19. Generalized Linear Madness

Statistical Rethinking





Generalized Linear

GUN



Generalized Linear Habits

GLMs and GLMMs: Flexible association description machines

With external causal model, causal interpretation possible

But only a fraction of scientific phenomena expressible as GLM(M)s

Even when GLM(M)s sufficient, starting with theory solves empirical problems





























 $V = \pi r^2 h$

 $V = \pi(ph)^2h$ radius as proportion of height



 $V = \pi r^2 h$

 $V = \pi(ph)^2h$

 $W = kV = k\pi(ph)^2h$ weight "density"



 $V = \pi r^2 h$

 $V = \pi(ph)^2h$

 $W = kV = k\pi(ph)^2h$

 $W = k\pi p^2 h^3$







 $W_i \sim \text{Distribution}(\mu_i, \ldots)$ $\mu_i = k\pi p^2 H_i^3$ $p \sim \text{Distribution}(...)$ $k \sim \text{Distribution}(\ldots)$

"error" distribution for W expected W for H prior for proportionality

prior for density

$p \sim \text{Distribution}(...)$ $k \sim \text{Distribution}(...)$

prior for proportionality

prior for density

kg



 $\mu_i = k\pi p^2 H_i^3$ $kg = kg/cm^3 \times cm^3$

 $\mu_i = k\pi p^2 H_i^3$ $kg = kg/cm^3 \times cm^3$

Measurement scales are artifice

If you can divide out all measurement units (kg, cm), often easier







$p \sim \text{Distribution}(...)$ $k \sim \text{Distribution}(\ldots)$

between 0-1, < 0.5

positive real, > 1

$p \sim \text{Beta}(25,50)$ $k \sim \text{Exponential}(0.5)$



Prior predictive simulation

```
# prior sim
n <- 30
p <- rbeta(n,25,50)
k <- rexp(n,0.5)
sigma <- rexp(n,1)

xseq <- seq(from=0,to=1.3,len=100)
plot(NULL,xlim=c(0,1.3),ylim=c(0,1.5))
for ( i in 1:n ) {
    mu <- log( pi * k[i] * p[i]^2 * xseq^3 )
    lines( xseq , exp(mu + sigma[i]^2/2) ,
lwd=3 , col=col.alpha(2,runif(1,0.4,0.8)) )
}</pre>
```



 $W_i \sim \text{Distribution}(\mu_i, \ldots)$ $\mu_i = k\pi p^2 H_i^3$ $p \sim \text{Beta}(25, 50)$ $k \sim \text{Exponential}(0.5)$

positive real, variance scales with mean



 $W_i \sim \text{LogNormal}(\mu_i, \sigma)$ $\exp(\mu_i) = k\pi p^2 H_i^3$ $p \sim \text{Beta}(25, 50)$ $k \sim \text{Exponential}(0.5)$ $\sigma \sim \text{Exponential}(1)$

Growth is multiplicative, log-normal is natural choice



 $W_i \sim \text{LogNormal}(\mu_i, \sigma)$ $\exp(\mu_i) = k\pi p^2 H_i^3$ $p \sim \text{Beta}(25, 50)$ $k \sim \text{Exponential}(0.5)$ $\sigma \sim \text{Exponential}(1)$

mu in log-normal is mean of log, not mean of observed

Growth is multiplicative, log-normal is natural choice



```
## R code 16.2
dat <- list(W=d$w,H=d$h)</pre>
m16.1 <- ulam(
    alist(
        W ~ dlnorm( mu , sigma ),
        exp(mu) <- 3.141593 * k * p^2 * H^3,
        p ~ beta( 25 , 50 ),
        k \sim exponential(0.5),
        sigma ~ exponential( 1 )
    ), data=dat , chains=4 , cores=4 )
```

 $W_i \sim \text{LogNormal}(\mu_i, \sigma)$ $\exp(\mu_i) = k\pi p^2 H_i^3$ $p \sim \text{Beta}(25, 50)$ $k \sim \text{Exponential}(0.5)$ $\sigma \sim \text{Exponential}(1)$



