

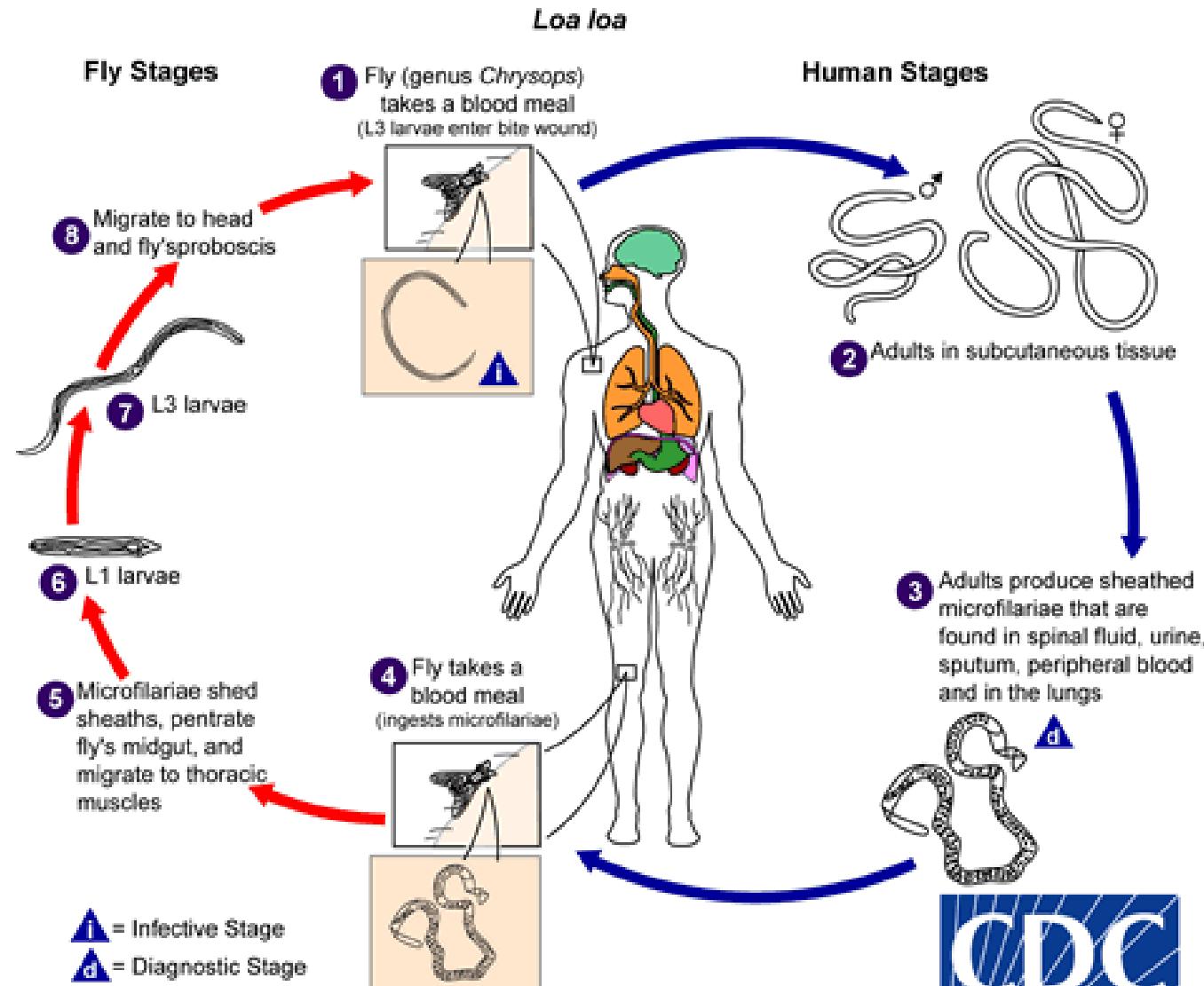
Point referenced data (pt. 2)

Lecture 22

Dr. Colin Rundel

Loa Loa Example

Loa Loa



SAFER • HEALTHIER • PEOPLE™

<http://www.dpd.cdc.gov/dpdx>

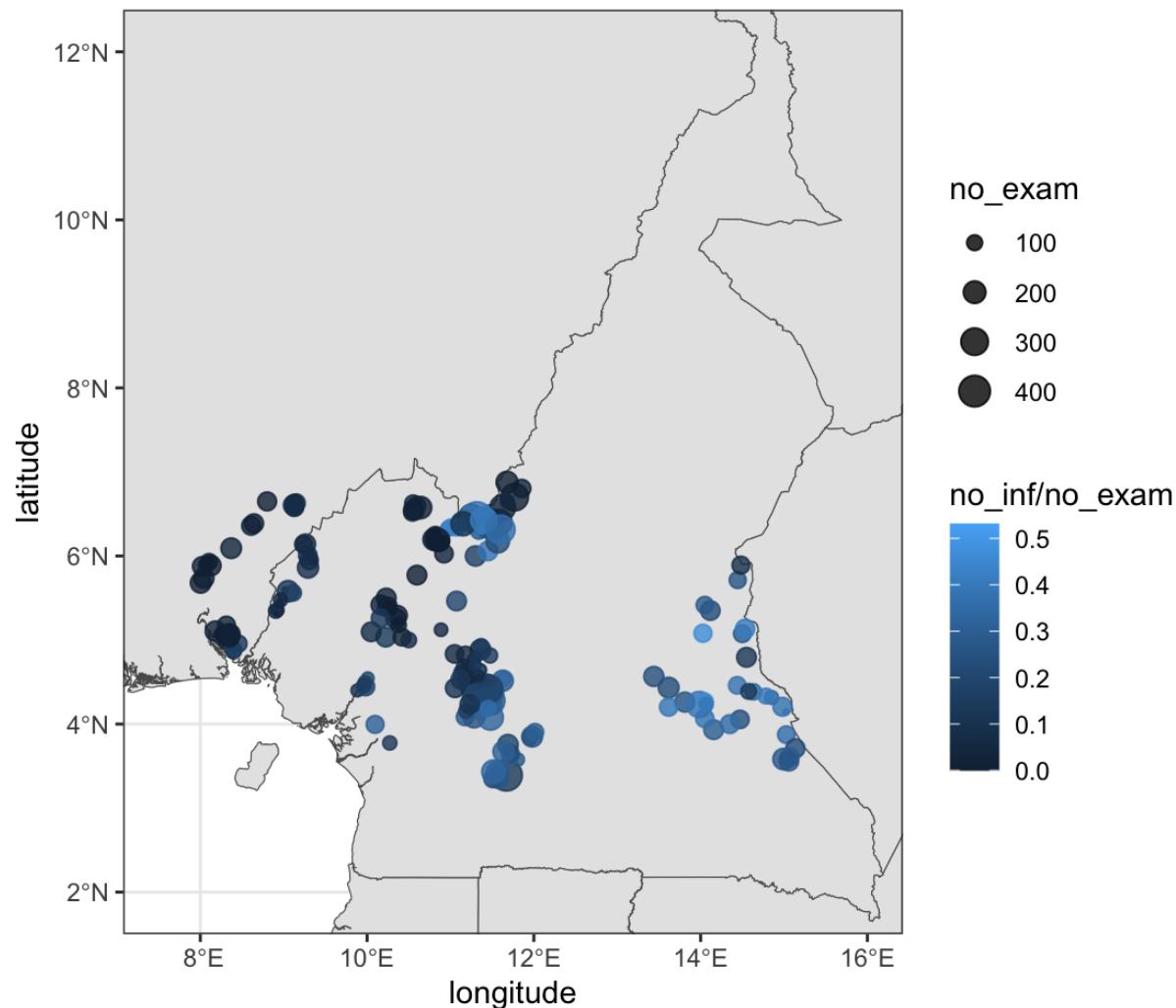
Data

```
1 loaloa = PrevMap::loaloa |>
2   as_tibble() |>
3   (\(x) setNames(x, tolower(names(x))))() |>
4   rename(elev=elevation)
5
6 loaloa
```

A tibble: 197 × 11

	row	villcode	longitude	latitude	no_exam	no_inf	elev	mean9901
	<int>	<int>	<dbl>	<dbl>	<int>	<int>	<int>	<dbl>
1	1	214	8.04	5.74	162	0	108	0.439
2	2	215	8.00	5.68	167	1	99	0.426
3	3	118	8.91	5.35	88	5	783	0.491
4	4	219	8.10	5.92	62	5	104	0.432
5	5	212	8.18	5.10	167	3	109	0.415
6	6	116	8.93	5.36	66	3	909	0.436
7	7	16	11.4	4.88	163	11	503	0.502
8	8	217	8.07	5.90	83	0	103	0.373
9	9	112	9.02	5.59	30	4	751	0.481
10	10	104	9.31	6.00	57	4	268	0.487
	# i	187 more rows						
	# i	3 more variables:	max9901 <dbl>, min9901 <dbl>, stdev9901 <dbl>					

Spatial Distribution



Normalized Difference Vegetation Index (NDVI)

Paper / Data summary

Original paper - Diggle, et. al. (2007). *Spatial modelling and prediction of Loa loa risk: decision making under uncertainty*. Annals of Tropical Medicine and Parasitology, 101, 499-509.

- `no_exam` and `no_inf` - Collected between 1991 and 2001 by NGOs (original paper mentions 168 villages and 21,938 observations)
- `elev` - USGS gtopo30 (1km resolution)
- `mean9901` to `stdev9901` - aggregated data from 1999 to 2001 from the Flemish Institute for Technological Research (1 km resolution)

