

# Methods 4 - 11

Chris Mathys



BSc Programme in Cognitive Science

Spring 2022

# Repeat observations

12 stories ( $S$ )

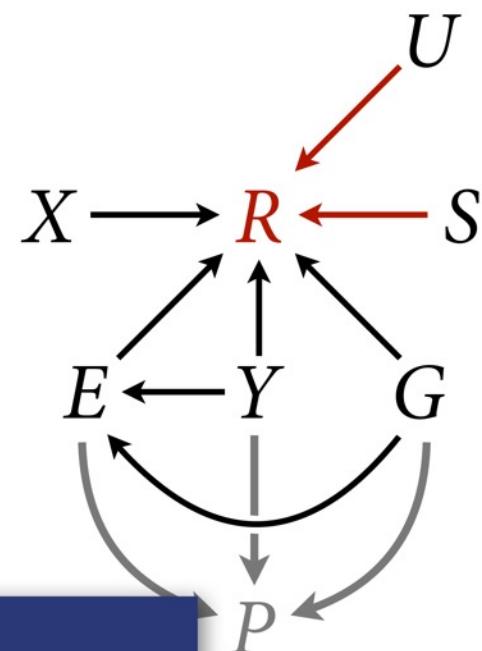
```
> table(d$story)
```

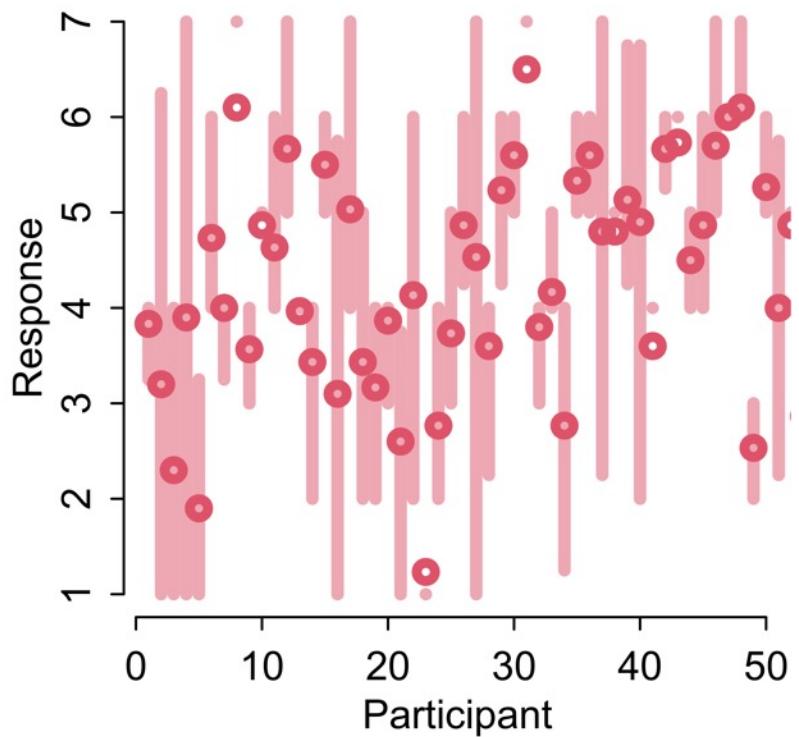
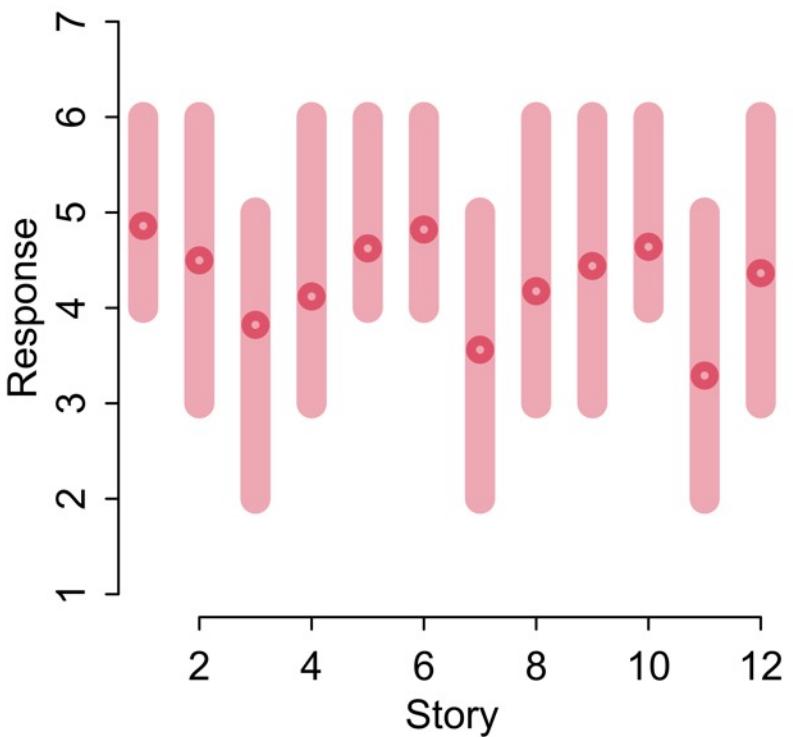
aqu	boa	box	bur	car	che	pon	rub	sha	shi	spe	swi
662	662	1324	1324	662	662	662	662	662	662	993	993

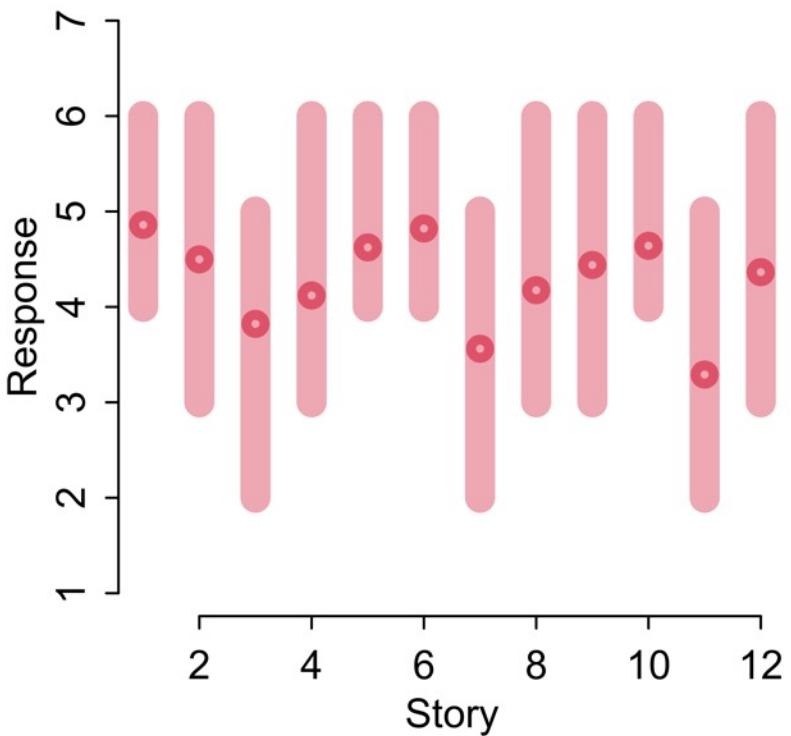
331 individuals ( $U$ )

```
> table(d$id)
```

96;434	96;445	96;451	96;456	96;458	96;466	96;467	96;474	96;480	96;481	96;497
30	30	30	30	30	30	30	30	30	30	30
96;498	96;502	96;505	96;511	96;512	96;518	96;519	96;531	96;533	96;538	96;547
30	30	30	30	30	30	30	30	30	30	30
96;550	96;553	96;555	96;558	96;560	96;562	96;566	96;570	96;581	96;586	96;591
30	30	30	30	30	30	30	30	30	30	30







$$R_i \sim \text{OrderedLogit}(\phi_i, \alpha)$$

$$\phi_i = \beta_{S[i]}$$

*This model has  
anterograde amnesia*

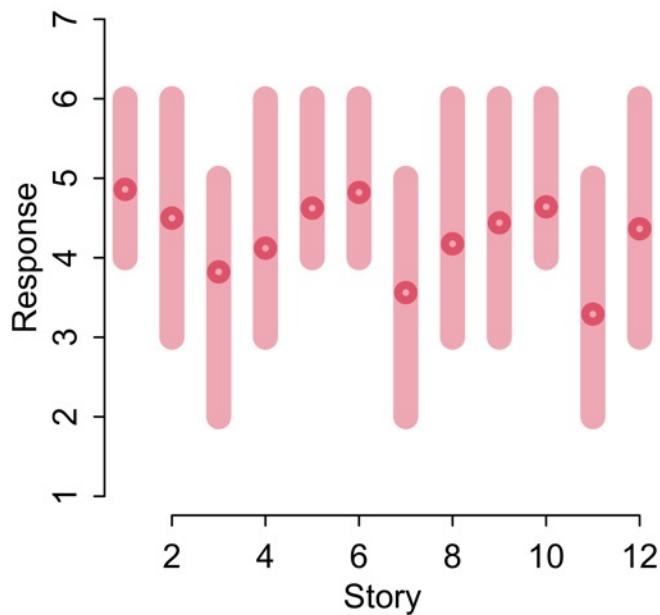
# Models With Memory

Multilevel models are models within models

(1) Model observed groups/individuals

(2) Model of population of groups/individuals

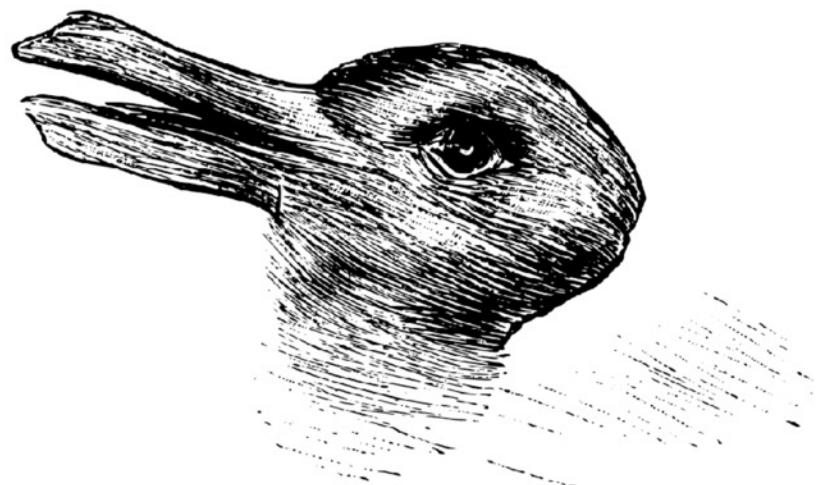
The population model creates a kind of memory