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```





一 1.2

Insightful errors

Not bad for a cylinder Poor fit for children

In scientific model, poor fit is informative — p different for kids

Bad epicycles harder to read





一 1.2

 $\mu_i = k\pi p^2 H_i^3$



 $\mu_i = k\pi p^2 H_i^3$



 $\mu_i = k\pi p^2 H_i^3$ $(1) = k\pi p^2 (1)^3$



 $\mu_i = k\pi p^2 H_i^3$ $(1) = k\pi p^2 (1)^3$ 1, $= \frac{1}{\pi p^2}$



 $\mu_i = k\pi p^2 H_i^3$ $(1) = k\pi p^2 (1)^3$ $= \frac{1}{\pi p^2}$



 $(1) = k\pi p^2 (1)^3$ $(1) = \pi \theta(1)^3$ $\theta \approx \pi^{-1}$



```
mWH2 <- ulam(
    alist(
        W ~ dlnorm( mu , sigma ),
        exp(mu) < - H^3,
        sigma ~ exponential( 1 )
    ), data=dat , chains=4 , cores=4 )
```

In dimensionless model, W is H^3

$W_i \sim \text{LogNormal}(\mu_i, \sigma)$ $\exp(\mu_i) = H_i^3$ $\sigma \sim \text{Exponential}(1)$





```
mWH2 <- ulam(
    alist(
        W ~ dlnorm( mu , sigma ),
        exp(mu) <- H^3 ,
        sigma ~ exponential( 1 )
    ), data=dat , chains=4 , cores=4 )
```

In dimensionless model, W is H^3



```
mWH2 <- ulam(
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    ), data=dat , chains=4 , cores=4 )</pre>
```


Geometric People

Most of the relationship $H \rightarrow W$ is just relationship between length and volume

Changes in body shape explain poor fit for children?

Problems provide insight when model is scientific instead of purely statistical

There is no empiricism without theory





 $W = k\pi p^2 h^3$























































majority choice (1) minority (2) choice











Social Conformity

Do children copy the majority? If so, how does this develop?

Problem: Cannot see strategy, only choice

Majority choice consistent with many strategies





Social Conformity

Majority choice consistent with many strategies

Random color: Choose majority 1/3 of time

Random demonstrator: 3/4 of time

Random demonstration: 1/2 of time







N <- 100 # number of children

half choose random color # sample from 1,2,3 at random for each y1 <- sample(1:3 , size=N/2 , replace=TRUE)</pre>

half follow majority
y2 <- rep(2 , N/2)</pre>

combine and shuffle y1 and y2
y <- sample(c(y1,y2))</pre>



State-Based Model

Majority choice does not indicate majority preference

Instead infer the unobserved strategy (state) of each child

Strategy space: (1) Majority (2) Minority (3) Maverick (4) Random Color (5) Follow First



$Y_i \sim \text{Categorical}(\theta)$

vector with probability of each choice



Probability of (1) unchosen, (2) majority, (3) minority





$Y_i \sim \text{Categorical}(\theta)$ $\theta_j = \sum p_S \Pr(Y = j | S)$ S=1

$p \sim \text{Dirichlet}([4, 4, 4, 4, 4])$ **Prior for strategy space**





```
data{
   int N;
   int y[N];
    int majority_first[N];
}
parameters{
   simplex[5] p;
}
model{
   vector[5] theta_j;
   // prior
   p \sim dirichlet(rep_vector(4,5));
    // probability of data
    for ( i in 1:N ) {
       theta_j = rep_vector(0,5); // clear it out
       if (y[i]==2) theta_j[1]=1; // majority
       if (y[i]==3) theta_j[2]=1; // minority
       if (y[i]==1) theta_j[3]=1; // maverick
       theta_j[4]=1.0/3.0; // random color
       if ( majority_first[i]==1 ) // follow first
           if (y[i]==2) theta_j[5]=1;
       else
           if (y[i] = 3) theta_j[5]=1;
```

$Y_i \sim \text{Categorical}(\theta)$ $\theta_{i} = \sum_{i=1}^{N} p_{S} \Pr(Y = j | S)$ S=1



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int y[N];

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   else
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```

Categorical(θ) $\theta_j = \sum_{j=1}^{5} p_S \Pr(Y = j \mid S)$ S=1



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data{
    int N;
    int y[N];
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simplex[5] p;

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```

$Y_i \sim \text{Categorical}(\theta)$ $\theta_j = \sum_{j=1}^{5} p_S \Pr(Y = j \mid S)$ S=1~ Dirichlet([4,4,4,4,4])



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$Y_i \sim \text{Categorical}(\theta)$ $\theta_j = \sum_{j=1}^{5} p_S \Pr(Y = j \mid S)$ S=1





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p \sim dirichlet(rep_vector(4,5));
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// probability of data for (i in 1:N) {

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$$\theta_j = \sum_{S=1}^5 p_S \Pr(Y = j \mid S)$$



