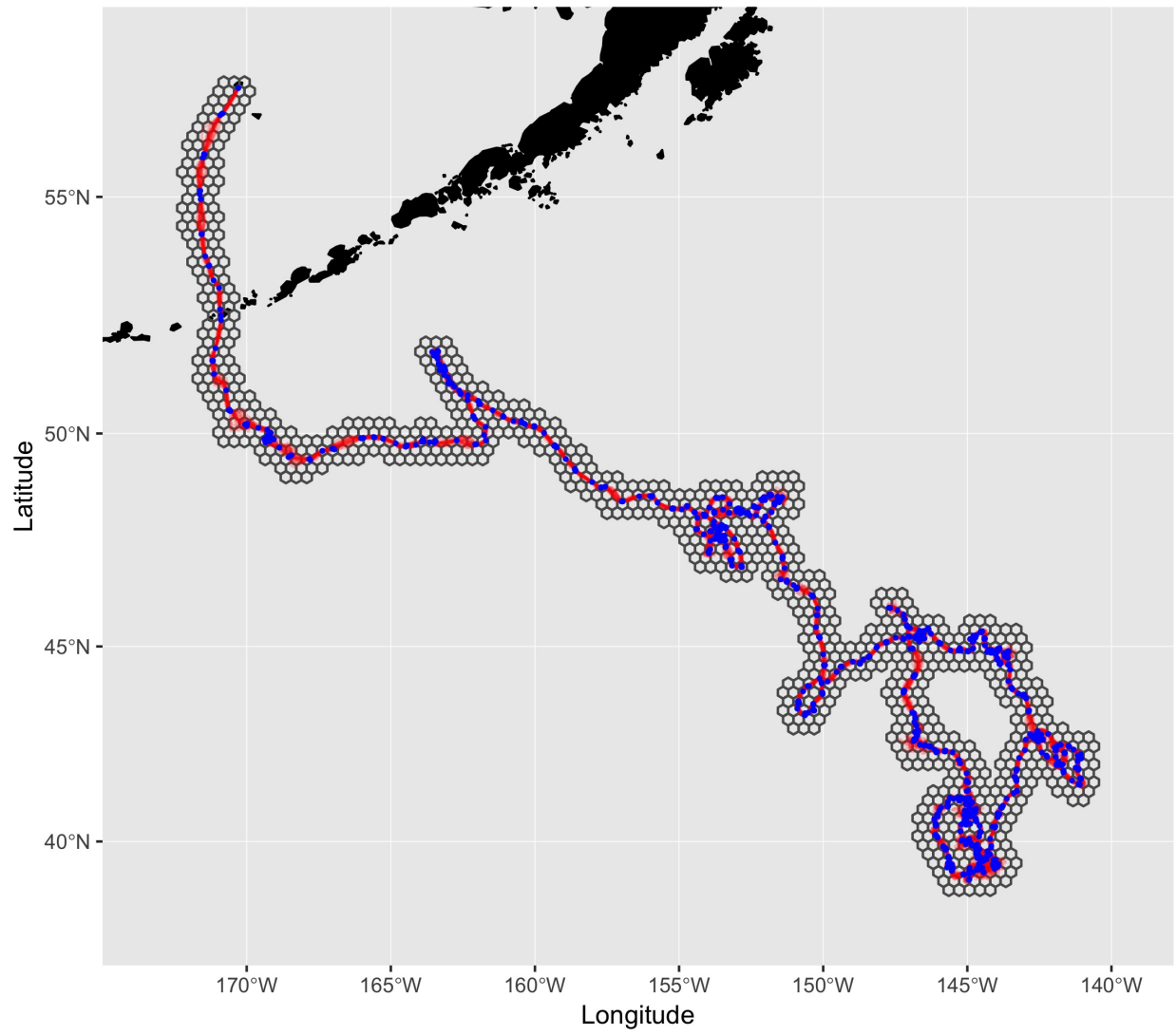
Animal ID: 380



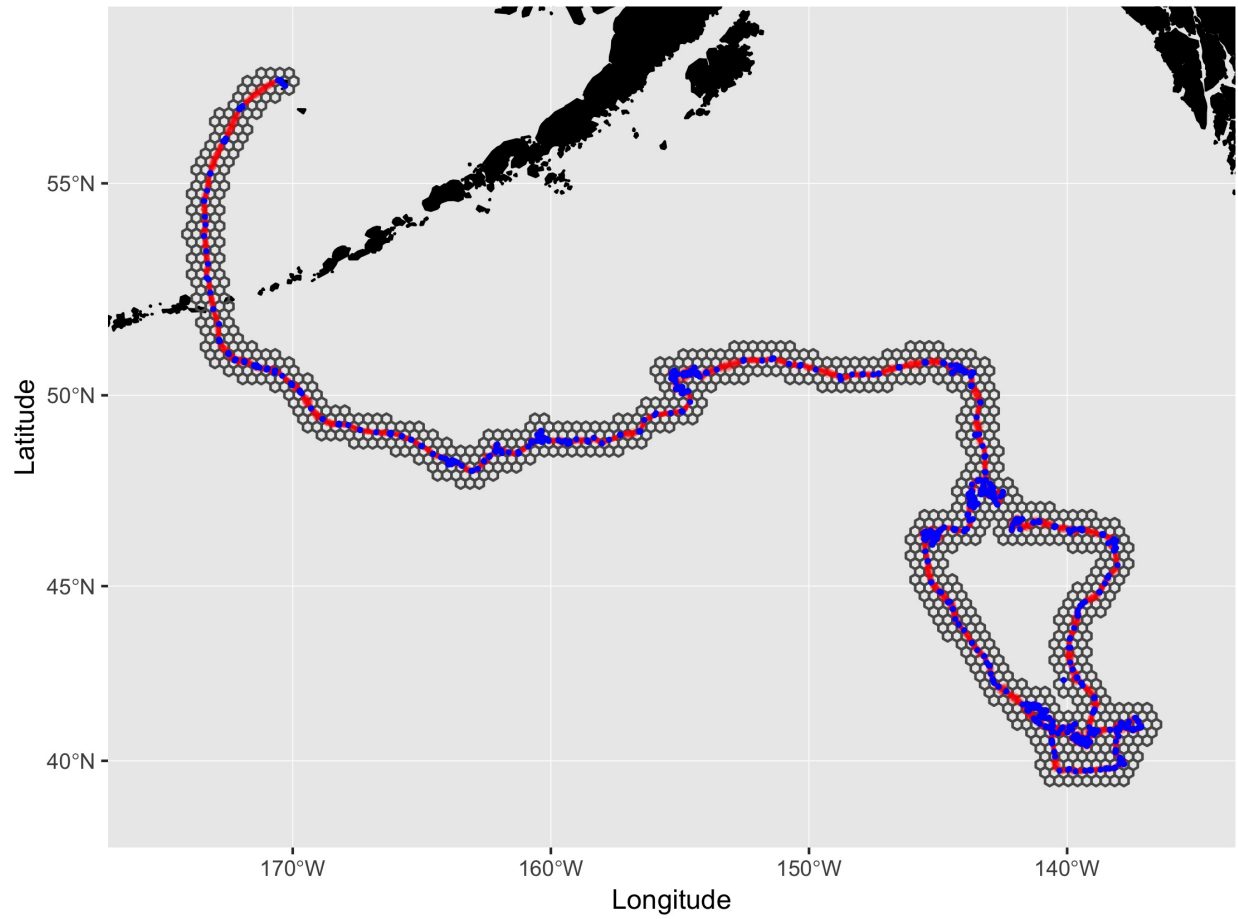