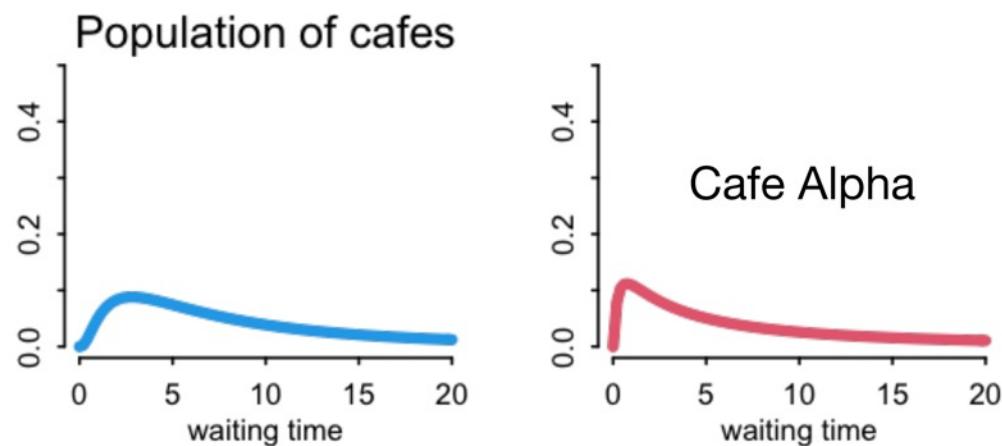
# Two Perspectives

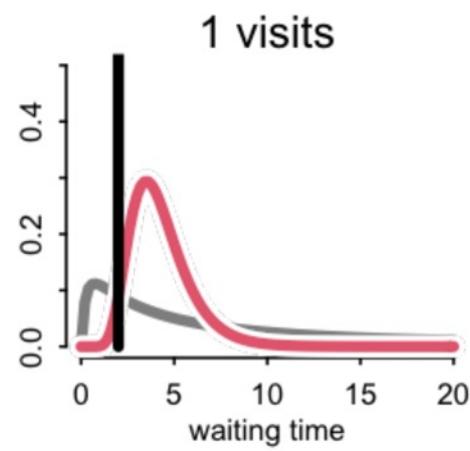
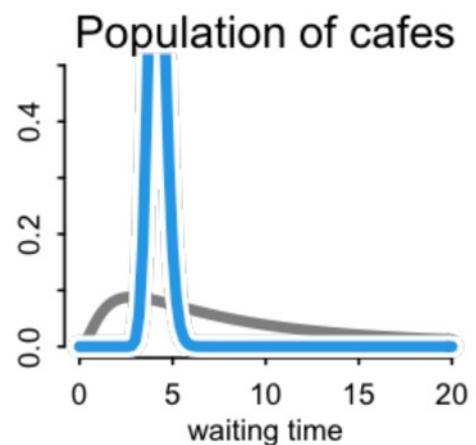
- (1) Models with memory learn faster, better
- (2) Models with memory resist overfitting

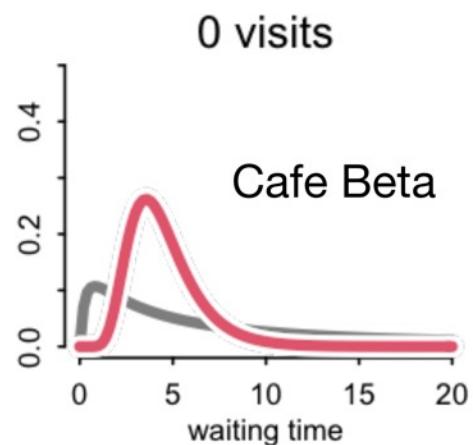
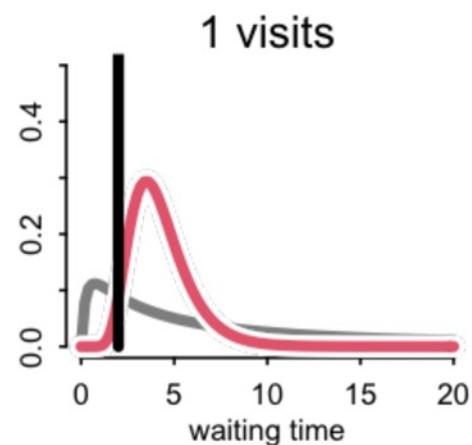
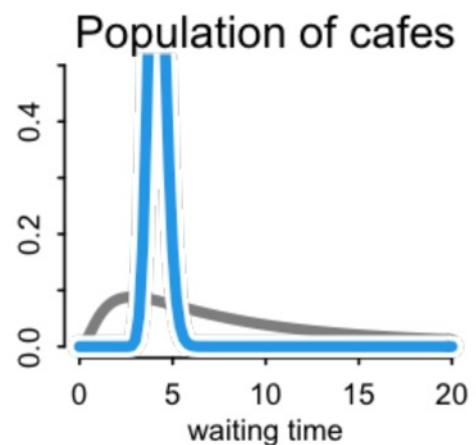
Welche Thiere gleichen einander am meisten?

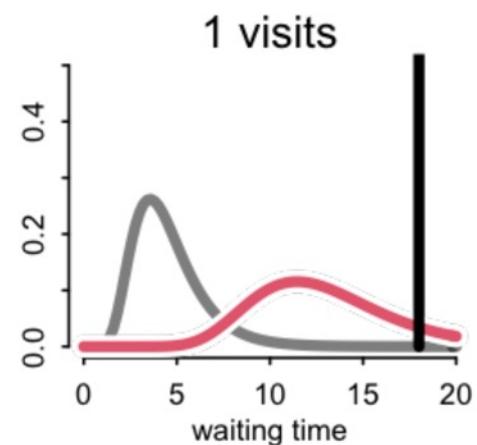
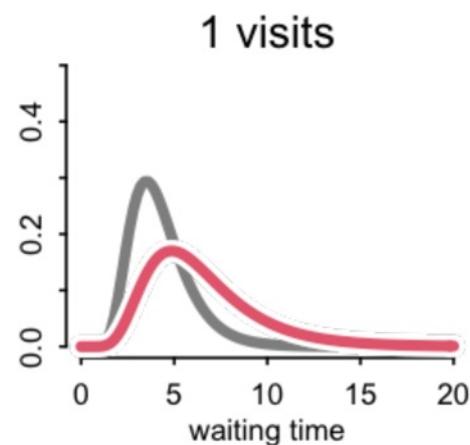
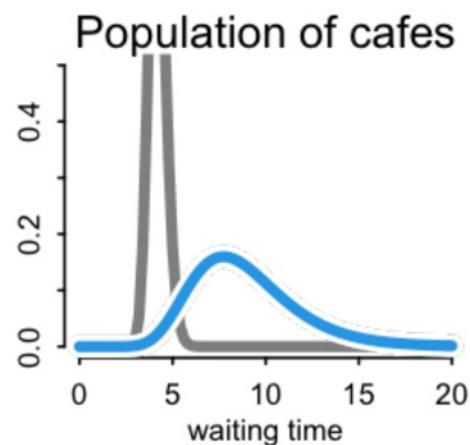


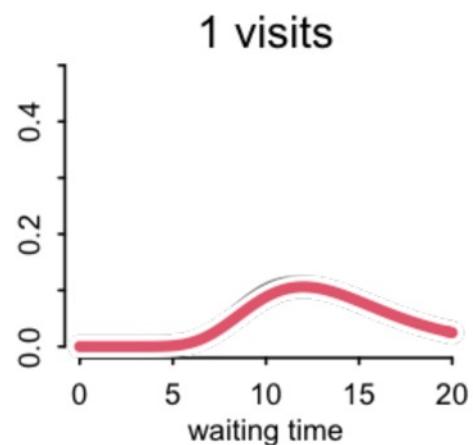
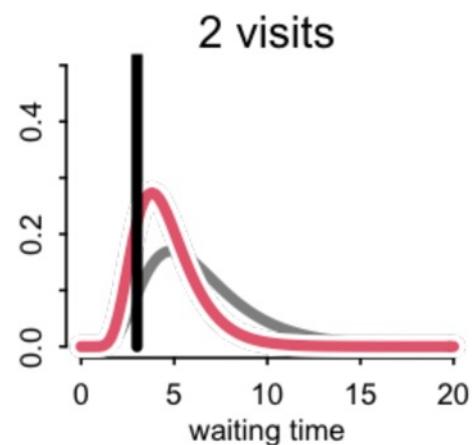
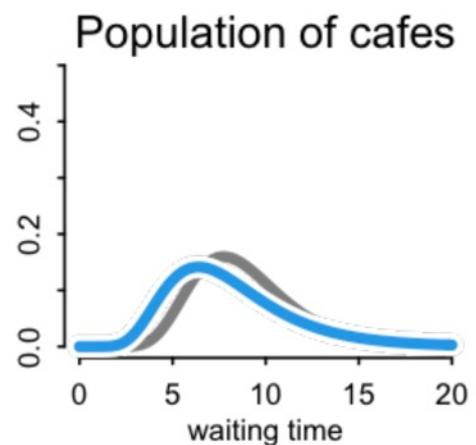
Kaninchen und Ente.

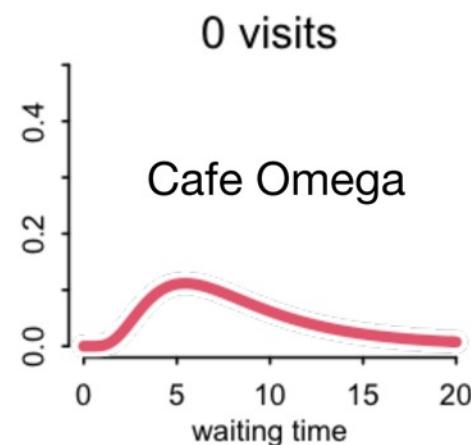
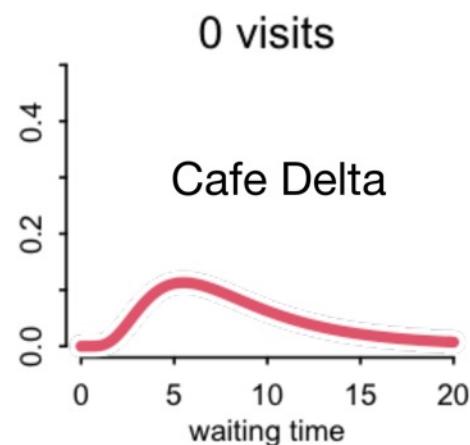
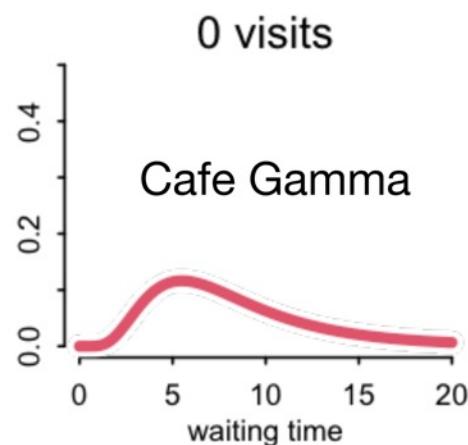
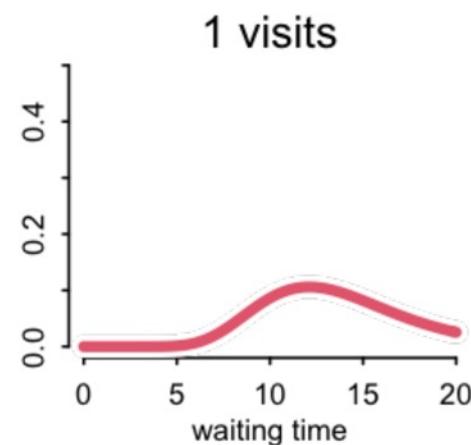
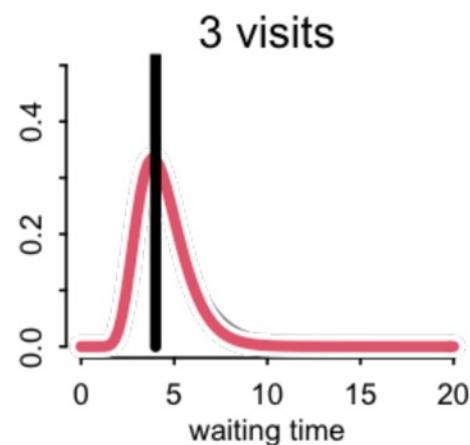
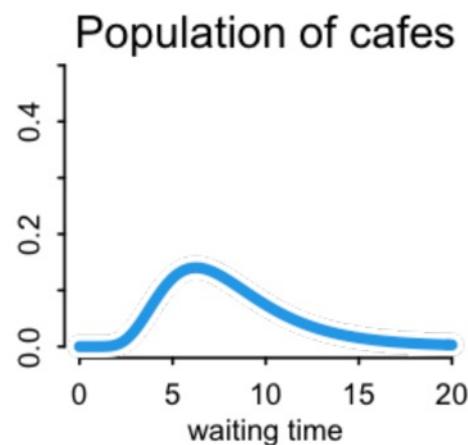