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   else
       if (y[i]==3) theta_j[5]=1;
```

// compute log($p_S * Pr(y_i|S)$) for (S in 1:5) theta_j[S] = $log(p[S]) + log(theta_j[S]);$

// compute average log-probability of y_i target += log_sum_exp(theta_j);

$Y_i \sim \text{Categorical}(\theta)$ 5

$$\partial_j = \sum_{S=1}^{J} p_S \Pr(Y = j \mid A)$$



vector[5] theta_j;

```
// prior
p \sim dirichlet(rep_vector(4,5));
// probability of data
for ( i in 1:N ) {
   theta_j = rep_vector(0,5); // clear it out
    if (y[i]==2) theta_j[1]=1; // majority
   if (y[i]==3) theta_j[2]=1; // minority
   if (y[i]==1) theta_j[3]=1; // maverick
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       if (y[i] = 2) theta_j[5]=1;
   else
       if (y[i] = 3) theta_j[5]=1;
    // compute log( p_S * Pr(y_i|S) )
    for ( S in 1:5 )
       theta_j[S] = log(p[S]) + log(theta_j[S]);
    // compute average log-probability of y_i
```

$$Y_i \sim \text{Categorical}(\theta)$$

$$\theta_j = \sum_{S=1}^5 p_S \Pr(Y = j \mid A)$$





$$Y_i \sim \text{Categorical}(\theta)$$
$$\theta_j = \sum_{S=1}^5 p_S \Pr(Y = j | S)$$
$$p \sim \text{Dirichlet}([4, 4, 4, 4, 4])$$





State-Based Models

What we want: Latent states

What we have: Emissions

Typically lots of uncertainty, but being honest is only ethical choice

Large family: Movement, learning, population dynamics, international relations, family planning, ...



Population Dynamics

Latent states can be time varying

Example: Ecological dynamics, numbers of different species over time

Estimand: How do different species interact; how do interactions influence population dynamics

How to Draw a Lynx

Page 541

$\frac{dH}{dt} = H_t \times \text{(birth rate)} - H_t \times \text{(death rate)}$

$\frac{dL}{dt} = L_t \times \text{(birth rate)} - L_t \times \text{(death rate)}$





 $\frac{dH}{dt} = H_t b_H - H_t (L_t m_H)$ birth rate *impact of lynx* on hares ofhares

 $\frac{dL}{dt} = L_t \times \text{(birth rate)} - L_t \times \text{(death rate)}$





 $\frac{dH}{dt} = H_t b_H - H_t (L_t m_H)$ birth rate *impact of lynx* ofhares on hares



depends upon hares







$h_t \sim \text{LogNormal}(\log(p_H H_t), \sigma_H)$

 $\frac{dH}{dt} = H_t b_H - H_t (L_t m_H)$ $H_T = H_1 + \int_1^I \frac{dH}{dt} dt$



$l_t \sim \text{LogNormal}(\log(p_L L_t), \sigma_L)$



observed hare pelts $h_t \sim \text{LogNormal}(\log(p_H H_t), \sigma_H)$

 $\frac{dH}{dt} = H_t b_H - H_t (L_t m_H)$ $H_T = H_1 + \int_1^T \frac{dH}{dt} dt$

observed lynx pelts $l_t \sim \text{LogNormal}(\log(p_L L_t), \sigma_L)$

 $\frac{dL}{dt} = L_t(H_t b_L) - L_t m_L$ $L_T = L_1 + \int_1^T \frac{dL}{dt} dt$

observed hare pelts $h_{t} \sim \text{LogNormal}(\log(p_{H}H_{t}), \sigma_{H})$

$$\frac{dH}{dt} = H_t b_H - H_t (L_t m_H)$$

$$H_T = H_1 + \int_1^T \frac{dH}{dt} dt$$

cumulative changes in H until time T

observed lynx pelts $l_t \sim \text{LogNormal}(\log(p_L L_t), \sigma_L)$



Prior Simulation



```
functions {
 real[] dpop_dt( real t,
              real[] theta, // parameters
              real[] x_r, int[] x_i) { // unused
   real L = pop_init[1];
   real H = pop_init[2];
   real bh = theta[1];
   real mh = theta[2];
   real ml = theta[3];
   real bl = theta[4];
   // differential equations
   real dH_dt = (bh - mh * L) * H;
   real dL_dt = (bl * H - ml) * L;
   return { dL_dt , dH_dt };
data {
 real<lower=0> pelts[N,2]; // measured populations
transformed data{
 real times_measured[N-1]; // N-1 because first time is initial state
 for ( i in 2:N ) times_measured[i-1] = i;
parameters {
```

// time real[] pop_init, // initial state {lynx, hares}

functions {