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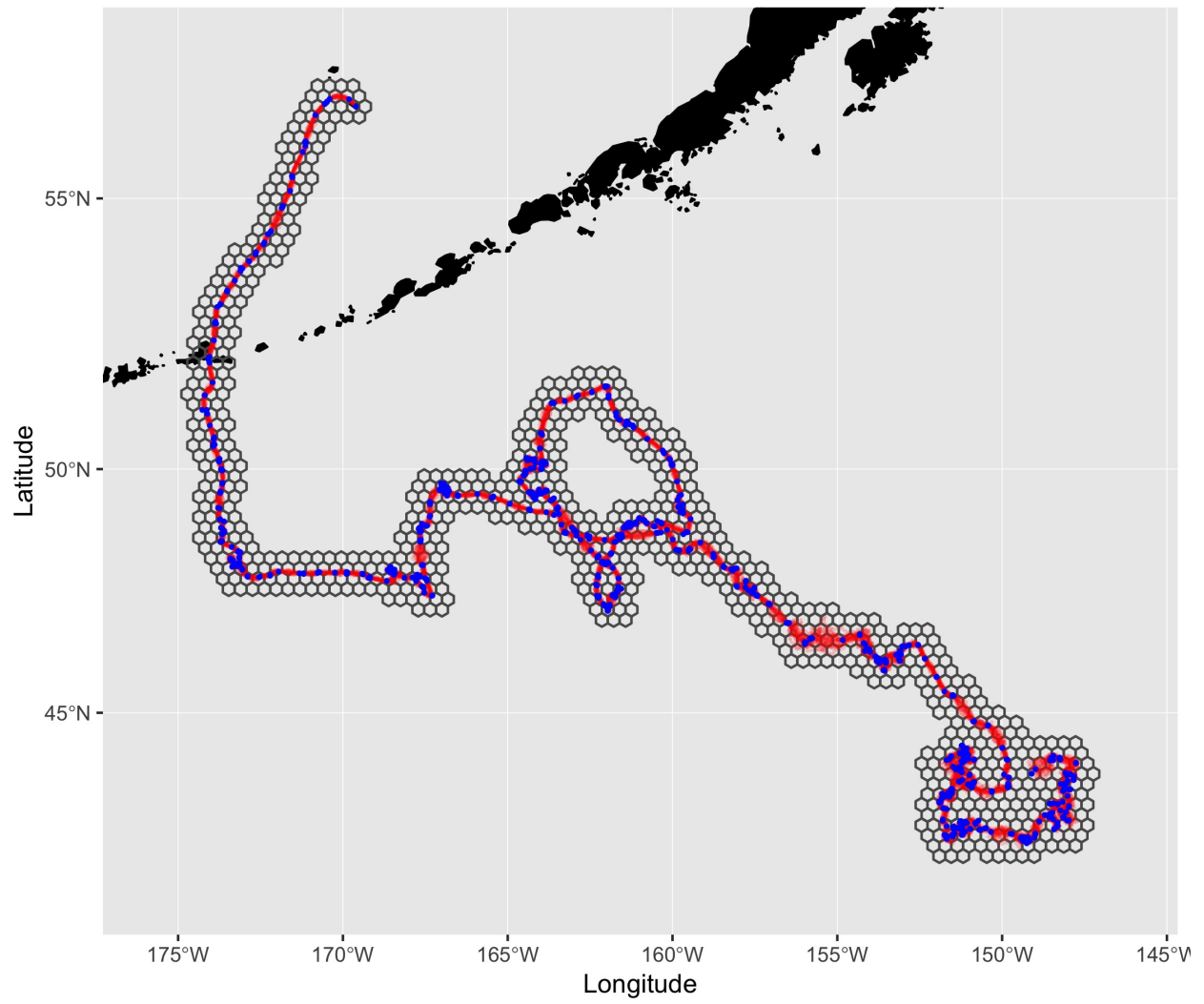