Diggle's Model

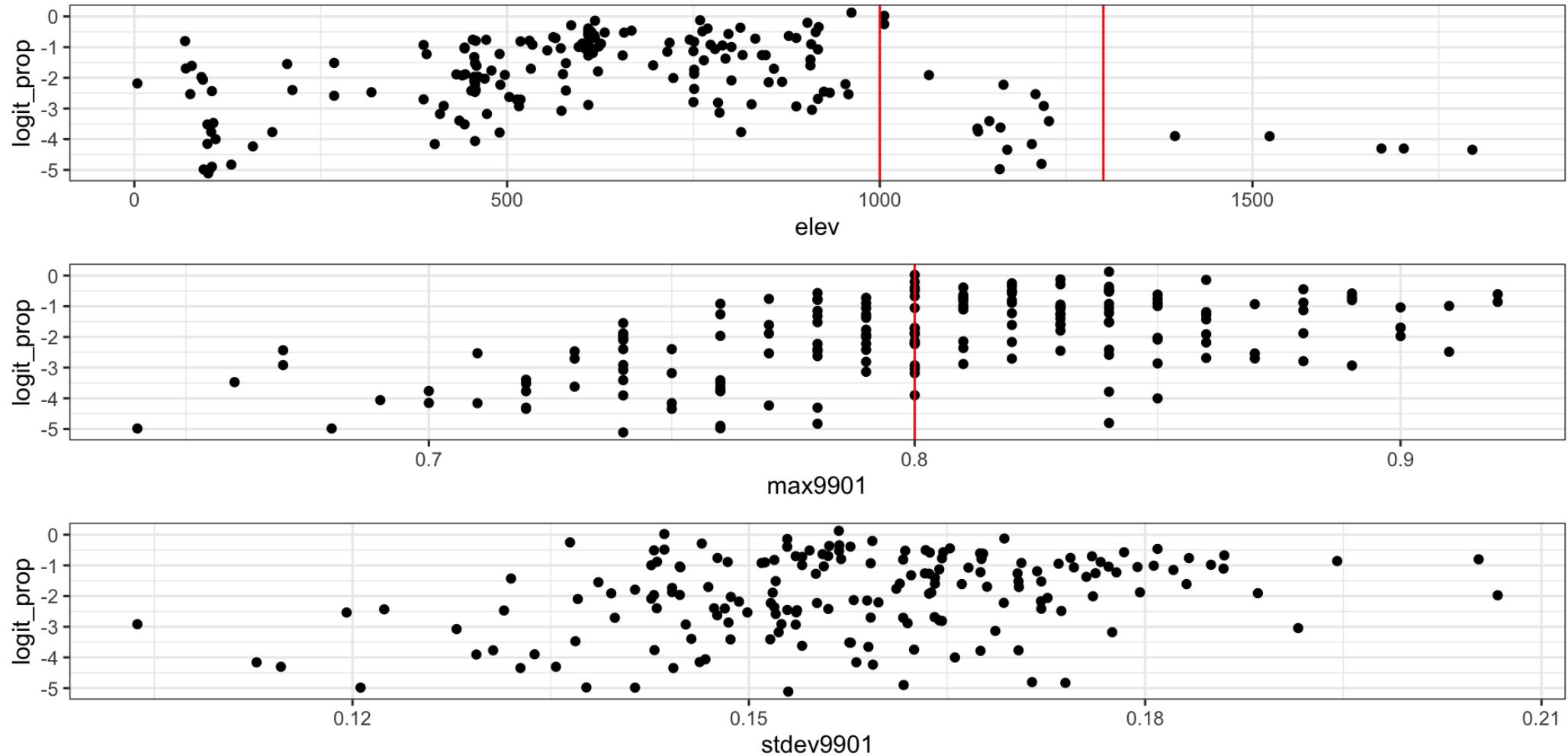
$$\begin{aligned}\log\left(\frac{p(s)}{1-p(s)}\right) = & \alpha + f_1(\text{elev}(s)) \\ & + f_2(\text{MAX.NDVI}(s)) \\ & + f_3(\text{SD.NDVI}(s)) + w(s)\end{aligned}$$

where

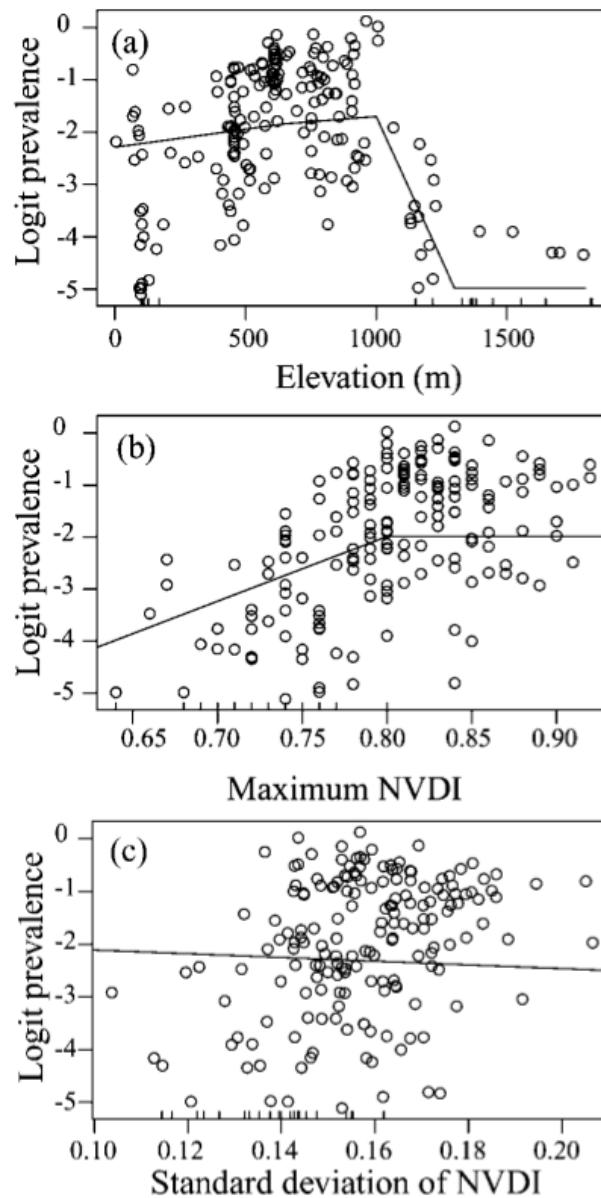
$$w(s) \sim N(0, \Sigma)$$

$$\{\Sigma\}_{ij} = \sigma^2 \exp(-d \phi)$$

EDA



Diggle's EDA



Feature engineering

```
1 loaloa = loaloa |>  
2   mutate(  
3     elev_f = cut(elev, breaks=c(0,1000,1300,2000), dig.lab=5),  
4     max_f  = cut(max9901, breaks=c(0,0.8,1))  
5   )  
6 loaloa |> select(elev, elev_f, max9901, max_f)
```

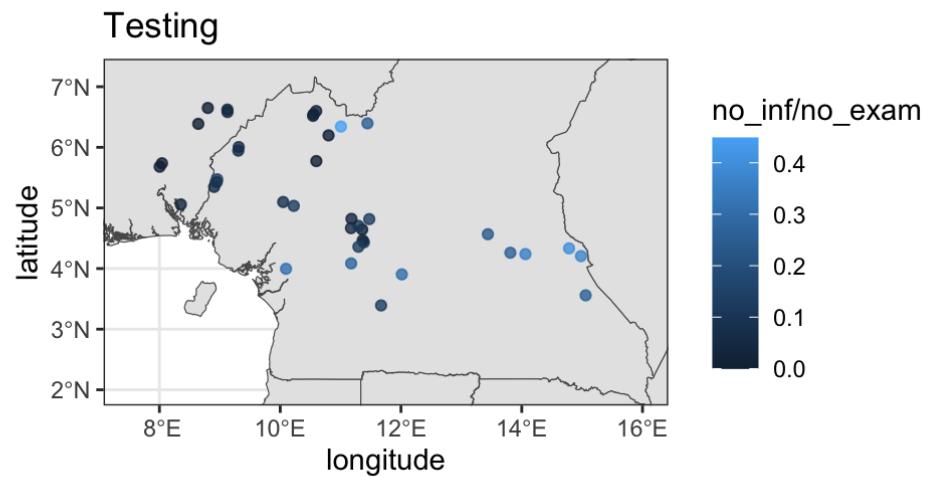
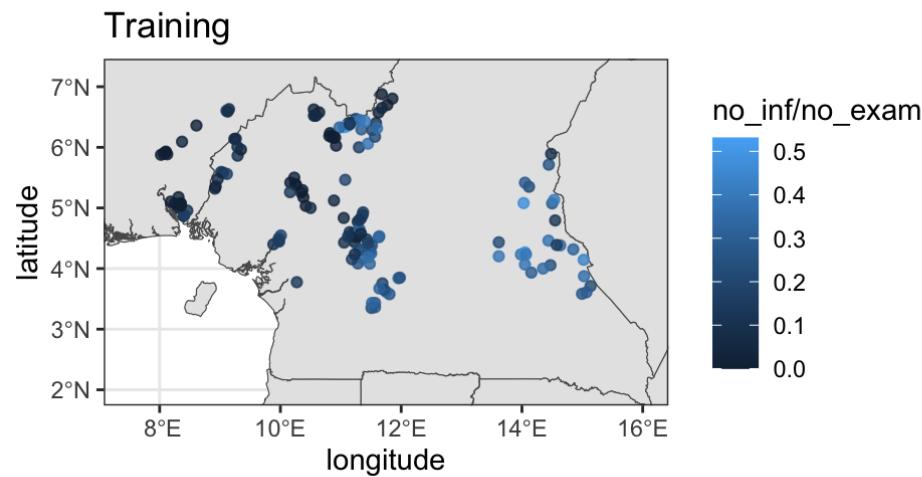
```
# A tibble: 197 × 4  
  elev elev_f    max9901 max_f  
  <int> <fct>      <dbl> <fct>  
1 108 (0,1000]    0.69 (0,0.8]  
2 99 (0,1000]     0.74 (0,0.8]  
3 783 (0,1000]    0.79 (0,0.8]  
4 104 (0,1000]    0.67 (0,0.8]  
5 109 (0,1000]    0.85 (0.8,1]  
6 909 (0,1000]    0.8 (0,0.8]  
7 503 (0,1000]    0.78 (0,0.8]  
8 103 (0,1000]    0.69 (0,0.8]  
9 751 (0,1000]    0.8 (0,0.8]  
10 268 (0,1000]   0.84 (0.8,1]  
# i 187 more rows
```

Model Matrix

```
1 model.matrix(  
2   ~ elev:elev_f - 1,  
3   data = loaloa  
4 ) |>  
5 as_tibble()  
  
# A tibble: 197 × 3  
#> `elev:elev_f(0,1000)` elev:elev_f(1000,1300)` elev:elev_f(1300,2000)`  
#> <dbl> <dbl> <dbl>  
#> 1 108 0 0  
#> 2 99 0 0  
#> 3 783 0 0  
#> 4 104 0 0  
#> 5 109 0 0  
#> 6 909 0 0  
#> 7 503 0 0  
#> 8 103 0 0  
#> 9 751 0 0  
#> 10 268 0 0  
#> # i 187 more rows  
#> # i abbreviated names: `elev:elev_f(1000,1300)`,  
#> # `elev:elev_f(1300,2000)`
```

OOS Validation

```
1 set.seed(12345)
2 loaloa_test = loaloa |> slice_sample(prop=0.20)
3 loaloa = anti_join(loaloa, loaloa_test, by="row")
```



Model

```
1 g = glm(no_inf/no_exam ~ elev:elev_f + max9901:max_f + stdev9901,  
2           data=loaloa, family=binomial, weights=loaloa$no_exam)  
3 summary(g)
```

Call:

```
glm(formula = no_inf/no_exam ~ elev:elev_f + max9901:max_f +  
    stdev9901, family = binomial, data = loaloa, weights = loaloa$no_exam)
```

Coefficients:

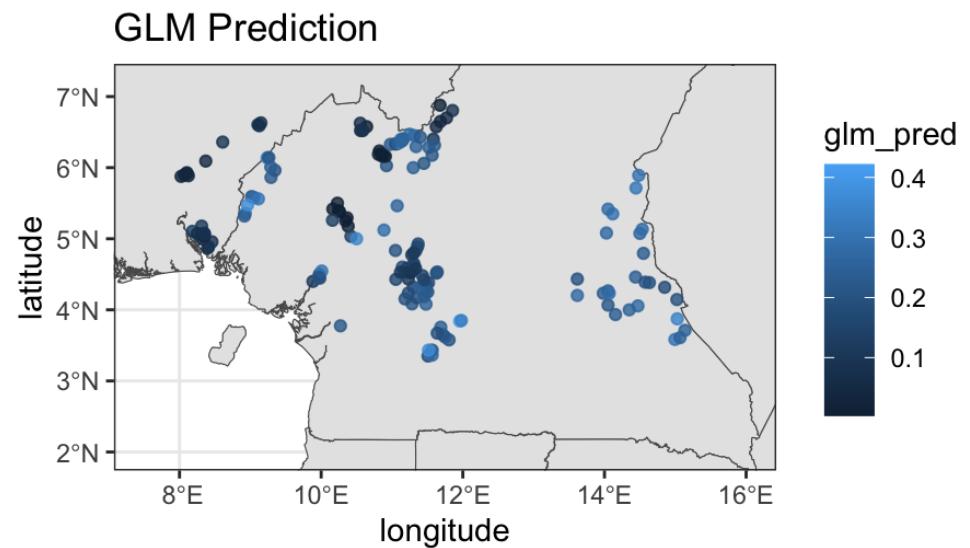
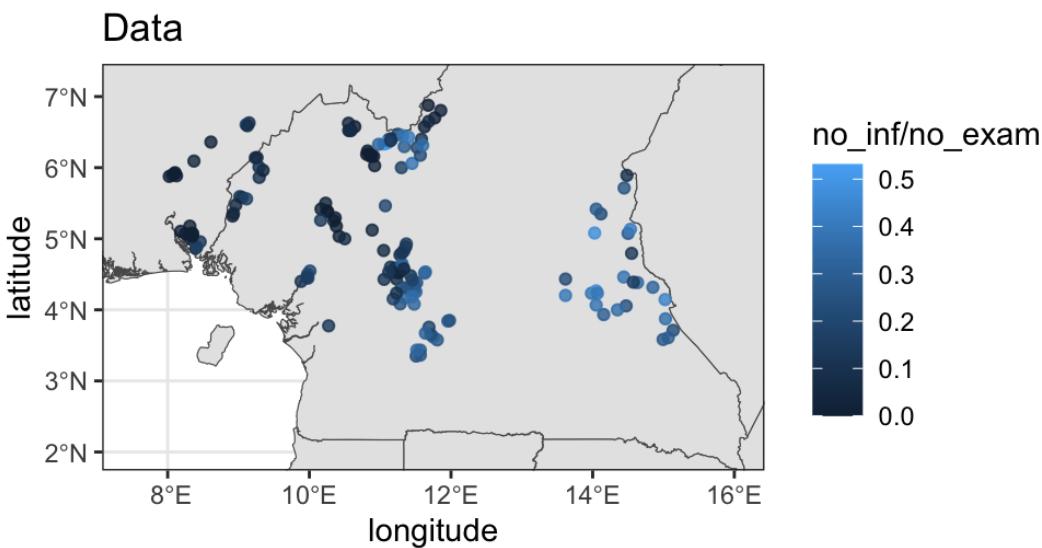
	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-8.537e+00	5.408e-01	-15.785	< 2e-16 ***
stdev9901	6.750e+00	1.449e+00	4.659	3.18e-06 ***
elev:elev_f(0,1000]	1.467e-03	9.481e-05	15.471	< 2e-16 ***
elev:elev_f(1000,1300]	1.940e-04	9.279e-05	2.091	0.0365 *
elev:elev_f(1300,2000]	-1.506e-03	1.912e-04	-7.880	3.29e-15 ***
max9901:max_f(0,0.8]	6.399e+00	6.951e-01	9.207	< 2e-16 ***
max9901:max_f(0.8,1]	6.364e+00	6.387e-01	9.965	< 2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

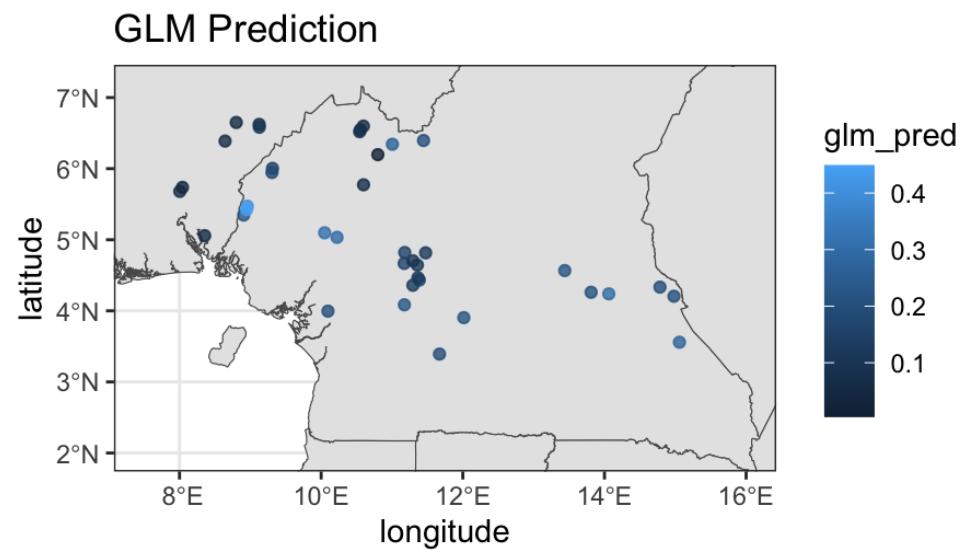
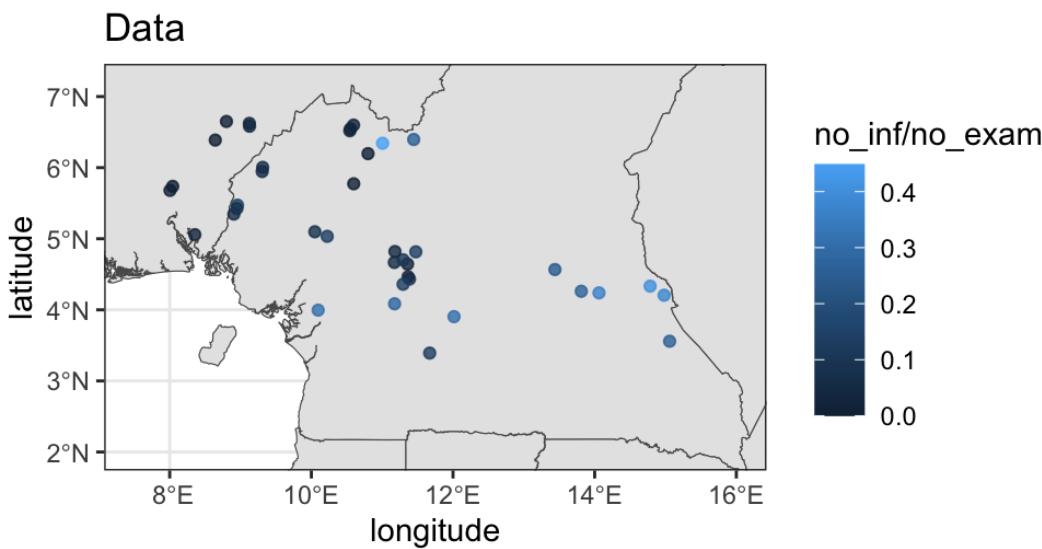
(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 3364.8 on 157 degrees of freedom  
Residual deviance: 1630.8 on 151 degrees of freedom
```

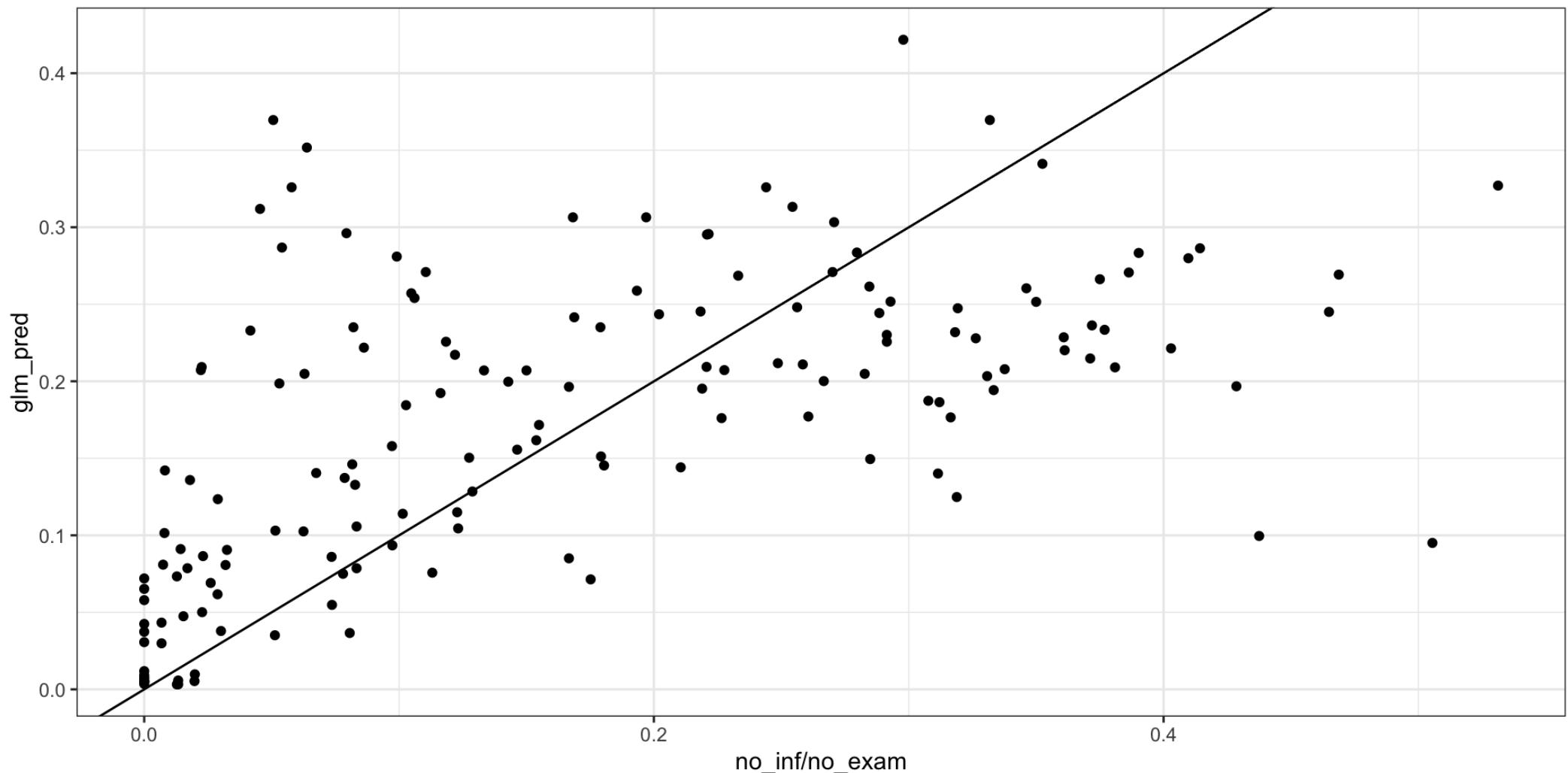
Predictions - Training



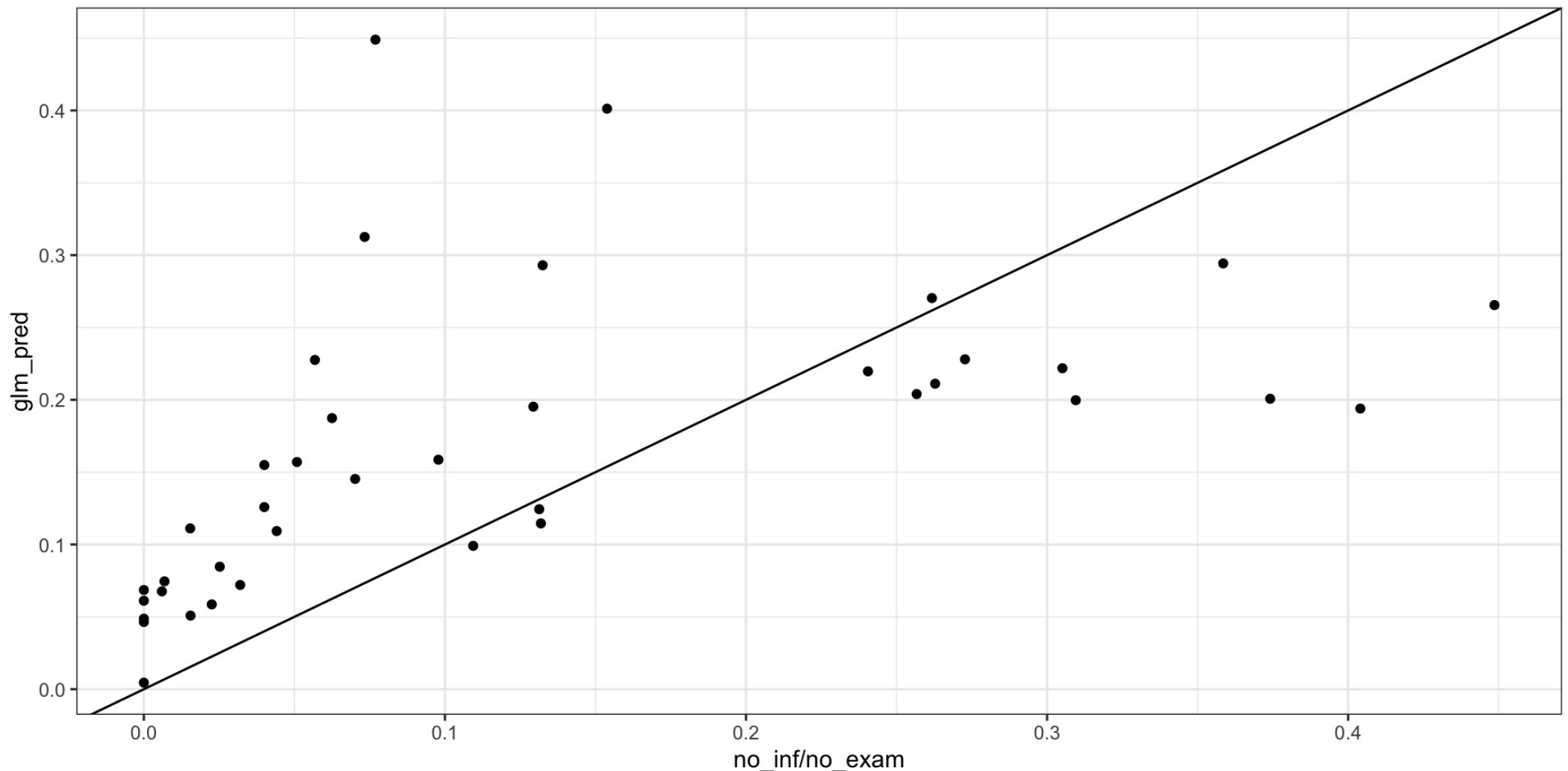
Predictions - Testing



Fit - Training



Fit - Testing



Fit - RMSE

Training