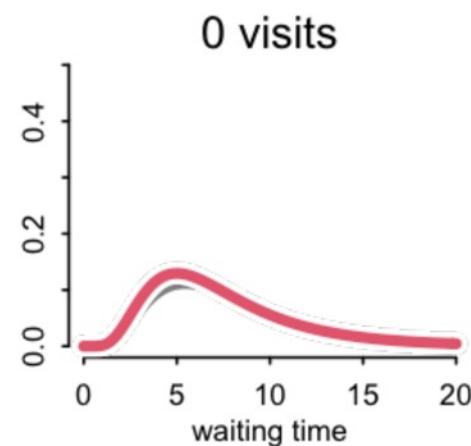
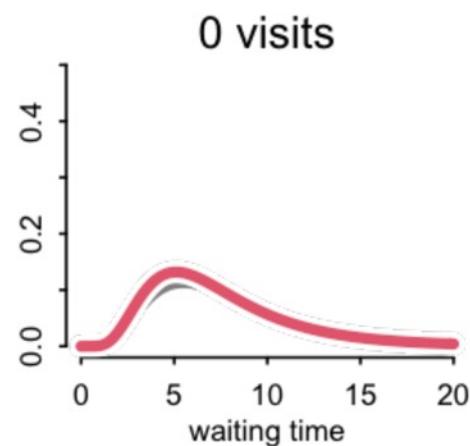
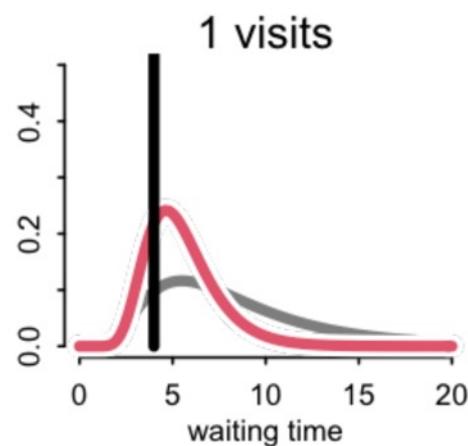
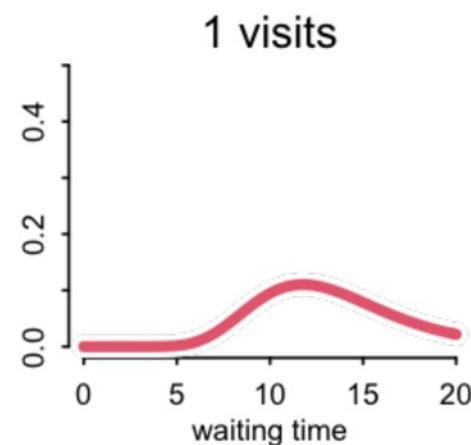
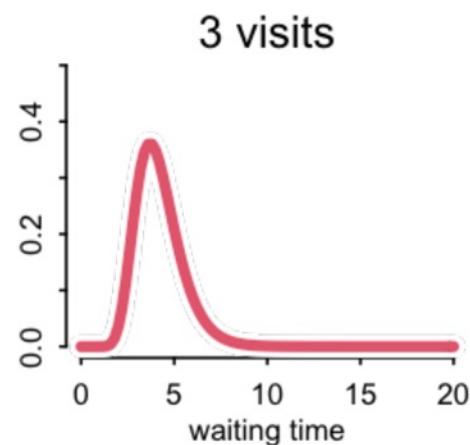
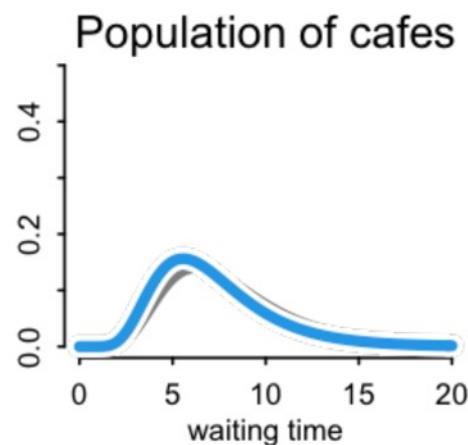


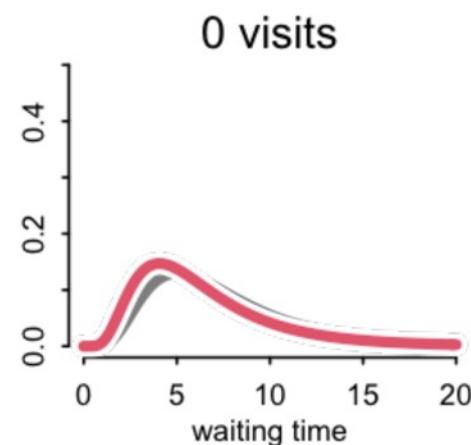
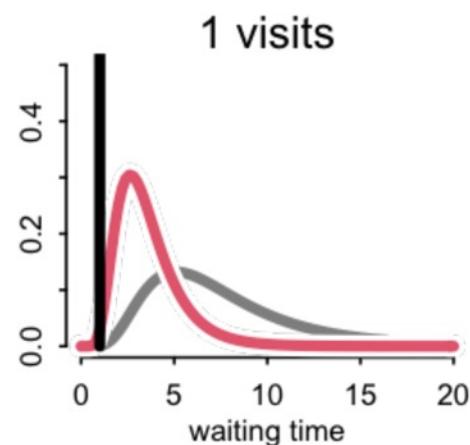
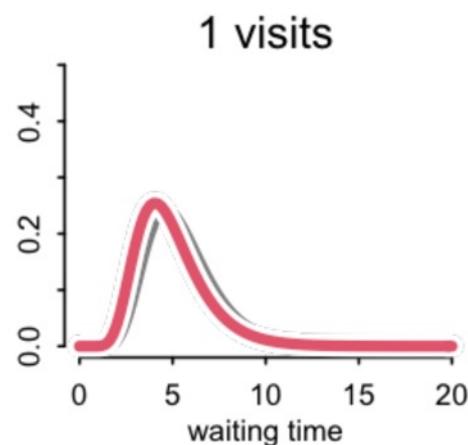
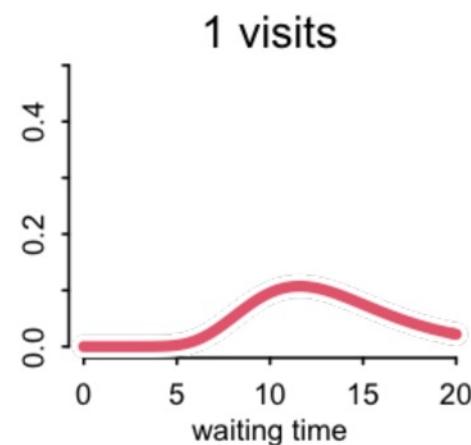
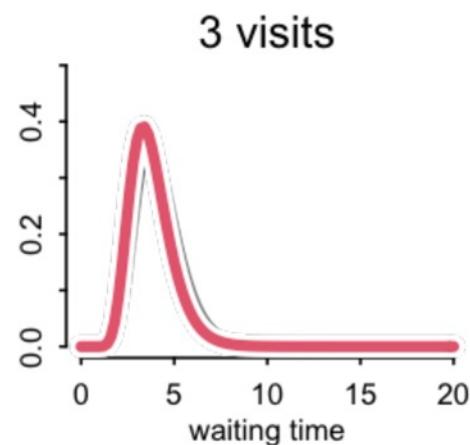
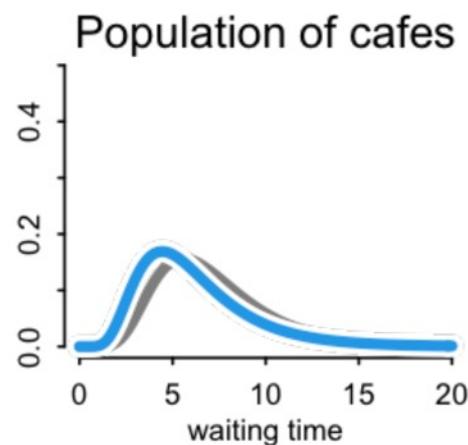