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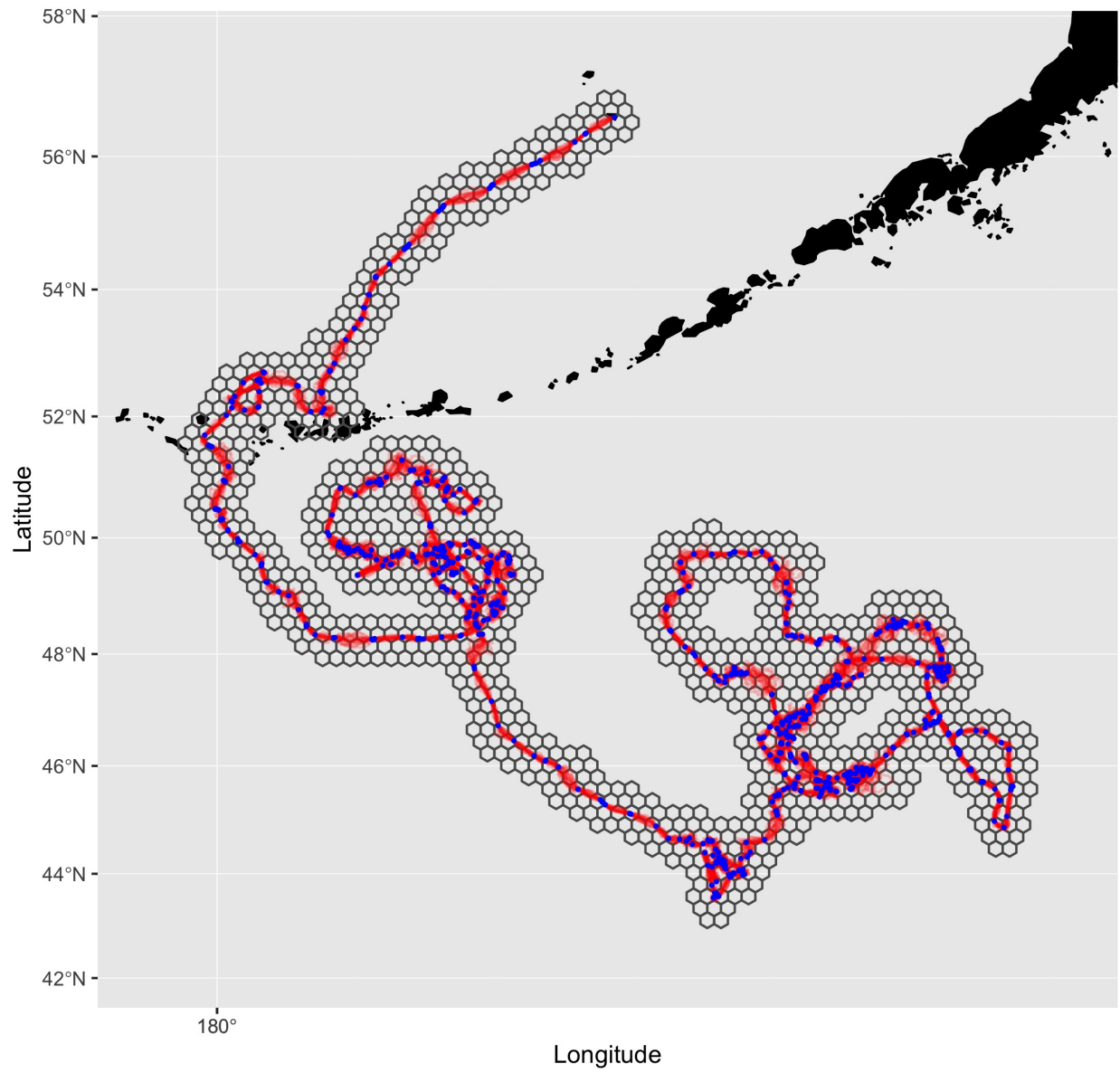
Animal ID: 388



Animal ID: 394



Animal ID: 405



Animal ID: 408

References

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