```
1 yardstick::rmse_vec(loaloa$no_inf/loaloa$no_exam, loaloa$glm_pred)  
[1] 0.111176
```

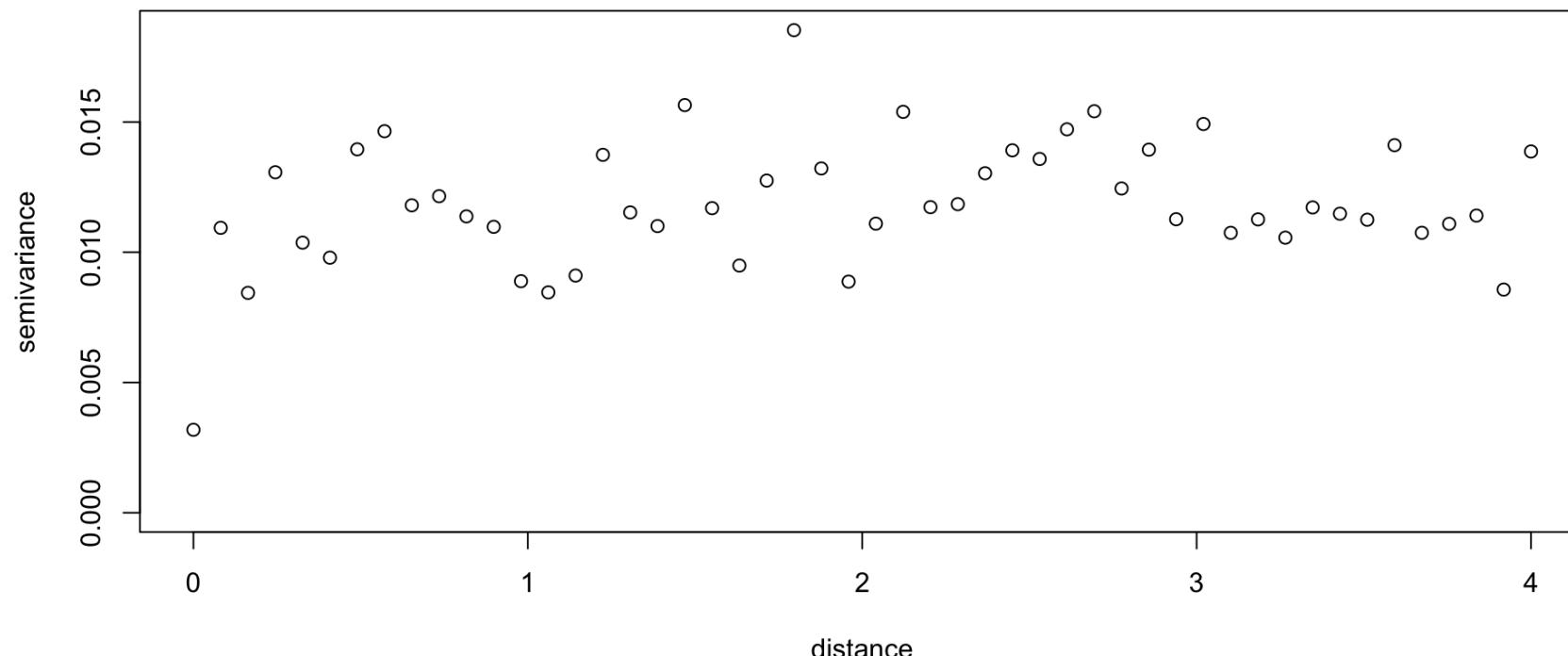
Testing

```
1 yardstick::rmse_vec(loaloa_test$no_inf/loaloa_test$no_exam, loaloa_test$glm_pred)  
[1] 0.1192507
```

Spatial Structure?

```
1 geoR:::variog(coords = cbind(loaloa$longitude, loaloa$latitude),  
2 data = loaloa$prop - loaloa$glm_pred,  
3 uvec = seq(0, 4, length.out = 50)) |> plot()
```

variog: computing omnidirectional variogram



gpglm model

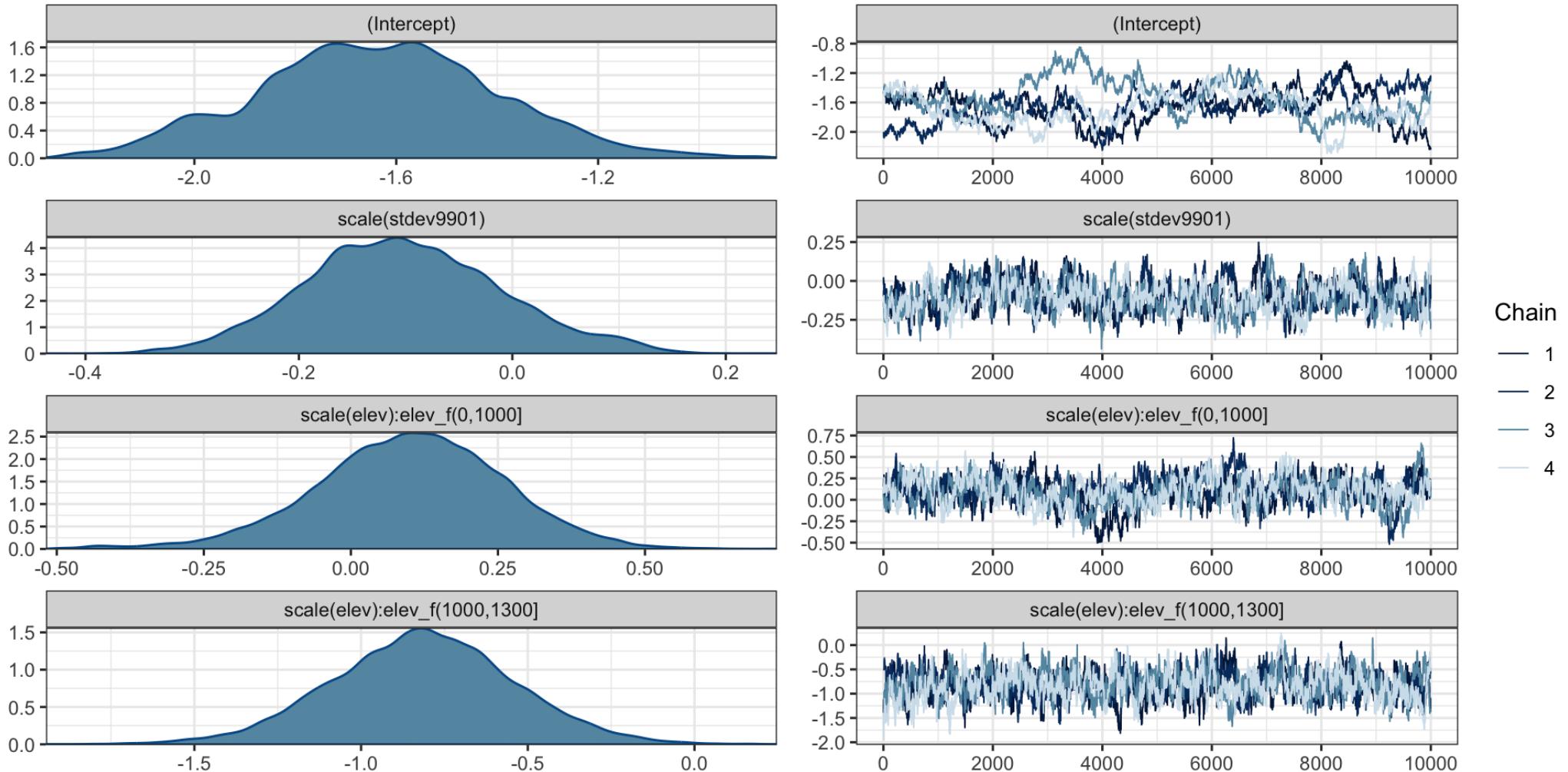
```
1 ll_gp = gpglm(
2   no_inf ~ scale(elev):elev_f + scale(max9901):max_f + scale(stdev9901),
3   data = loaloa, family="binomial", weights=loaloa$no_exam,
4   coords = c("longitude", "latitude"),
5   cov_model="exponential",
6   starting = list(
7     beta=rep(0,7),
8     phi=3, sigma.sq=1, w=0
9   ),
10  priors = list(
11    beta.Normal=list(rep(0,7), rep(10,7)),
12    phi.unif=c(3/4, 3/0.25), sigma.sq.ig=c(2, 2)
13  ),
14  tuning = list(
15    "beta"=rep(0.1, 7),
16    "phi"=0.6, "sigma.sq"=0.3, "w"=0.1
17  ),
18  n_batch = 400,
19  batch_len = 50,
20  verbose = TRUE,
21  n_report = 10,
22  chains=4
```