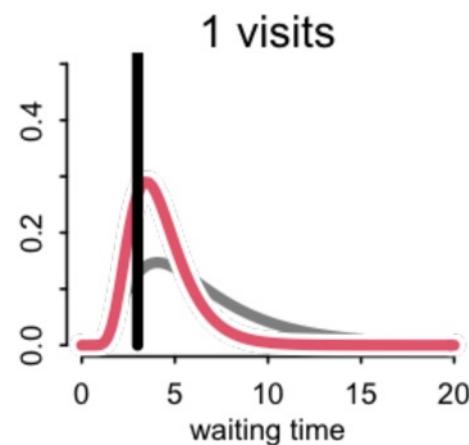
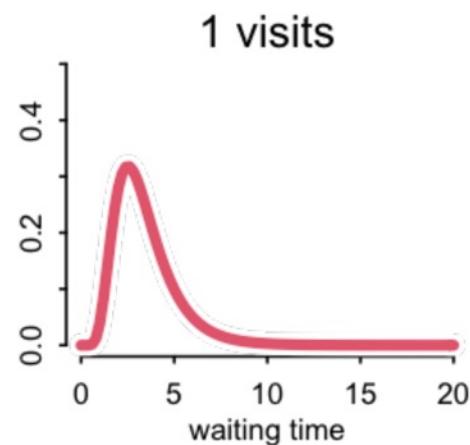
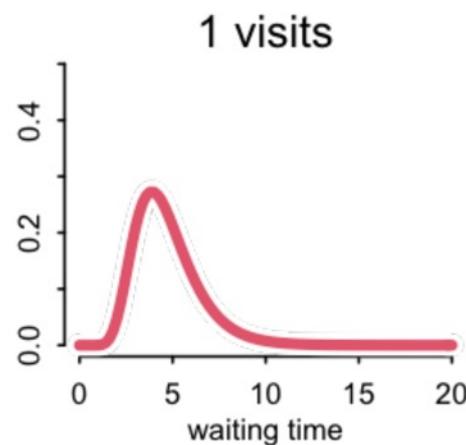
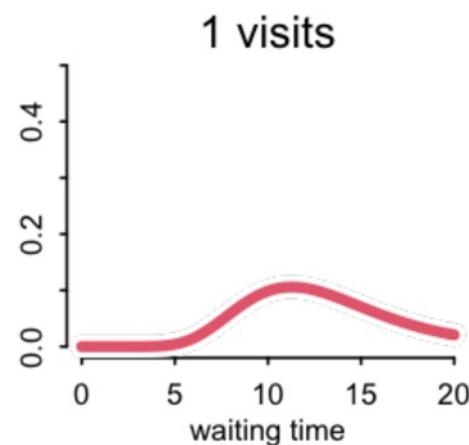
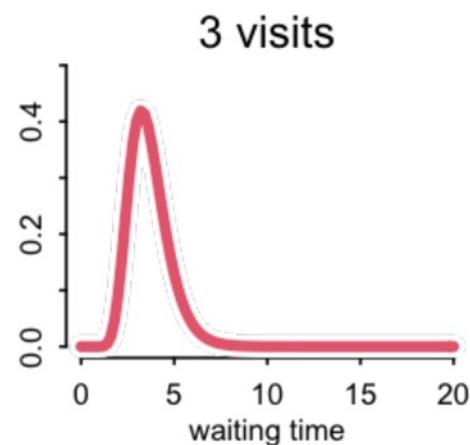
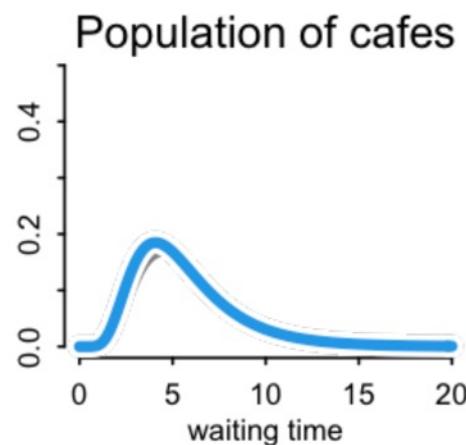


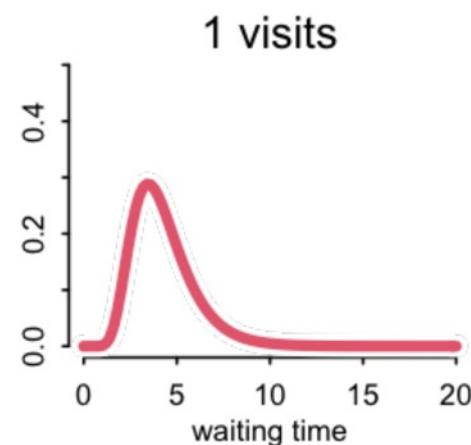
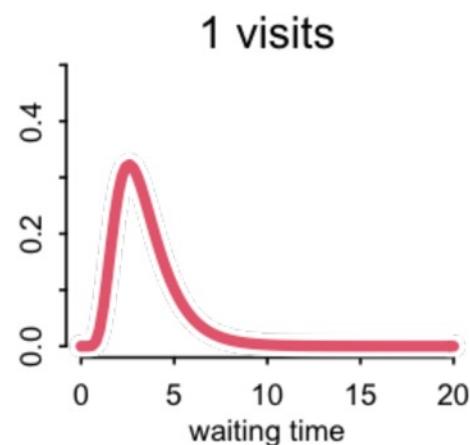
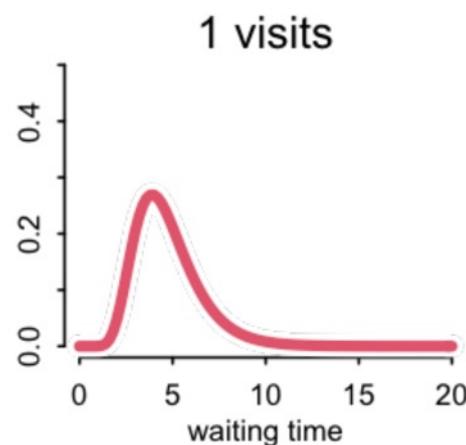
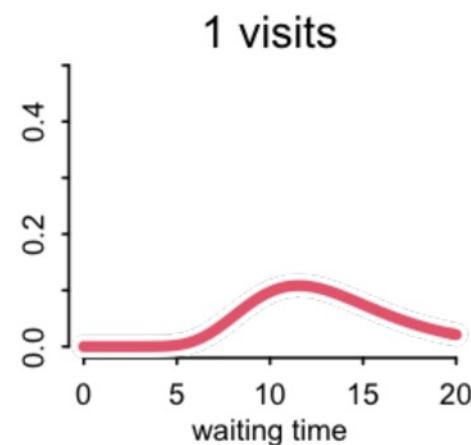
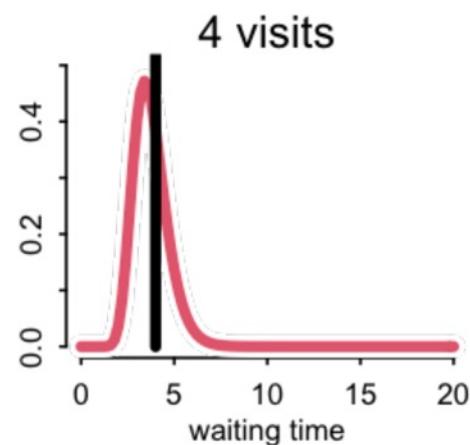
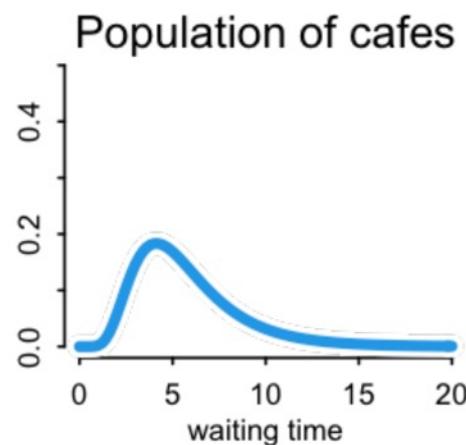


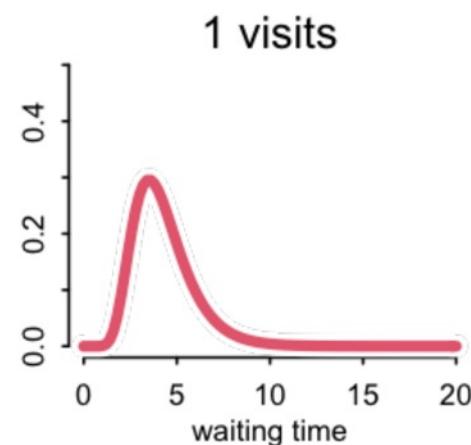
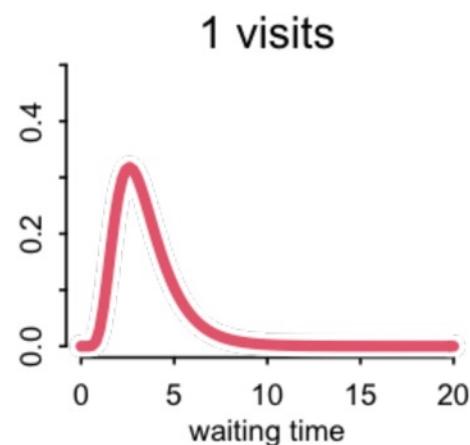
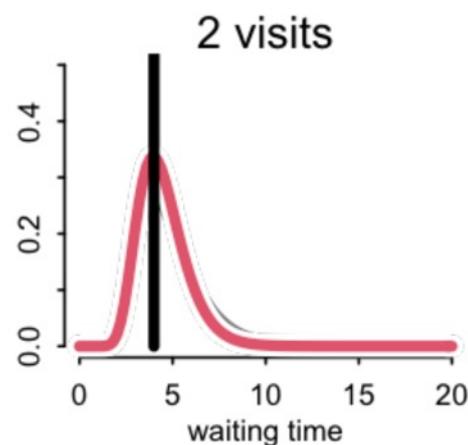
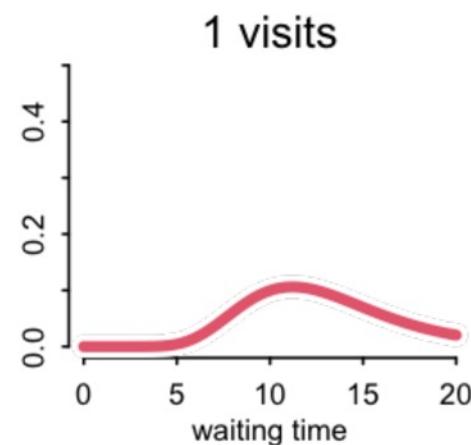
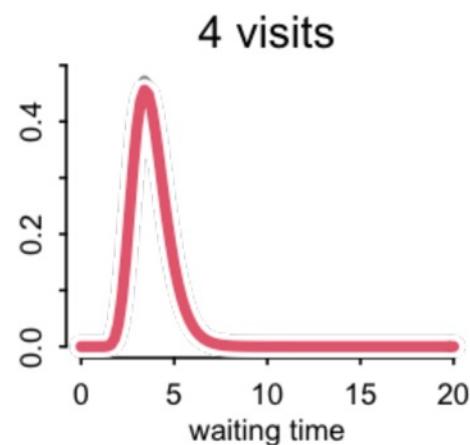
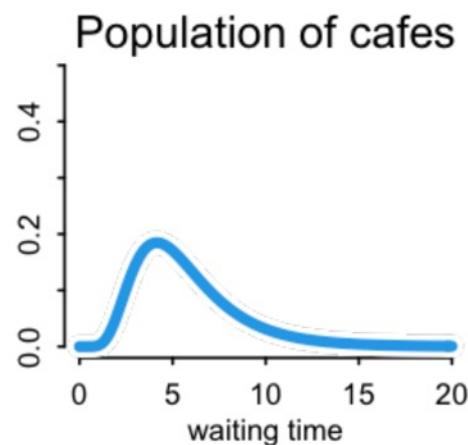


