Generalized Linear Models, part 2

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Generalized linear models

The components of a model

- Likelihood of the data (the small-world data generator): *e.g.* $y \sim Binomial(n, p)$
- The linear function and link function (converts likelihood parameters to linear combinations of predictors): *e.g.* $logit(p) = \alpha + \beta x$
- Priors (our initial beliefs about plausible parameter values) *e.g.*:

$$\alpha \sim Normal(0, 1)$$

$$\beta \sim Normal(0, 1)$$

The Binomial count model

When $n = 1$, a Binomial regression model with a logit link function is called a logistic regression. When $n > 1$, we are instead modeling counts of events as our outcome.

The expected value for a Binomial variable with probability p and number of trials n is np, and the variance is $np(1 - p)$.

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When n is large, and p is small, $np \approx np(1-p)$. This special case of the Binomial distribution is the Poisson distribution.

The Poisson likelihood

Where y is a non-negative integer (count)

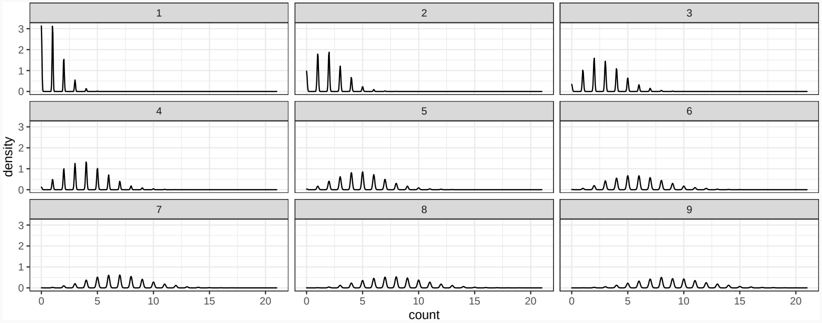
$$y \sim Poisson(\lambda)$$

$$E(y) = \bar{y} = \lambda$$

$$Var(y) = \lambda$$

The Poisson likelihood

```r
ggplot(pois_demo, aes(x=count)) +
  geom_density(adjust = 1/4) +
  facet_wrap(~lambda)
```



Let’s look at each Poisson variable

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```
pois_demo%>%group_by(lambda)%>%

  summarise(mean = mean(count),
            variance = var(count))
```

```
## # A tibble: 9 x 3
##   lambda  mean variance
##    <int> <dbl>    <dbl>
## 1      1  1.01     1.01
## 2      2  2.00     1.99
## 3      3  2.97     2.94
## 4      4  4.00     3.99
## 5      5  5.02     5.04
## 6      6  6.02     6.27
## 7      7  7.00     6.93
## 8      8  7.98     8.11
## 9      9  8.98     9.20
```

Poisson as a GLM

For a non-negative integer *y*

$$y_i \sim Poisson(\lambda)$$

$$\log \lambda_i = \alpha + \beta X$$

Using appropriate priors for α and β

The data for today: Fatal Encounters

Let’s use data on police-involved killings to estimate how many men of different racial groups are killed by police in the average US county.

```
fe<-read_csv(”./fe_demo.csv”)
### on your computer, run fe<-read_csv(”./slides/fe_demo.csv”)
head(fe)
```

```
## # A tibble: 6 x 5
##    fips state   pop deaths race.ethn
##   <dbl> <chr> <dbl>  <dbl> <chr>
## 1  1001 AL      483      0 latino
## 2  1003 AL     3218      0 latino
## 3  1005 AL      473      0 latino
## 4  1007 AL      163      0 latino
## 5  1009 AL     1713      0 latino
## 6  1011 AL      359      0 latino
```

A mortality model using a Poisson likelihood

Let's define a Poisson regression of death rates *d*

$$d_i \sim Poisson(\lambda)$$

$$\log \lambda_i = \alpha[race]_i$$

$$\alpha[race] \sim Normal(0, 2)$$

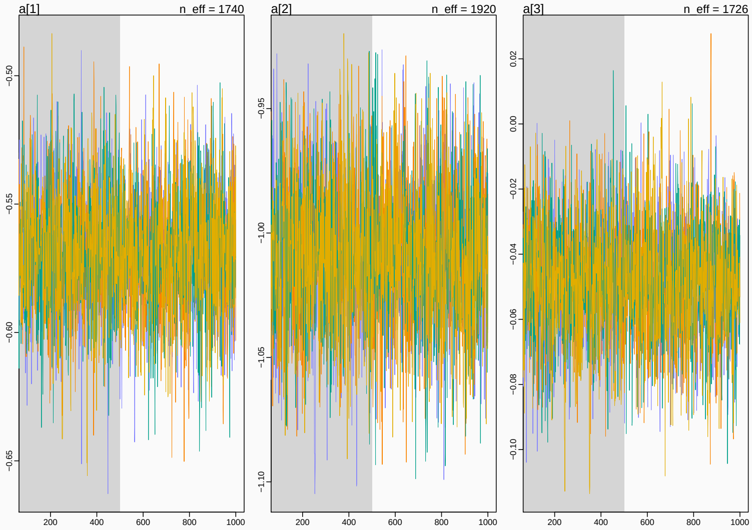
Estimation