```
1 11_gp
```

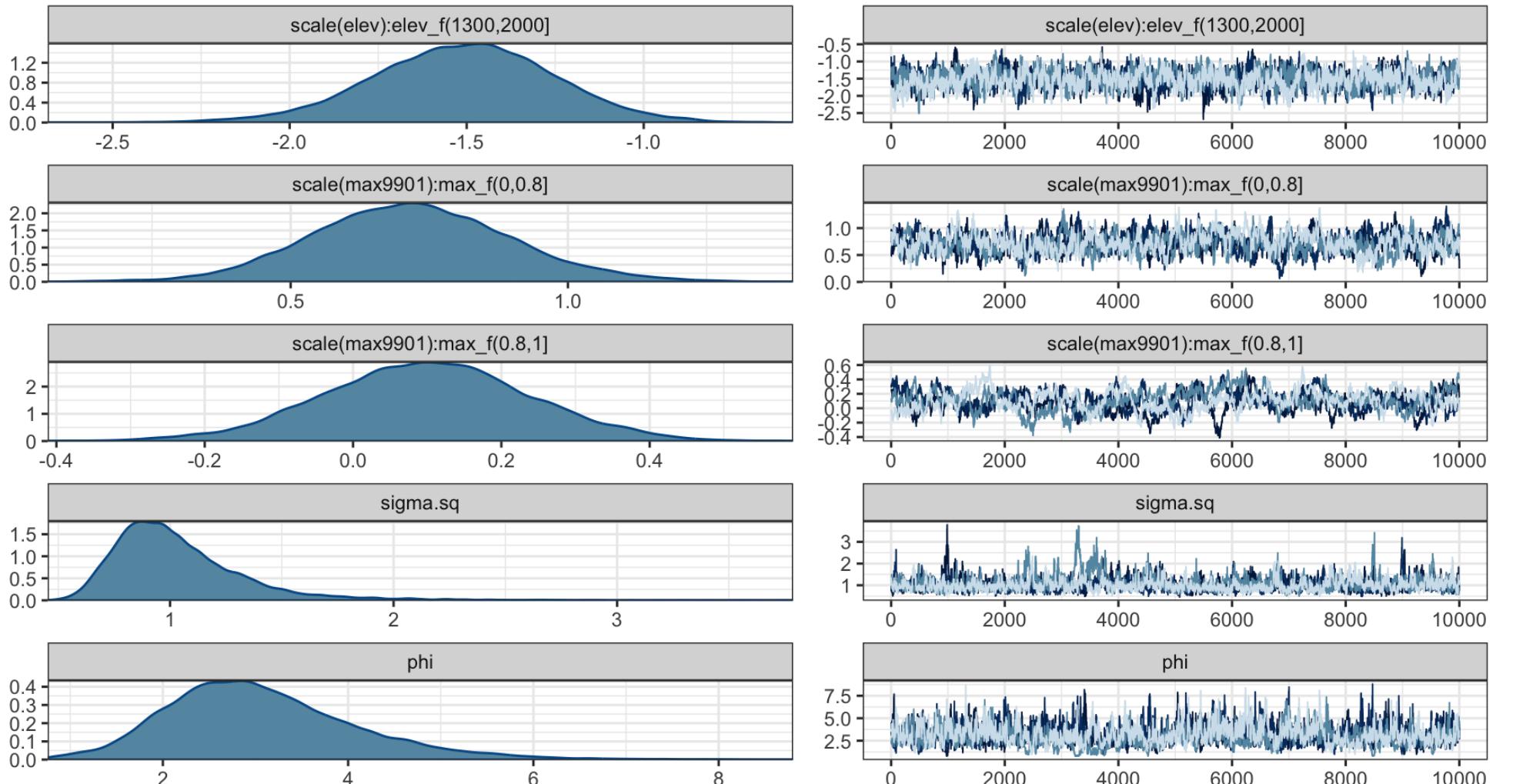
```
# A gpglm model (spBayes spGLM) with 4 chains, 9 variables, and 80000 iterations.
# A tibble: 9 × 10
  variable      mean   median     sd    mad     q5     q95   rhat ess_bulk
  <chr>       <dbl>   <dbl>   <dbl>   <dbl>   <dbl>   <dbl> <dbl>   <dbl>
1 (Interce... -1.64   -1.64   0.237  0.234  -2.03  -1.24   1.15   22.1
2 scale(st... -0.101  -0.105  0.0914 0.0916 -0.248  0.0573  1.01   299.
3 scale(el...  0.0992  0.104   0.160  0.154  -0.170  0.352   1.02   127.
4 scale(el... -0.815  -0.813  0.274  0.265  -1.27  -0.363  1.01   378.
5 scale(el... -1.51   -1.50   0.257  0.254  -1.94  -1.10   1.01   534.
6 scale(ma...  0.718   0.715  0.179  0.176  0.432   1.02   1.01   318.
7 scale(ma...  0.0990  0.100   0.139  0.137  -0.128  0.329   1.03   137.
8 sigma.sq   1.04    0.977  0.306  0.235  0.682   1.58   1.02   221.
9 phi        3.07    2.94   1.03   0.940  1.64    4.95   1.03   178.
# i 1 more variable: ess_tail <dbl>
```

Diagnostics

```
1 vars = colnames(ll_gp$mcmc)  
2 plot(ll_gp, vars=vars[1:4])
```



```
1 plot(ll_gp, vars=vars[5:9])
```

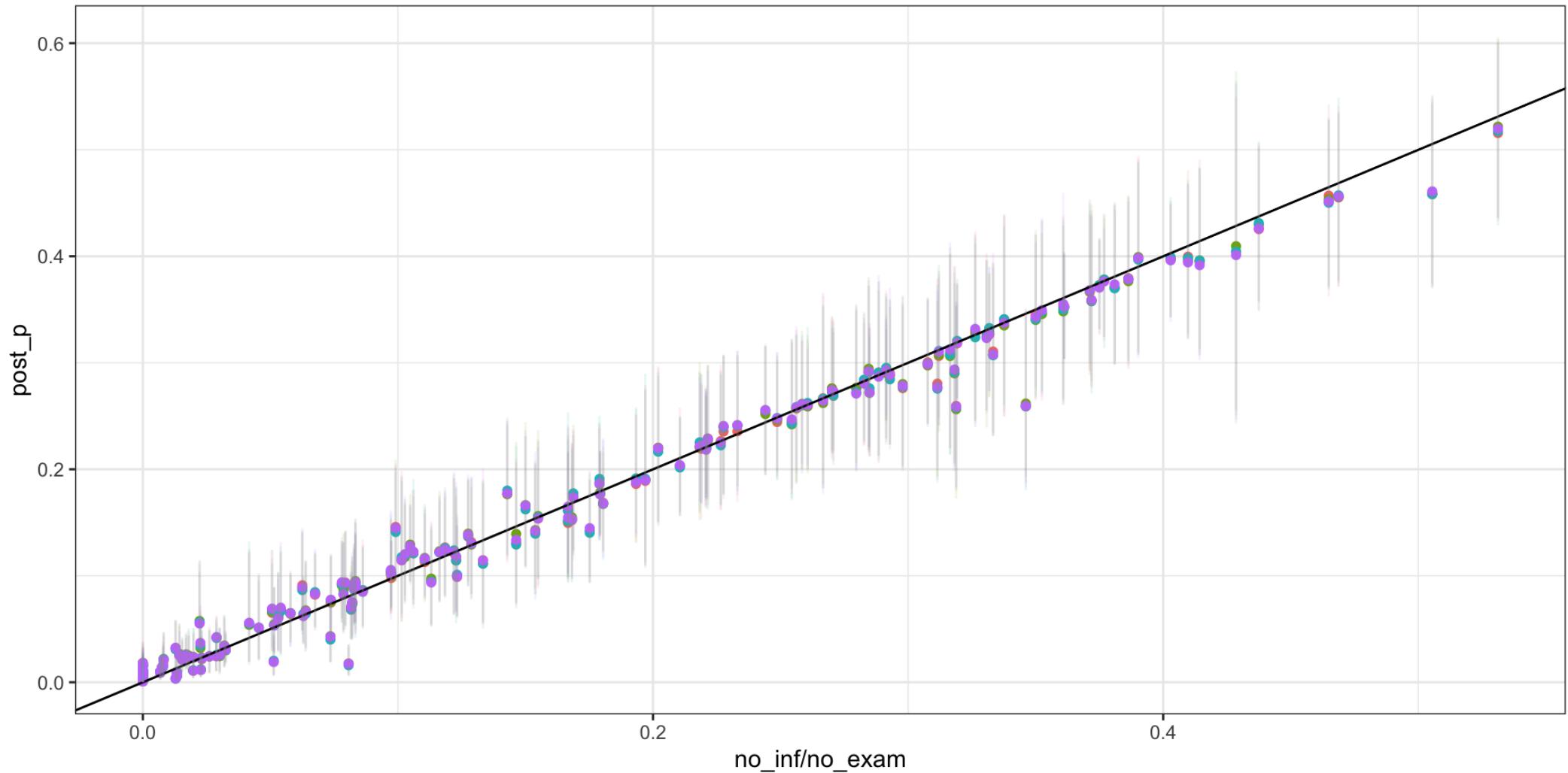


Chain

- 1
- 2
- 3
- 4

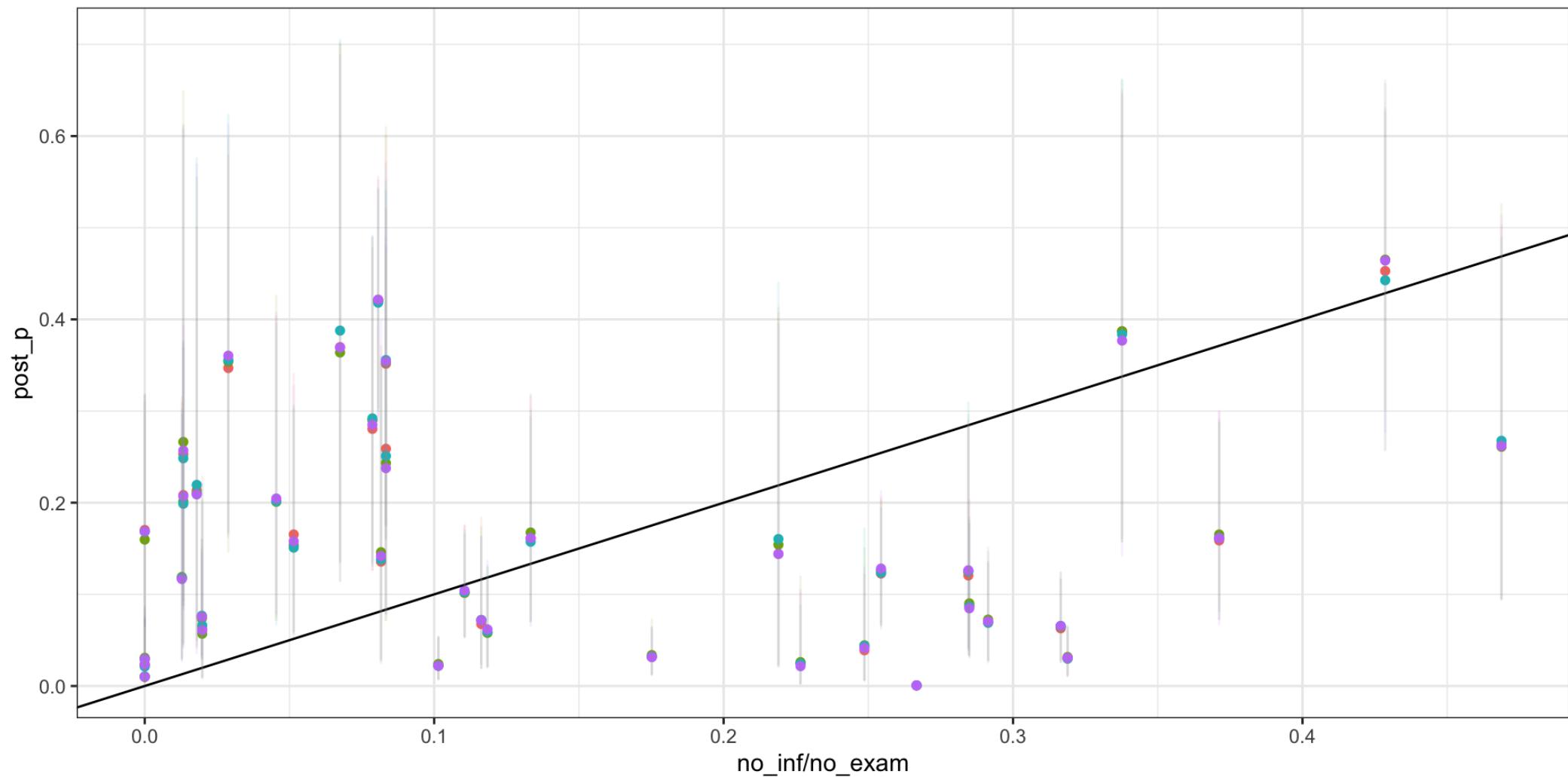
Prediction (training)