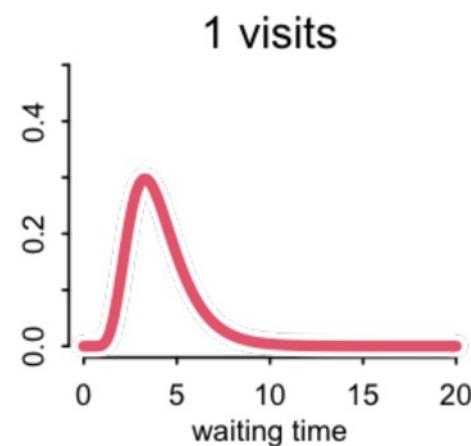
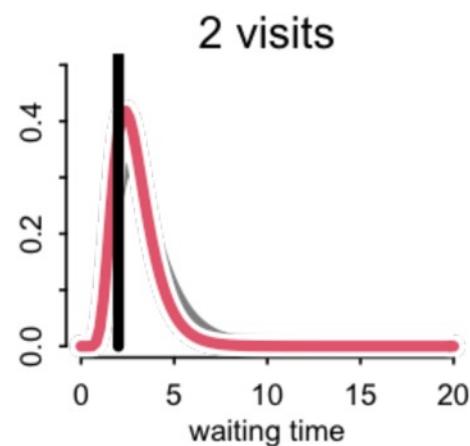
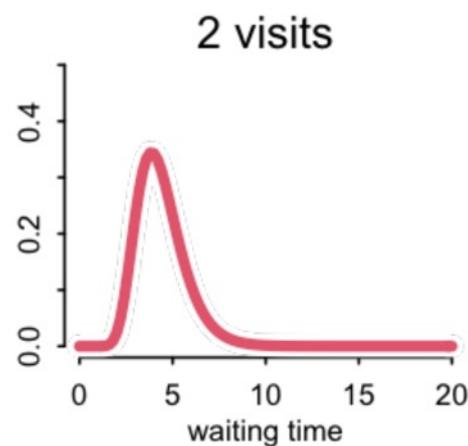
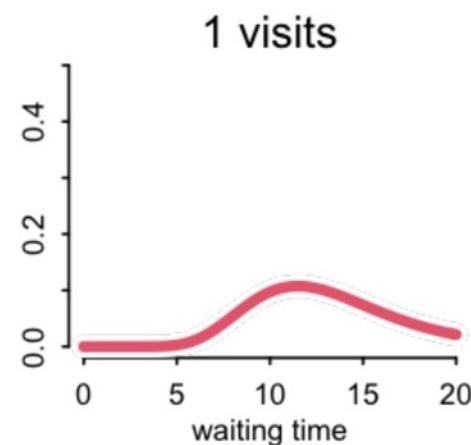
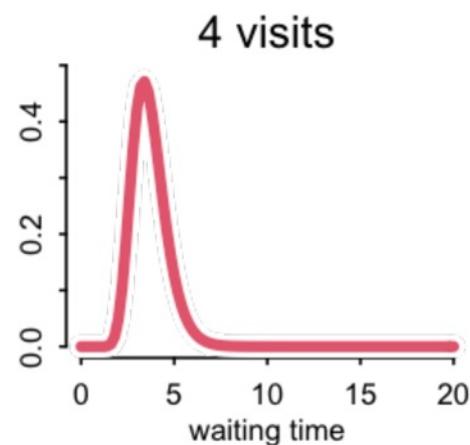
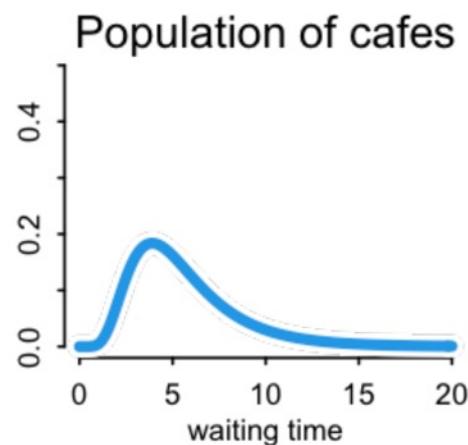


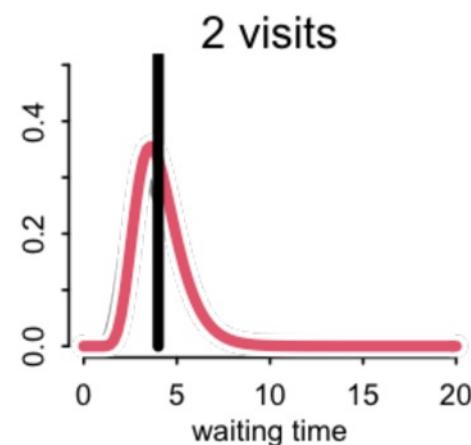
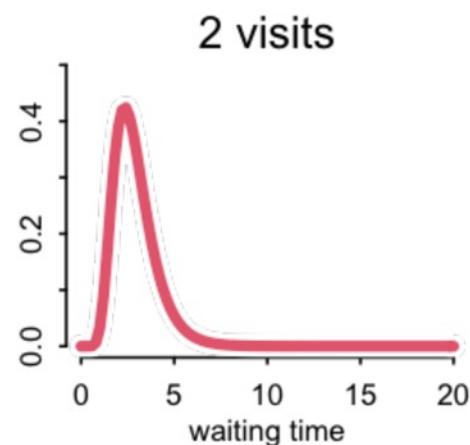
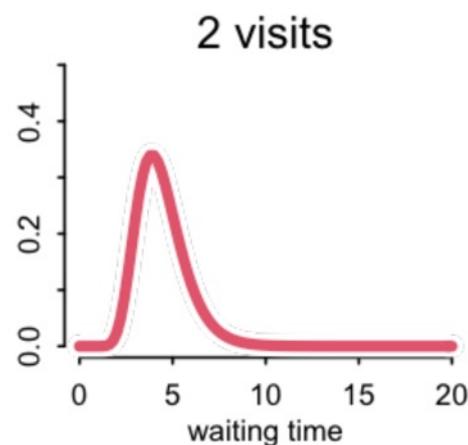
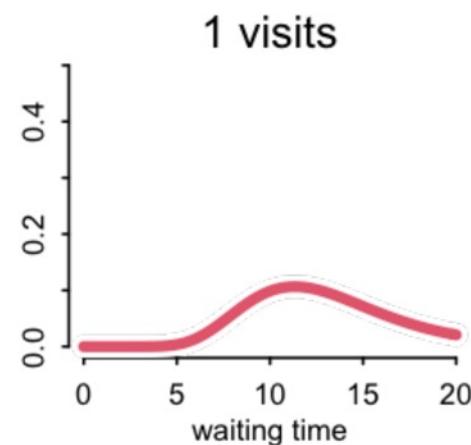
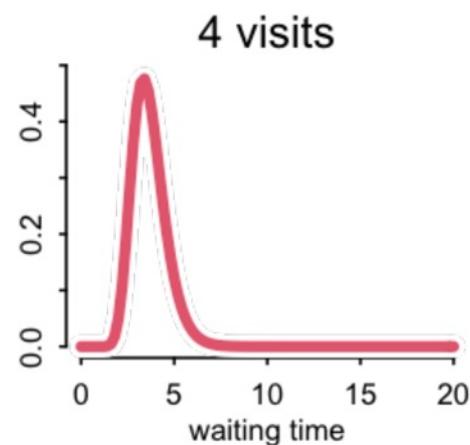
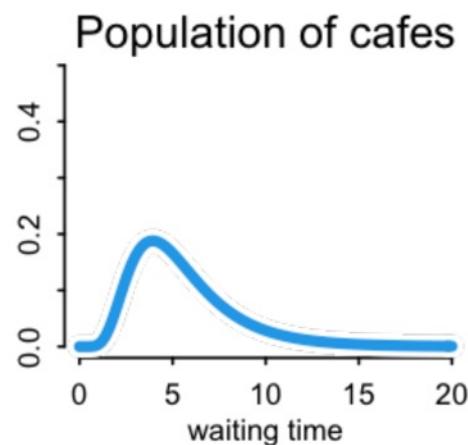


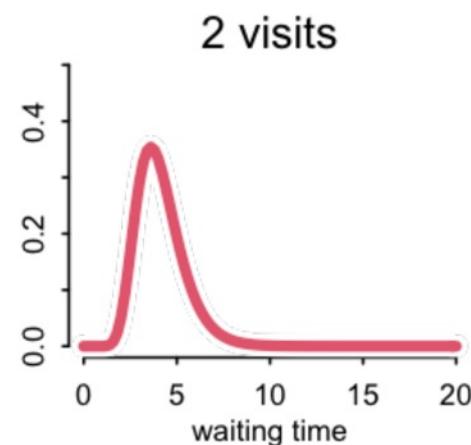
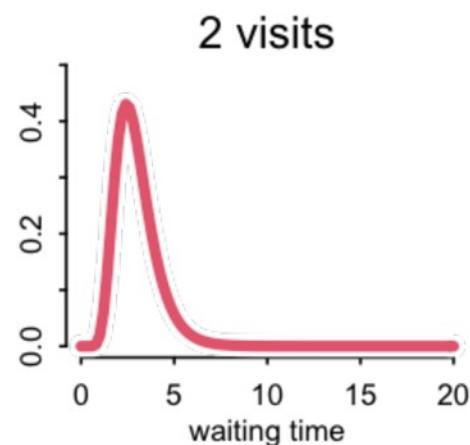
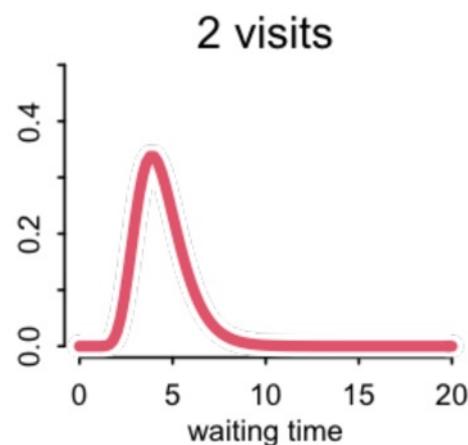
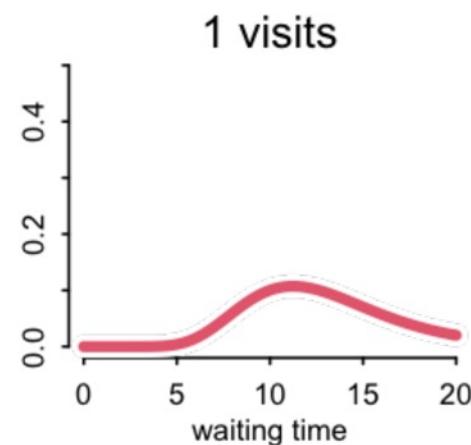
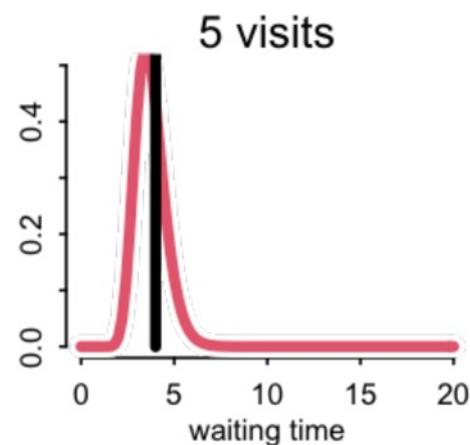
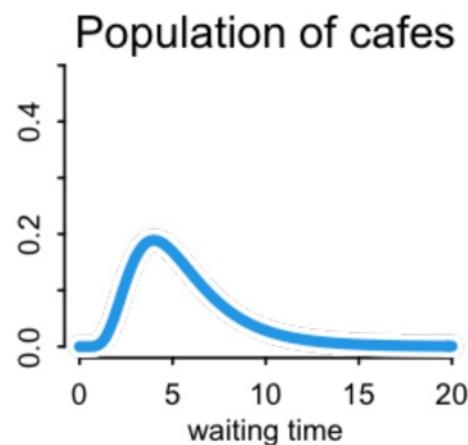