```r
fe_model<-fe %>%
  mutate(race_ethn = factor(race.ethn),
         log_pop = log(pop + 1)) %>%
  select(deaths, race_ethn, log_pop)

fe_pois<-ulam(alist(
  deaths ~ dpois(l),
  log(l) <-  a[race_ethn],
  a[race_ethn] ~ dnorm(0,2)
), data = fe_model, chains = 4, cores = 2)
```

Check convergence

```r
traceplot(fe_pois)
```



Log-scale parameters are hard to interpret...

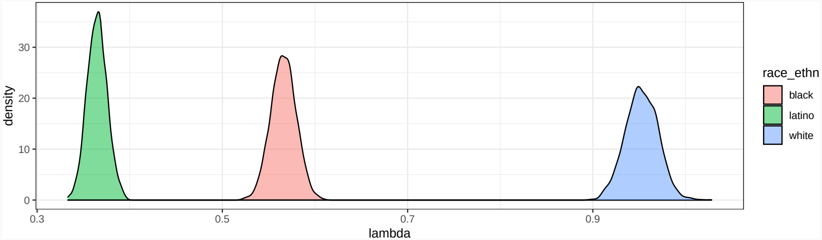
```r
precis(fe_pois)
```

```
## [1] mean  sd    5.5%  94.5% n_eff Rhat4
## <0 rows> (or 0-length row.names)
```

Average expected deaths per county

```r
post_a<-extract.samples(fe_pois)
post_a<-as.data.frame(post_a)
names(post_a)<-c("black", "latino", "white")
post_a<-post_a %>%
  pivot_longer(cols = everything(),
               names_to = "race_ethn",
               values_to = "log_lambda")
# inverse link function to get lambda on E(deaths) scale
post_a<-post_a %>%
  mutate(lambda = exp(log_lambda))

ggplot(post_a,
       aes(x = lambda, fill = race_ethn)) +
  geom_density(alpha = 0.5)
```



Problem: these don't adjust for population size

The standard Poisson model is *unbounded*, and assumes each observation is drawn from a similar unit. However, we can use Poisson models to estimate event *rates* using an *offset*.

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The standard Poisson model is *unbounded*, and assumes each observation is drawn from a similar unit. However, we can use Poisson models to estimate event *rates* using an *offset*.

An offset (or exposure) scales λ to the size of the exposure, turning λ into a rate per unit of the offset.

Including an offset in the model

Let's now estimate a model that includes population p as an exposure variable (typically time, population, or some other measure of event opportunity).

$$d_i \sim Poisson(\lambda)$$

$$\log \frac{\lambda_i}{p_i} = \log \lambda_i - \log p_i = \alpha + \beta x_i$$

Including an offset in the model

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$$\log \frac{\lambda_i}{p_i} = \log \lambda_i - \log p_i = \alpha + \beta x_i$$

Which we can rewrite as

$$\log \lambda_i = \log p_i + \alpha + \beta x_i$$

We add the offset to the regression without including a parameter.

Let’s re-estimate the model with an offset

$$d_i \sim Poisson(\lambda)$$

$$\log \lambda_i = \log p_i + \alpha[race]_i$$

$$\alpha[race] \sim Normal(0, 2)$$

$$\sigma \sim Exp(1)$$

```
fe_pois_offset<-ulam(alist(
  deaths ~ dpois(l),
  log(l) <- log_pop + a[race_ethn],
  a[race_ethn] ~ dnorm(0,2)
), data = fe_model, chains = 4, cores = 2)
```

Interpreting the model, checking convergence diagnostics