```
1 ll_gp_pred = predict(  
2   ll_gp,  
3   newdata=loaloa,  
4   coords = c("longitude", "latitude"),  
5   thin = 25,  
6   verbose=FALSE  
7 )  
8  
9 ll_gp_pred_y = tidybayes::gather_draws(ll_gp_pred, y[i]) |>  
10 group_by(.chain, i) |>  
11 summarize(  
12   post_p = mean(.value),  
13   q025 = quantile(.value, 0.025),  
14   q975 = quantile(.value, 0.975)  
15 )
```



Prediction - Testing

```
1 ll_gp_test_pred = predict(  
2   ll_gp,  
3   newdata=loaloa_test,  
4   coords = c("longitude", "latitude"),  
5   thin = 25,  
6   verbose=FALSE  
7 )  
8  
9 ll_gp_test_pred_y = tidybayes::gather_draws(ll_gp_test_pred, y[i]) |>  
10 group_by(.chain, i) |>  
11 summarize(  
12   post_p = mean(.value),  
13   q025 = quantile(.value, 0.025),  
14   q975 = quantile(.value, 0.975)  
15 )
```



Diggle's Predictive Surface

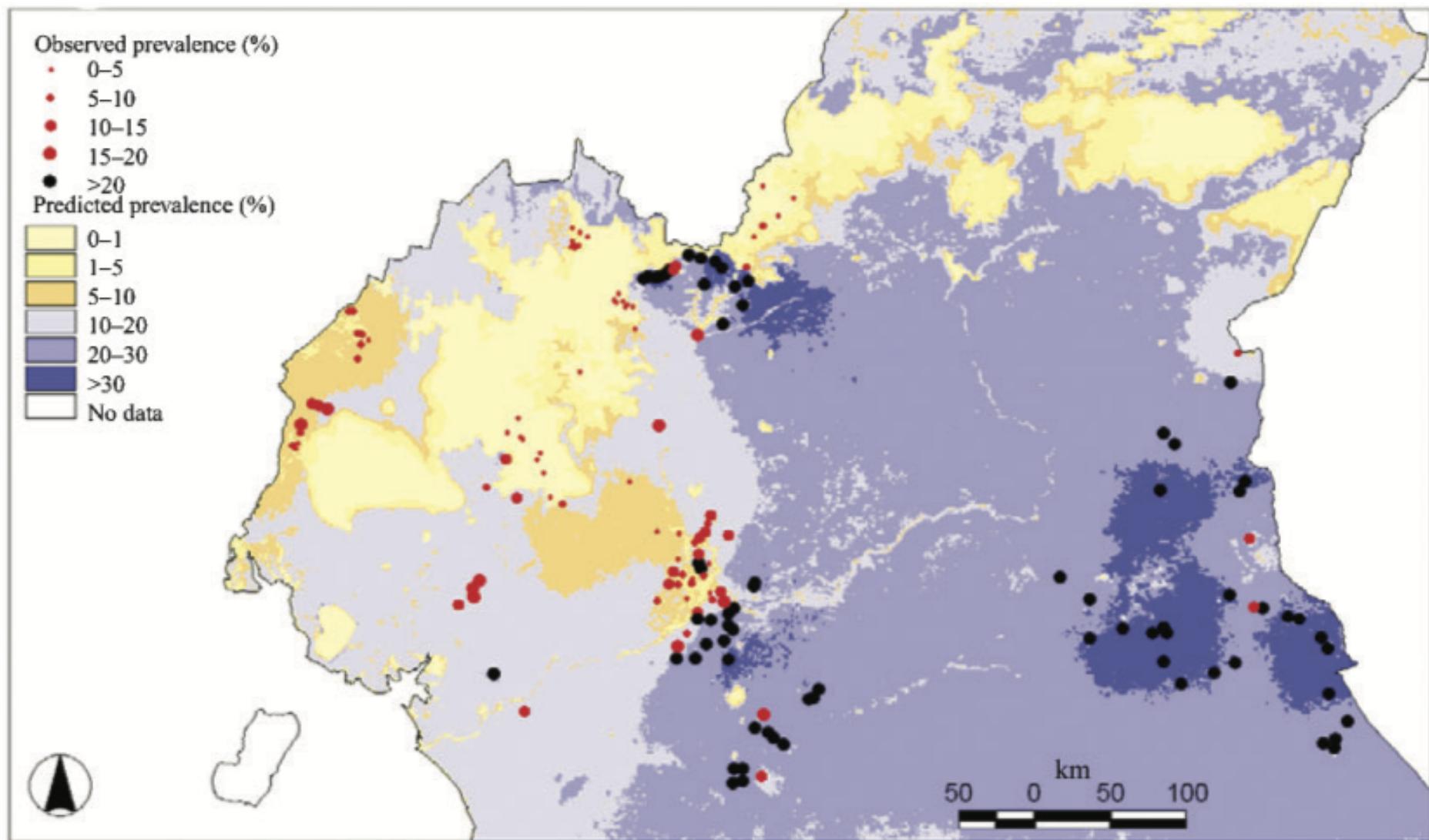
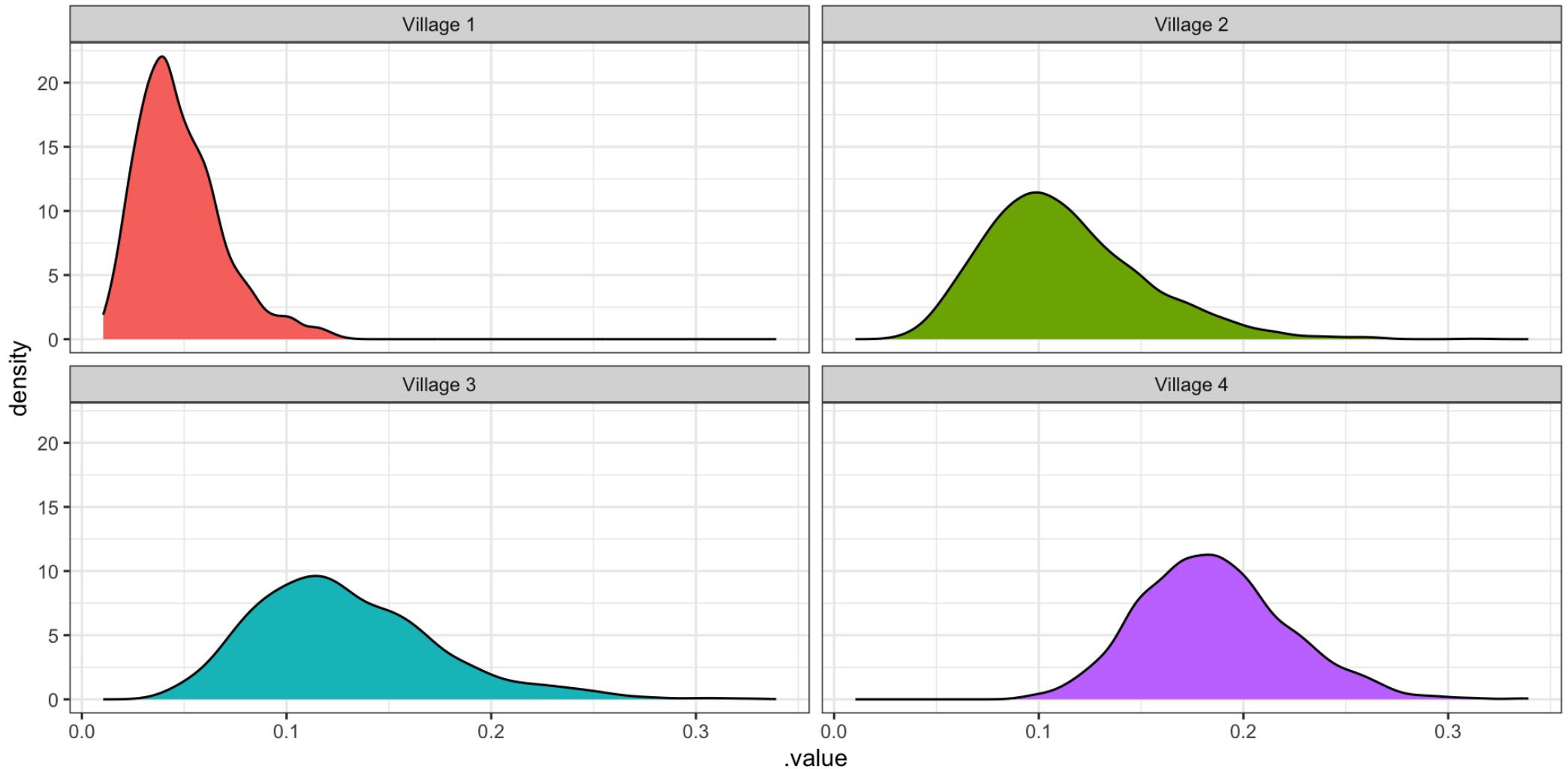


FIG. 2. Point estimates of the prevalence of *Loa loa* microfilaraemia, over-laid with the prevalences observed in field studies.

Exceedance Probability



Exceedance Probability Predictive Surface