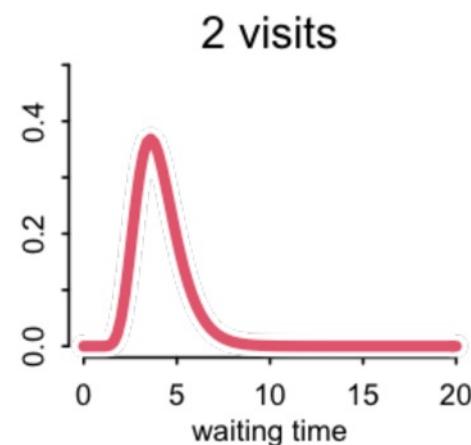
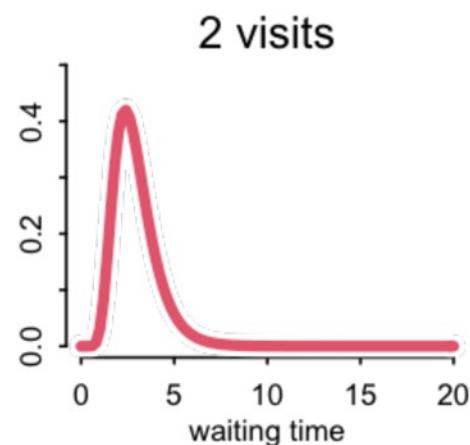
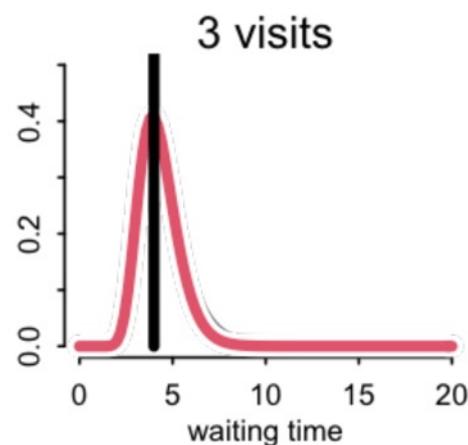
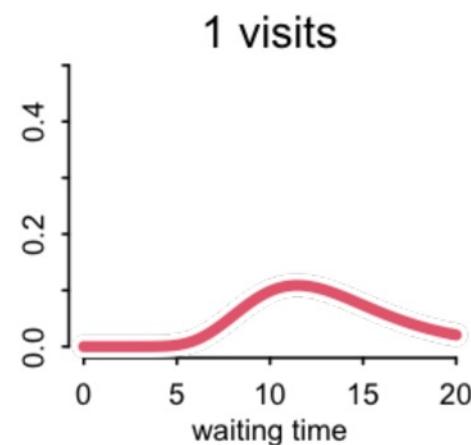
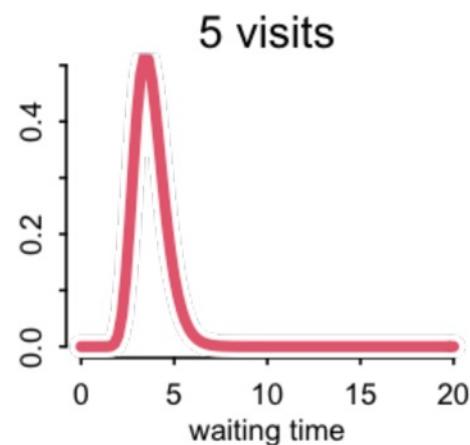
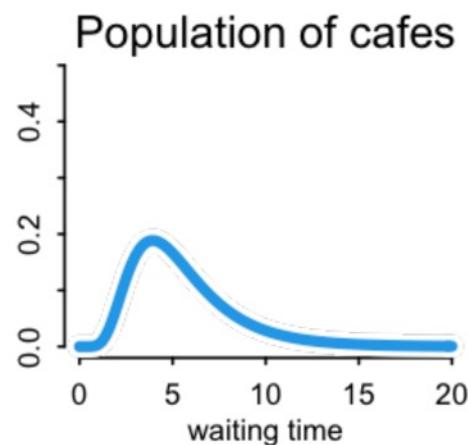


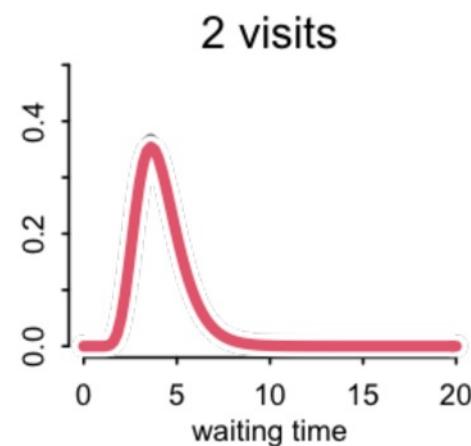
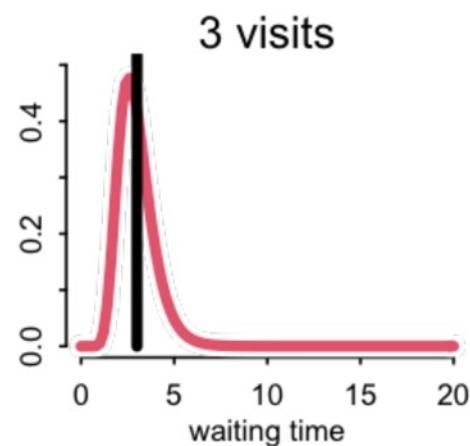
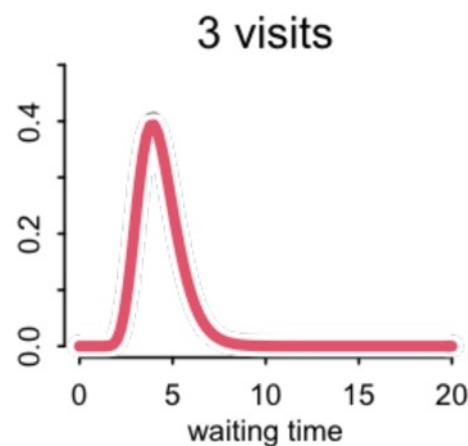
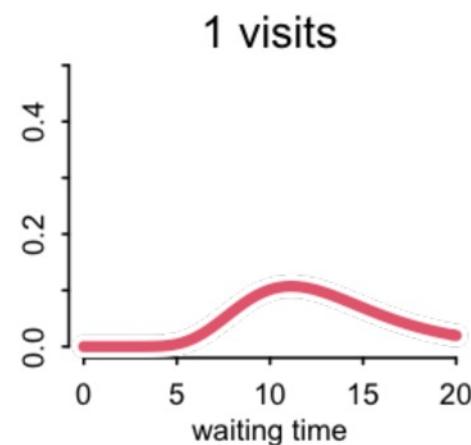
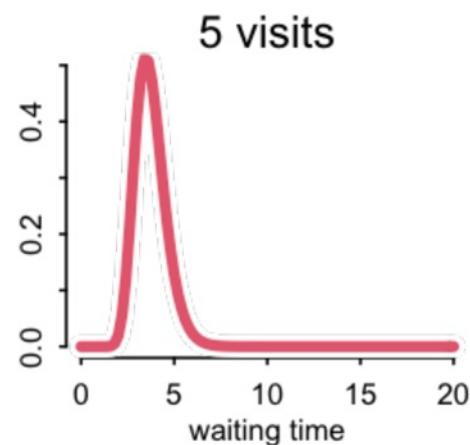
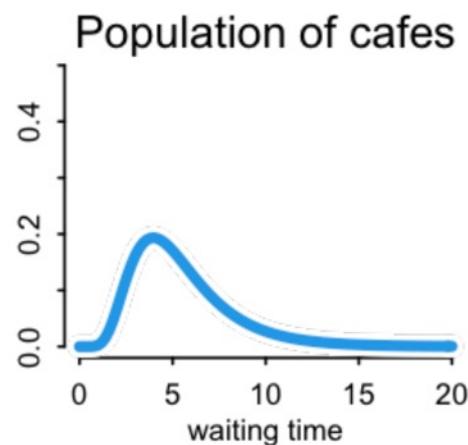


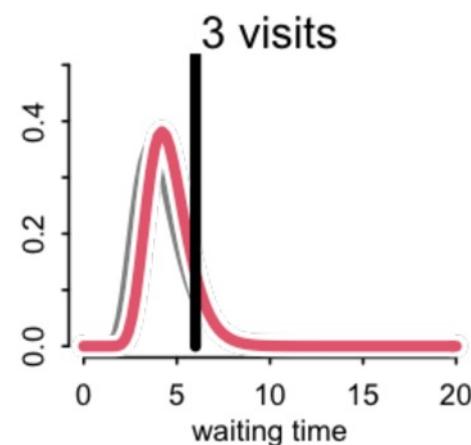
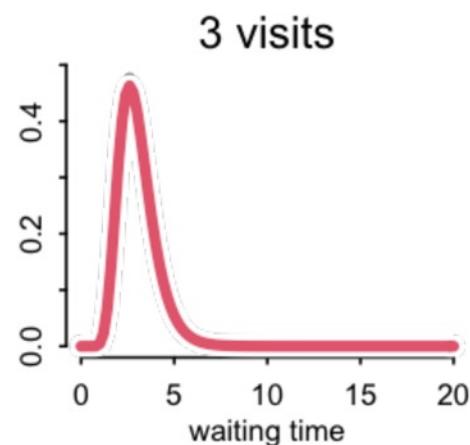
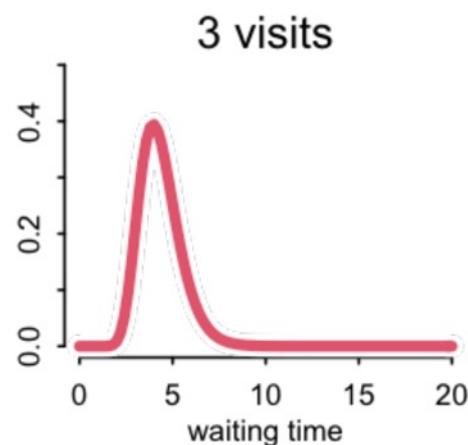
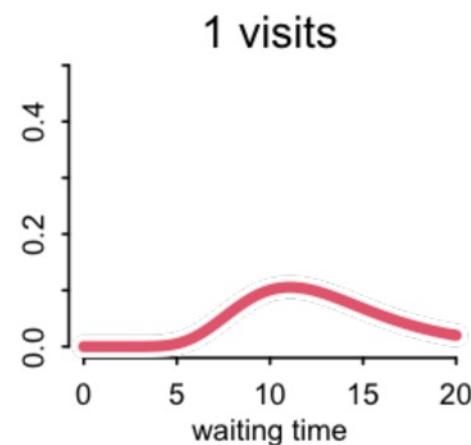
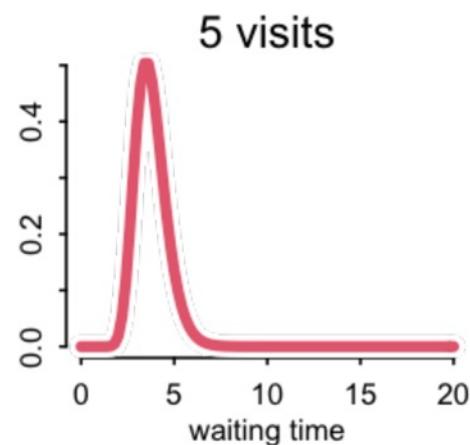
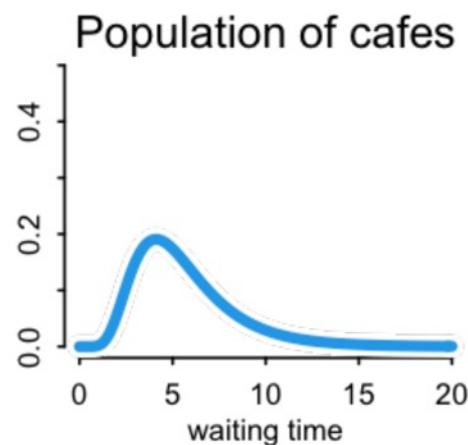