```r
precis(fe_pois_offset, depth = 2)
```

```
##            mean         sd       5.5%      94.5%    n_eff     Rhat4
## a[1]  -8.951253 0.02438574  -8.989470  -8.912355 1951.683 0.9994298
## a[2]  -9.682579 0.02897562  -9.729369  -9.635760 1891.496 0.9998911
## a[3] -10.159628 0.01881547 -10.190347 -10.129502 1640.717 1.0021529
```

Posterior inference

Let’s check the expected number of deaths for each group assuming a population of 100,000.

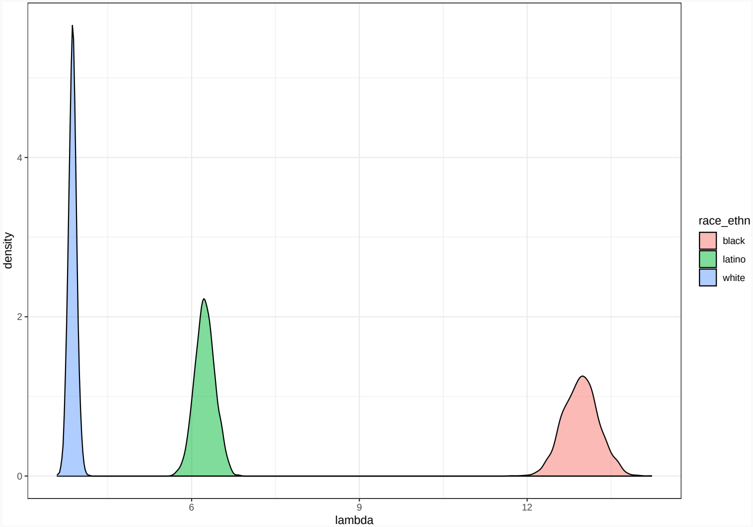
```r
sim_dat<-data.frame(race_ethn =
                      c("black", "latino", "white"),
                    log_pop = log(1e5))

post_lambda<-link(fe_pois_offset, sim_dat)
post_lambda<-as.data.frame(post_lambda)
names(post_lambda)<-c("black", "latino", "white")

post_lambda<-post_lambda %>%
  pivot_longer(cols = everything(),
               names_to = "race_ethn",
               values_to = "lambda")
```

Posterior inference

```r
ggplot(post_lambda,
       aes(x = lambda, fill = race_ethn)) +
  geom_density(alpha = 0.5)
```



Categorical regression

Categorical data

Categorical data falls into a fixed set of categories. It may be *unordered*, meaning that there is no inherent ranking of categories, or it may be *ordered*. Ordered categorical data has an explicit hierarchical ranking of values.

Categorical data, examples

Are these variables ordered or unordered?

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- Candidate choice in a primary election
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- Graduate program to attend

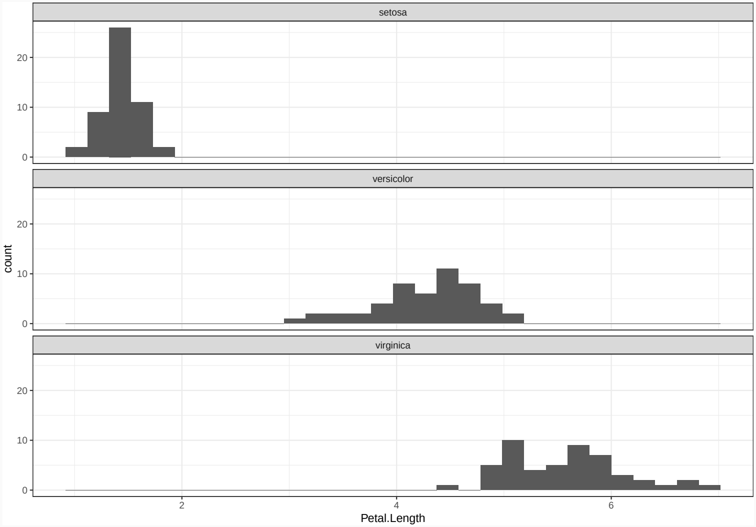
Categorical data, examples

Are these variables ordered or unordered?

- Candidate choice in a primary election
- Zip code for people choosing a place to move
- Cause of death
- Opinions on a political issue on a thermometer / Likert scale (e.g. Strongly oppose, oppose, neutral, support, strongly support)
- Graduate program to attend
- Ranking of graduate program

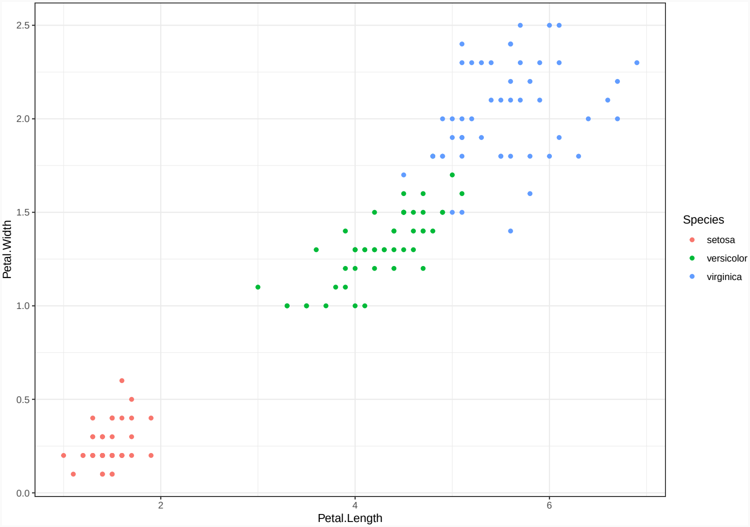
Visualizing categorical data, facets