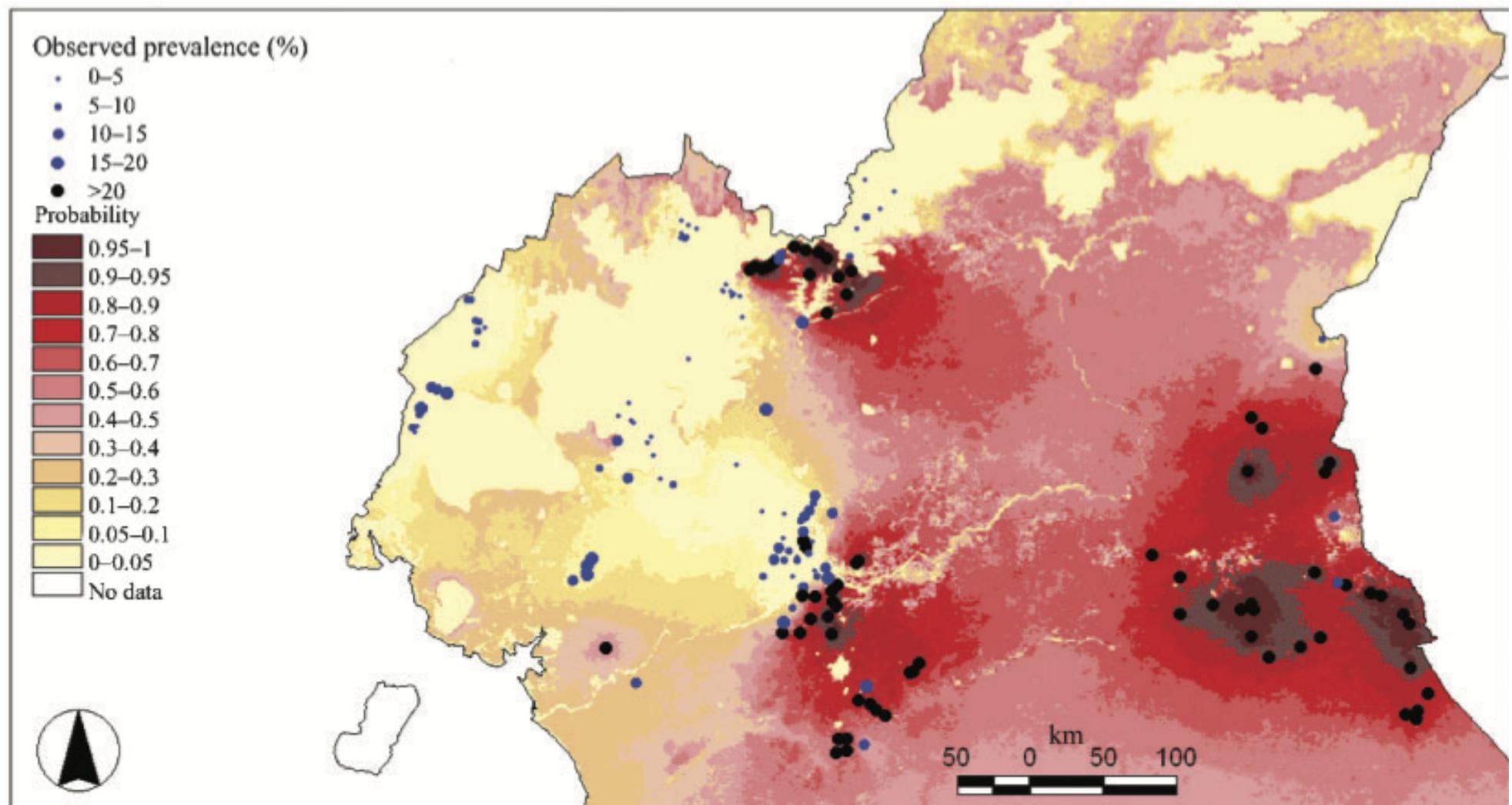


FIG. 4. A probability contour map, indicating the probability that the prevalence of *Loa loa* microfilaraemia in each area exceeds 20%, over-laid with the prevalences observed in field studies.

Spatial Assignment of Migratory Birds

Background

Using intrinsic markers (genetic and isotopic signals) for the purpose of inferring migratory connectivity.

- Existing methods are too coarse for most applications
- Large amounts of data are available (150,000 feather samples from 500 species)
- Genetic assignment methods are based on Wasser, et al. (2004)
- Isotopic assignment methods are based on Wunder, et al. (2005)

Data - DNA microsatellites and $\delta^2\text{H}$

Hermit Thrush
(Catharus guttatus)

138 individuals

14 locations

6 loci

9-27 alleles / locus

Wilson's Warbler
(Wilsonia pusilla)

163 individuals

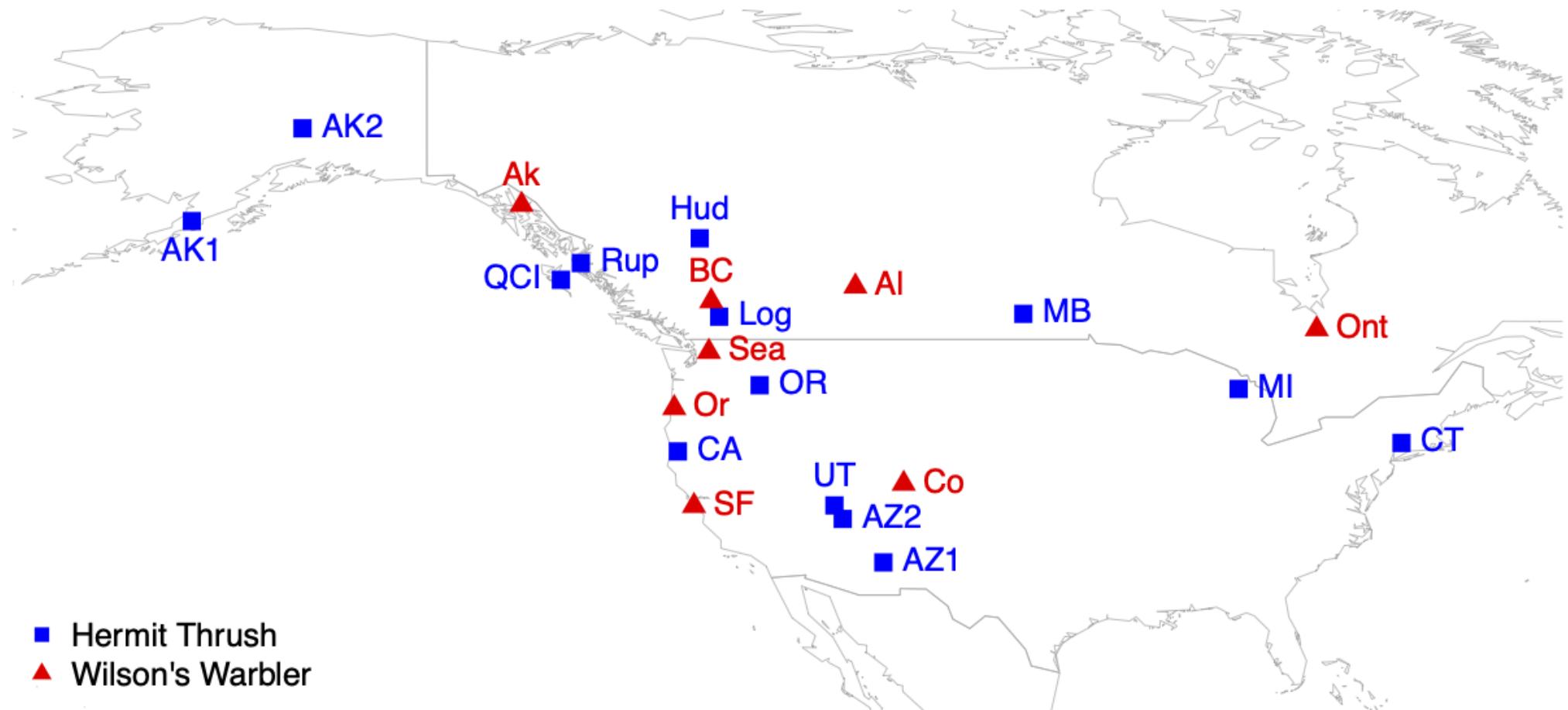
8 locations

9 loci

15-31 alleles / locus



Sampling Locations



Allele Frequency Model

For the allele i , from locus l , at location k

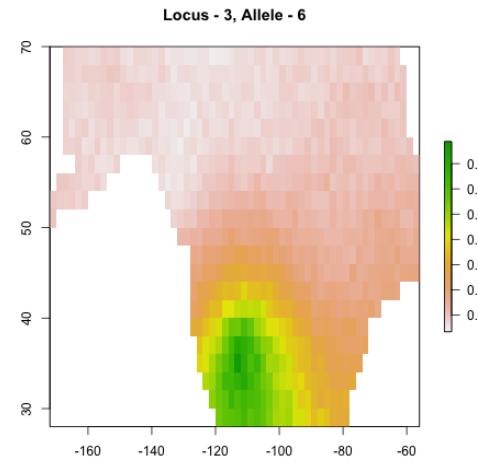
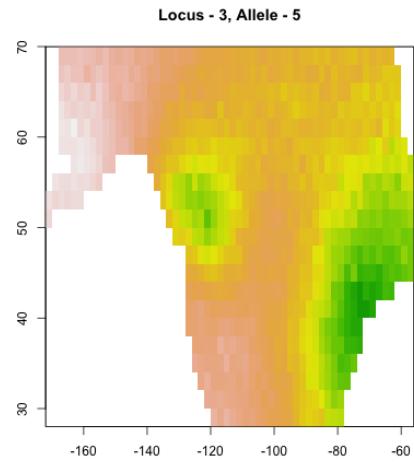