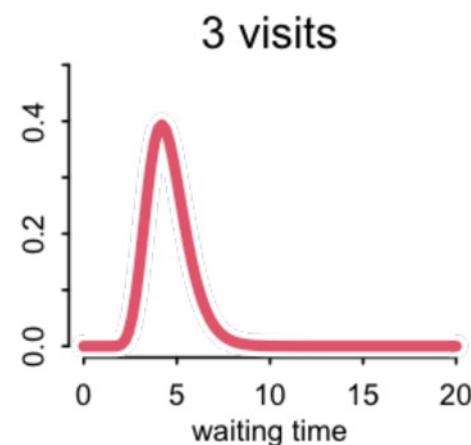
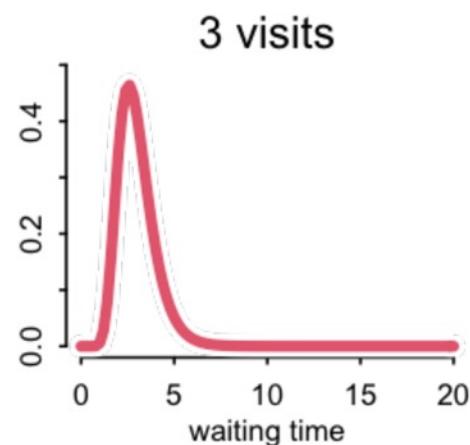
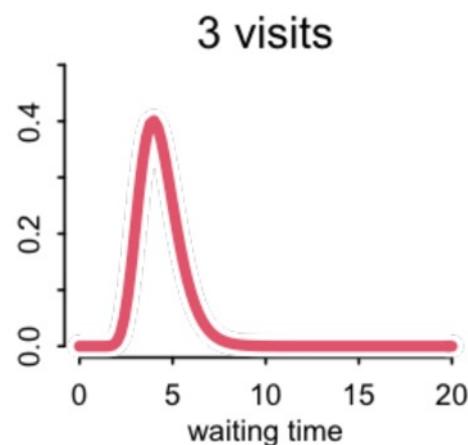
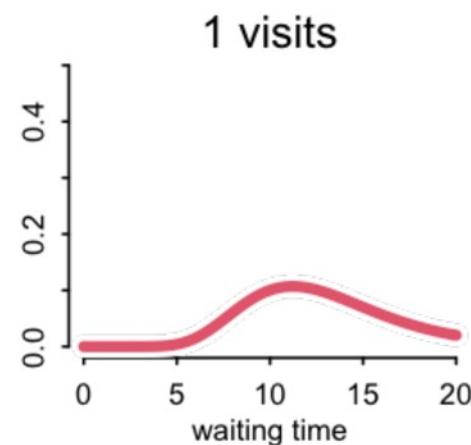
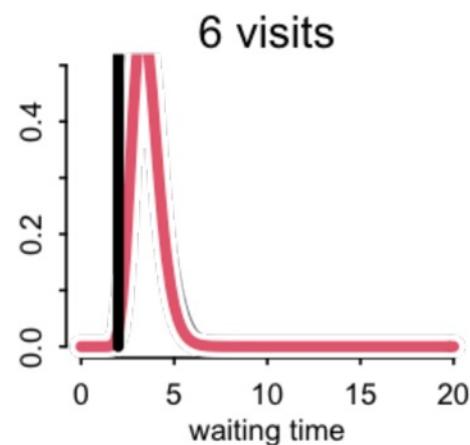
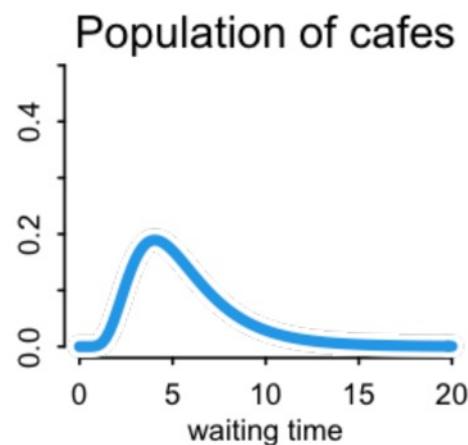


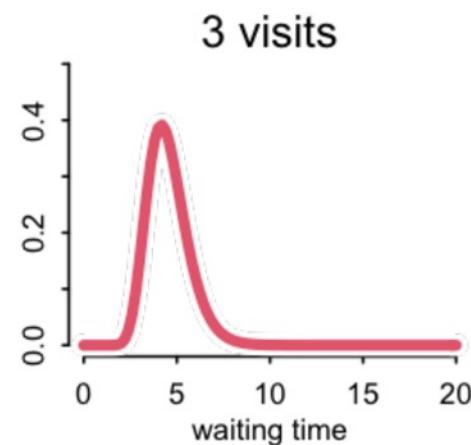
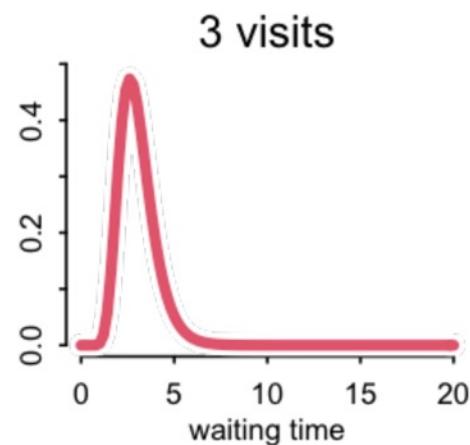
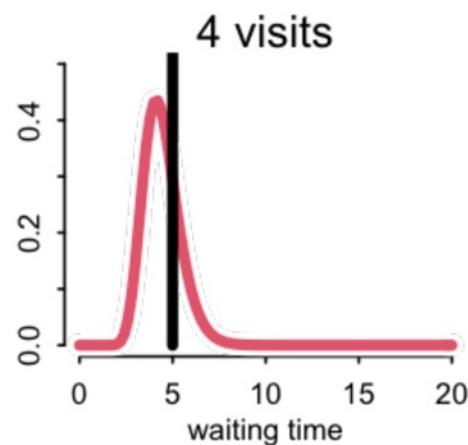
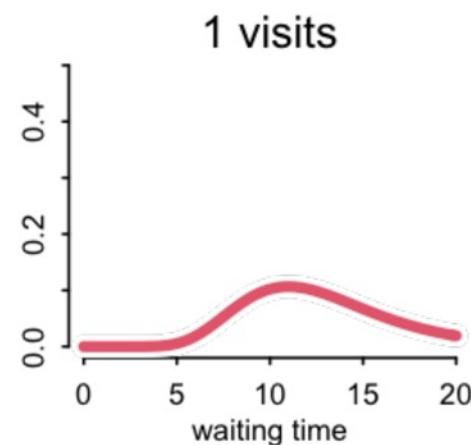
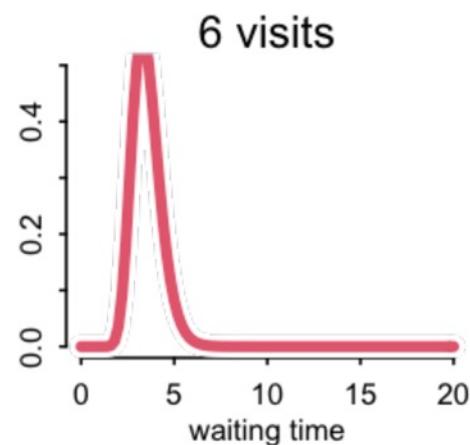
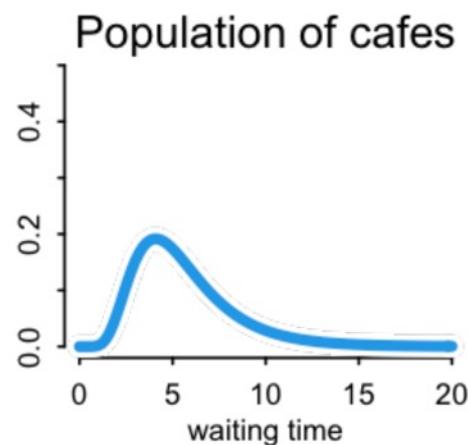


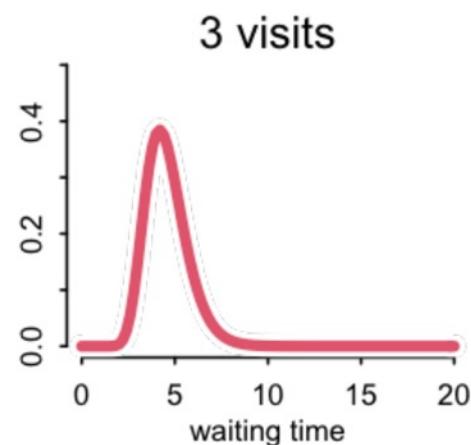
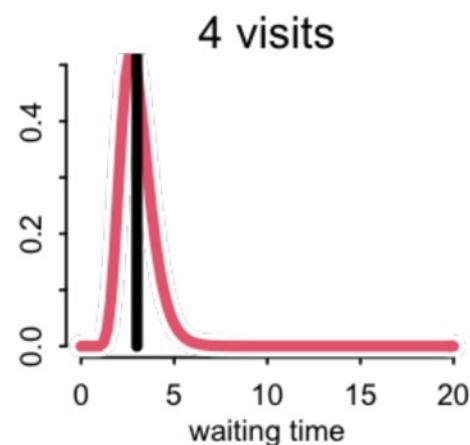
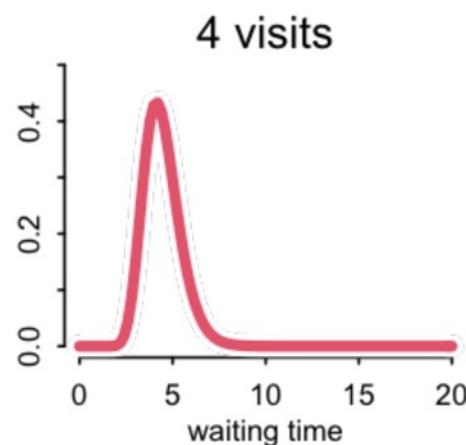
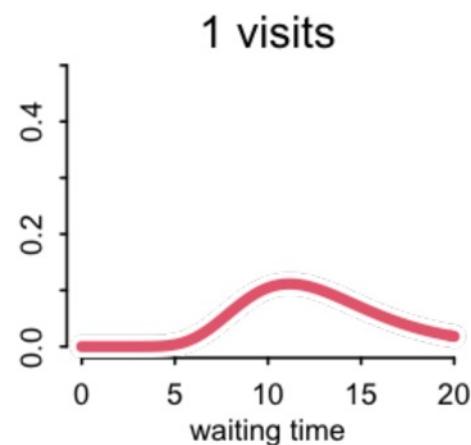
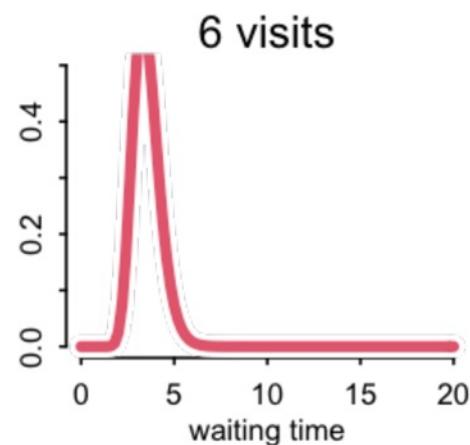
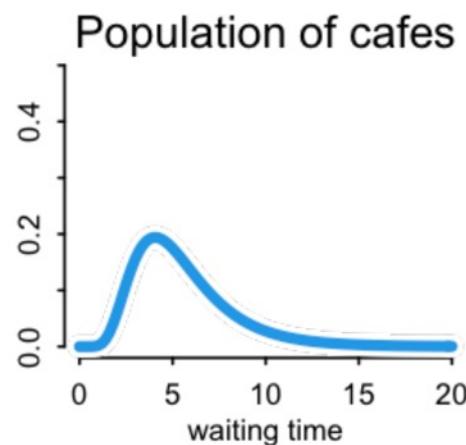