```r
ggplot(iris, aes(x = Petal.Length)) +
  geom_histogram() +
  facet_wrap(~Species, ncol=1)
```



Visualizing categorical data, color

```r
ggplot(iris, aes(x = Petal.Length, y = Petal.Width,
                 color = Species)) +
  geom_point()
```



Predicting Iris species from petal length and width

Can we successfully classify Iris species based on the observed length of the petals?

We will use a *multinomial regression*, which is conceptually similar to running $k - 1$ logistic regressions, where k is the number of categories in our outcome.

Multinomial regression: basics

For a categorical outcome with K categories, estimate $K-1$ models where 1,2,3 stand in for membership in group 1, 2, 3:

$$log \frac{Pr(y_i = 1)}{Pr(y_i = K)} = \beta x_i$$

$$log \frac{Pr(y_i = 2)}{Pr(y_i = K)} = \beta x_i$$

$$\cdots$$

$$log \frac{Pr(y_i = K-1)}{Pr(y_i = K)} = \beta x_i$$

Key assumtion: Independence of irrelevant alternatives. Odds of choice do not depend on the presence or absence of other alternatives (i.e. car vs bus or car vs red bus vs blue bus)

Implementation

The book provides details on using Stan directly, but this is tricky with ulam(). I'm using the brms package here (I'll show you more of this later!)

```
library(brms)

iris_model<-brm(Species ~ Petal.Length,
                family = categorical,
                data = iris)
```

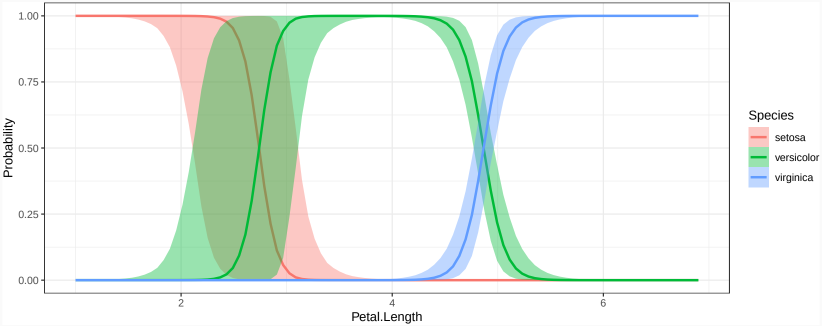
These are hard to interpret...

```r
summary(iris_model)
```

```
##  Family: categorical 
##   Links: muversicolor = logit; muvirginica = logit 
## Formula: Species ~ Petal.Length 
##    Data: iris (Number of observations: 150) 
## Samples: 4 chains, each with iter = 2000; warmup = 1000; thin = 1;
##          total post-warmup samples = 4000
## 
## Population-Level Effects: 
##                           Estimate Est.Error l-95% CI u-95% CI Rhat Bulk_ESS
## muversicolor_Intercept      -43.09     29.16  -116.91   -12.96 1.01      361
## muvirginica_Intercept       -93.08     33.06  -173.24   -50.83 1.01      380
## muversicolor_Petal.Length    15.70      9.87     5.00    41.12 1.01      329
## muvirginica_Petal.Length     25.98     10.52    13.47    51.81 1.01      333
##                           Tail_ESS
## muversicolor_Intercept         342
## muvirginica_Intercept          378
## muversicolor_Petal.Length      332
## muvirginica_Petal.Length       342
## 
## Samples were drawn using sampling(NUTS). For each parameter, Bulk_ESS
## and Tail_ESS are effective sample size measures, and Rhat is the potential
## scale reduction factor on split chains (at convergence, Rhat = 1).
```

Let’s predict flower species

```r
conditional_effects(iris_model, categorical = T)
```



Summary

- We added two new likelihoods into our GLM tool-belt: the Poisson and the multinomial
- Poisson regression can handle counts and rates easily
- Multinomial regression models categorical outcomes
- Homework: Chapter 11 Easy and Medium questions. If you want practice with Poisson models, add 11H4. Note that map == quap and map2stan == ulam.