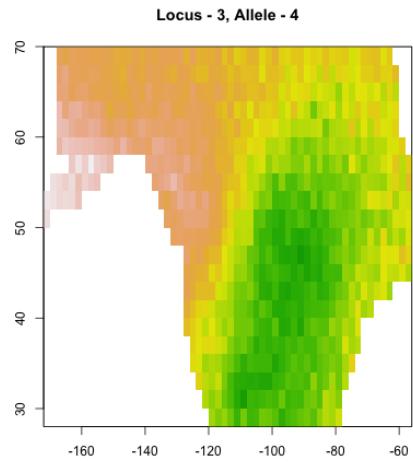
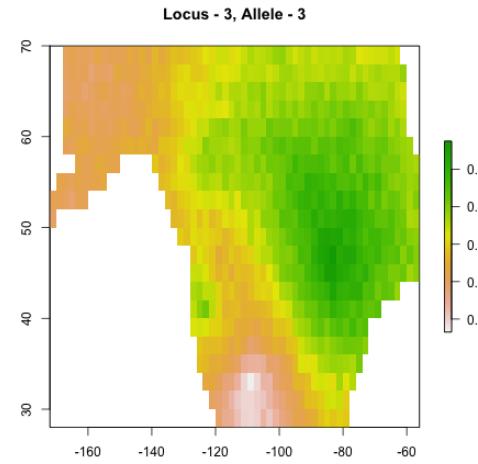
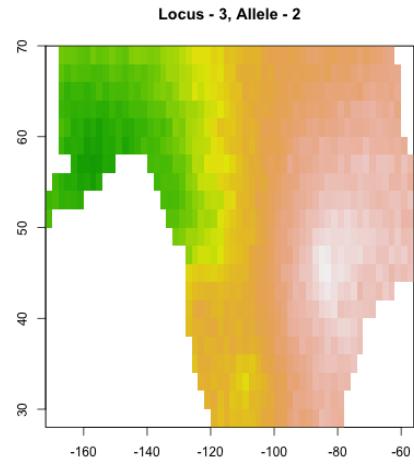
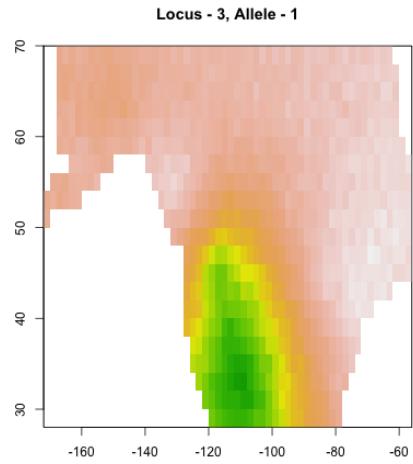
$$y_{\cdot lk} | \Theta \sim N \left(\sum_i y_{ilk}, f_{\cdot lk} \right)$$

$$f_{ilk} = \frac{\exp(\Theta_{ilk})}{\sum_i \exp(\Theta_{ilk})}$$

$$\Theta_{il} | \alpha, \mu \sim N(\mu_{il}, \Sigma)$$

$$\{\Sigma\}_{ij} = \sigma^2 \exp \left(- (\{d\}_{ij} r)^\psi \right) + \sigma_n^2 \mathbf{1}_{i=j}$$

Predictions by Allele (Locus 3)



Genetic Assignment Model

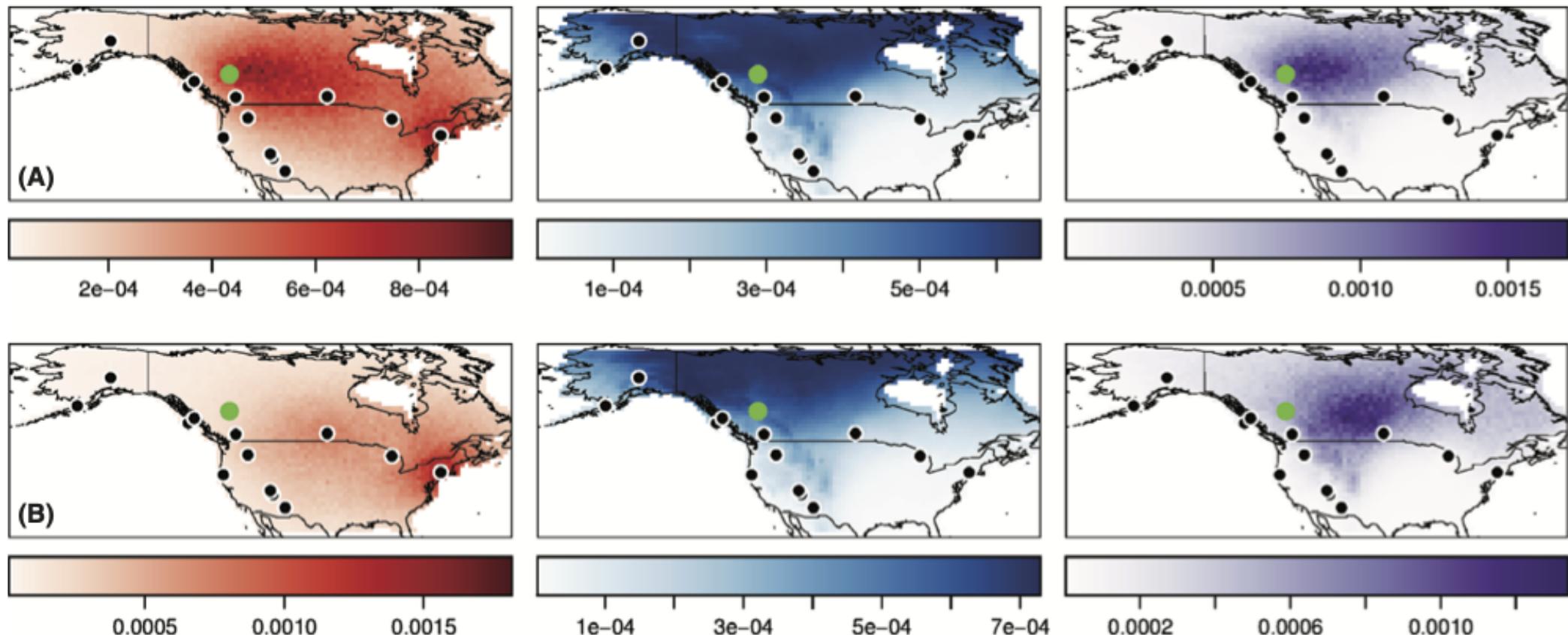
Assignment model assuming Hardy-Weinberg equilibrium and allowing for genotyping (δ) and single amplification (γ) errors.

$$P(S_G | f, k) = \prod_1 P(i_l, j_l | f, k)$$

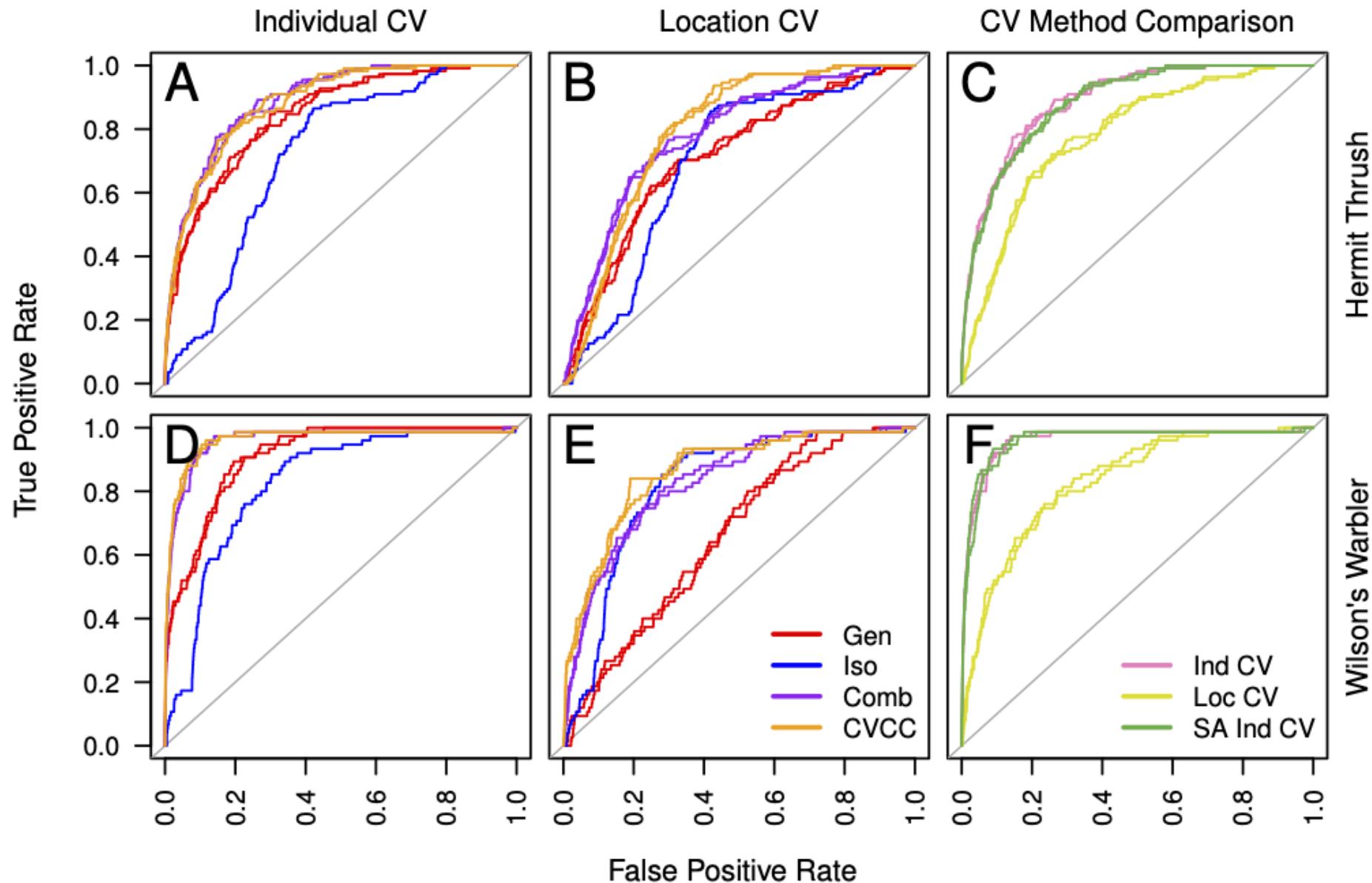
$$P(i_l, j_l | f, k) = \begin{cases} \gamma P(i_l | f, k) + (1 - \gamma) P(i_l | \tilde{f}, k)^2 & \text{if } i = j \\ (1 - \gamma) P(i_l | f, k) P(j_l | f, k) & \text{if } i \neq j \end{cases}$$

$$P(i_l | f, k) = (1 - \delta) f_{lik} + \delta / m_l$$

Combined Model



Model Assessment



Migratory Connectivity