```
real[] dpop_dt( real t,
               real[] pop_init, // initial state {lynx, hares}
               real[] theta, // parameters
               real[] x_r, int[] x_i) { // unused
    real L = pop_init[1];
    real H = pop_init[2];
   real bh = theta[1];
    real mh = theta[2];
   real ml = theta[3];
   real bl = theta[4];
   // differential equations
    real dH_dt = (bh - mh * L) * H;
    real dL_dt = (bl * H - ml) * L;
    return { dL_dt , dH_dt };
data {
 int<lower=0> N; // number of measurement times
  real<lower=0> pelts[N,2]; // measured populations
transformed data{
  real times_measured[N-1]; // N-1 because first time is initial state
 for ( i in 2:N ) times_measured[i-1] = i;
parameters {
```

time

Computes cumulative change to time t





```
functions {
 real[] dpop_dt( real t,
              real[] theta, // parameters
              real[] x_r, int[] x_i) { // unused
   real L = pop_init[1];
   real H = pop_init[2];
   real bh = theta[1];
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// time real[] pop_init, // initial state {lynx, hares}

Computes cumulative change to time t

 $\frac{dH}{dt} = H_t b_H - H_t (L_t m_H)$ $\frac{dL}{dt} = L_t (H_t b_L) - L_t m_L$







```
real pop[N, 2];
pop[1,1] = pop_init[1];
pop[1,2] = pop_init[2];
pop[2:N,1:2] = integrate_ode_rk45(
 dpop_dt, pop_init, ⊙, times_measured, theta,
  rep_array(0.0, 0), rep_array(0, 0),
 1e-5, 1e-3, 5e2);
```

model {

// priors

theta[{1,3}] ~ normal(1 , 0.5); // bh,ml theta[$\{2,4\}$] ~ normal(0.05, 0.05); // mh,bl sigma ~ exponential(1); $pop_init ~ lognormal(log(10), 1);$ $p \sim beta(40, 200);$ observation model connect latent population state to observed pelts for (t in 1:N)for (k in 1:2)

Compute population state for each time



```
POP[T,T] - POP[IIIC[T]]
  pop[1,2] = pop_init[2];
  pop[2:N,1:2] = integrate_ode_rk45(
    dpop_dt, pop_init, 0, times_measured, theta,
    rep_array(0.0, 0), rep_array(0, 0),
   1e-5, 1e-3, 5e2);
model {
  // priors
  theta[{1,3}] ~ normal( 1 , 0.5 ); // bh,ml
  theta[\{2,4\}] ~ normal( 0.05, 0.05); // mh,bl
  sigma ~ exponential( 1 );
  pop_init \sim lognormal(log(10), 1);
  p ~ beta(40.200):
  // observation model
  // connect latent population state to observed pelts
  for ( t in 1:N )
    for ( k in 1:2 )
      pelts[t,k] ~ lognormal( log(pop[t,k]*p[k]) , sigma[k] );
generated quantities {
  real pelts_pred[N,2];
  for (t in 1:N)
    for ( k in 1:2 )
      pelts_pred[t,k] = lognormal_rng( log(pop[t,k]*p[k]) , sigma[k] );
```

Probability of data, given latent population





year

Population Dynamics

Ecologies much more complex Other animals prey on hare Without causal model, little hope to understand interventions

Same framework very successful in fisheries management





Science Before Statistics

Epicycles get you only so far

Scientific models also flawed, but flaws are more productive

Theory necessary for empiricism

Be patient; mastery takes time; experts learn safe habits



Student learning differential equations



Course Schedule

Week 1	Bayesian inference	Chapters 1, 2, 3
Week 2	Linear models & Causal Inference	Chapter 4
Week 3	Causes, Confounds & Colliders	Chapters 5 & 6
Week 4	Overfitting / MCMC	Chapters 7, 8, 9
Week 5	Generalized Linear Models	Chapters 10, 11
Week 6	Ordered categories & Multilevel models	Chapters 12 & 13
Week 7	More Multilevel models	Chapters 13 & 14
Week 8	Social Networks & Gaussian Processes	Chapter 14
Week 9	Measurement & Missingness	Chapter 15
Week 10	Generalized Linear Madness	Chapter 16

https://github.com/rmcelreath/stat_rethinking_2023