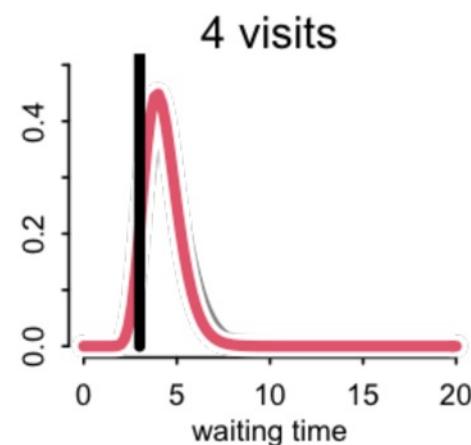
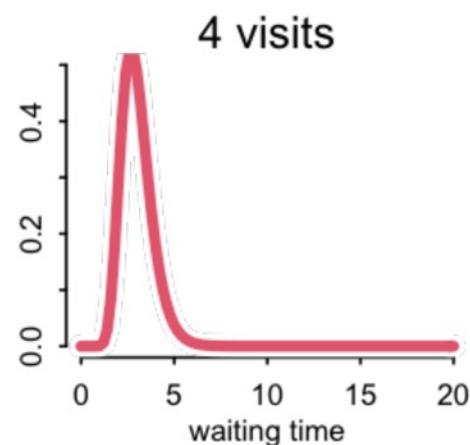
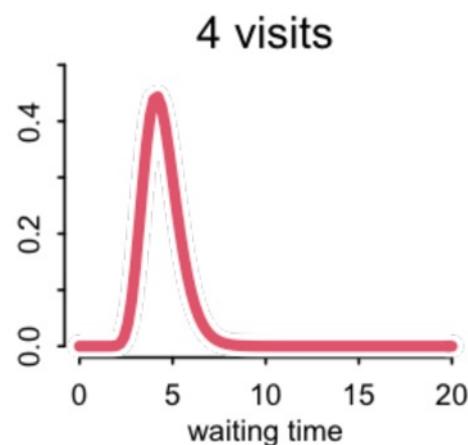
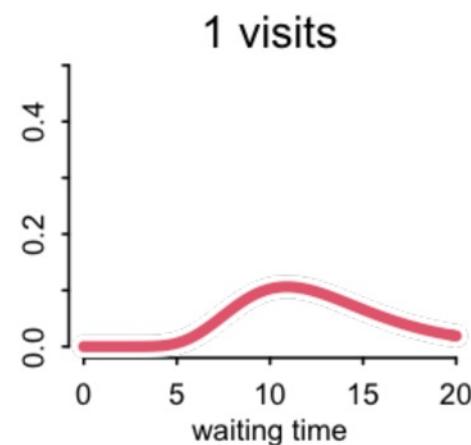
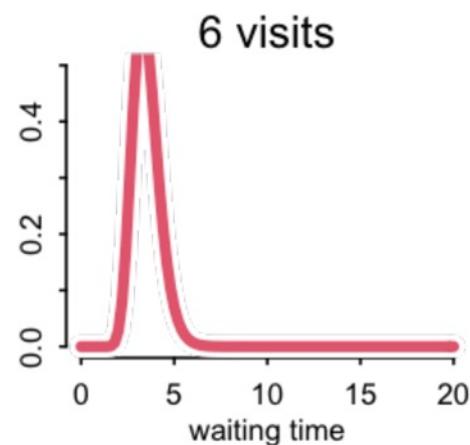
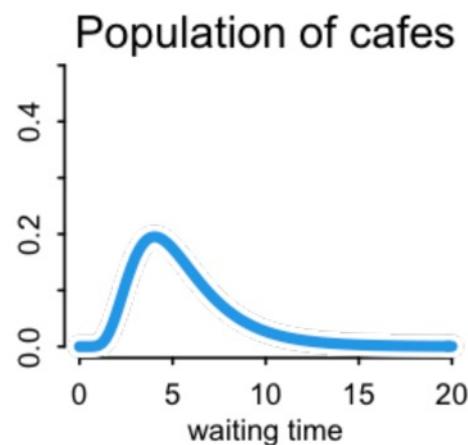


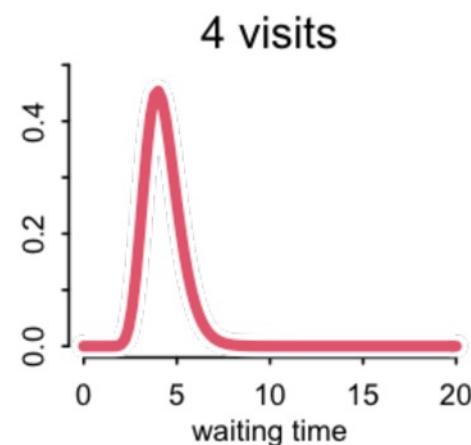
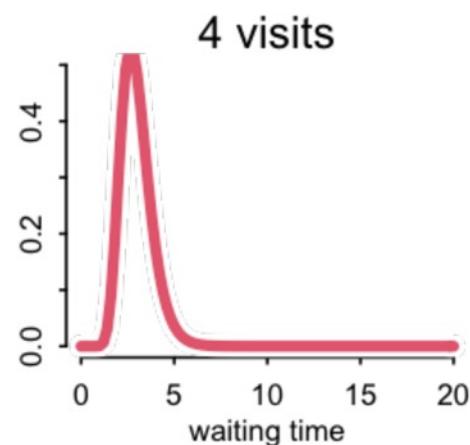
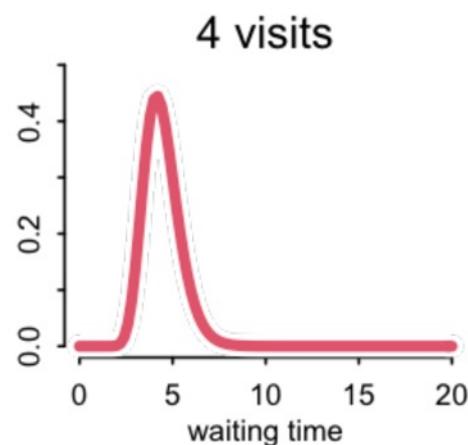
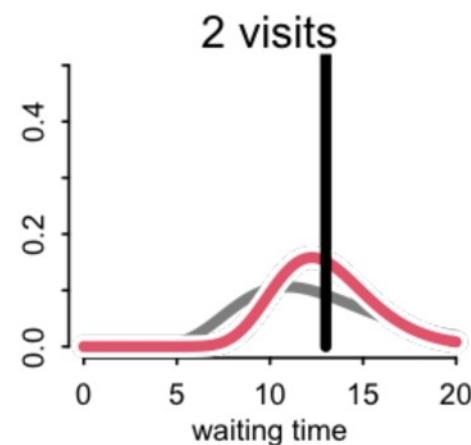
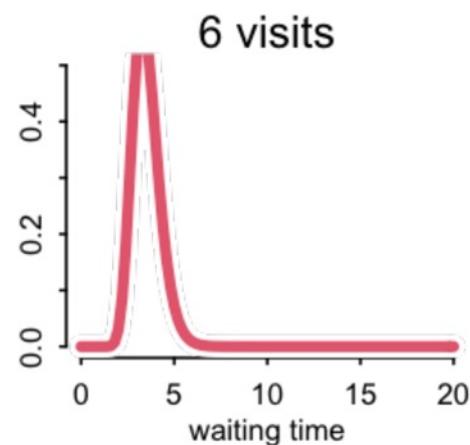
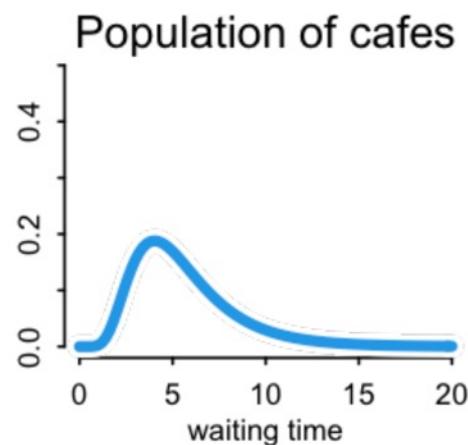












# Regularization

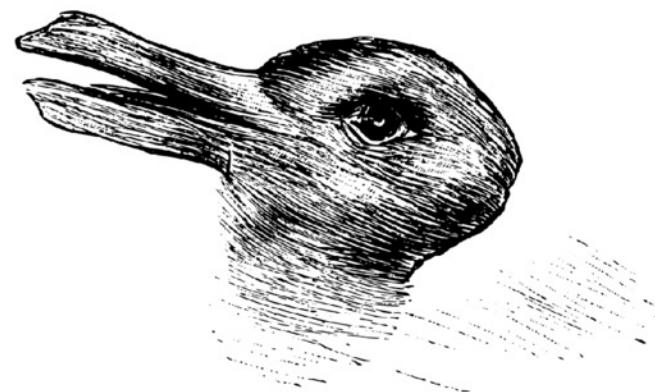
Another reason for multilevel models is that they adaptively regularize

**Complete pooling:** Treat all clusters as identical => underfitting

**No pooling:** Treat all clusters as unrelated => overfitting

**Partial pooling:** Adaptive compromise

Welche Thiere gleichen einander am meisten?



Raninchen und Ente.

# Reedfrogs in peril

---

data(reedfrogs)

48 groups (“tanks”) of tadpoles

Treatments: density, size, predation

Outcome: survival



Vonesh & Bolker (2005) Compensatory larval responses shift trade-offs associated with predator-induced hatching plasticity

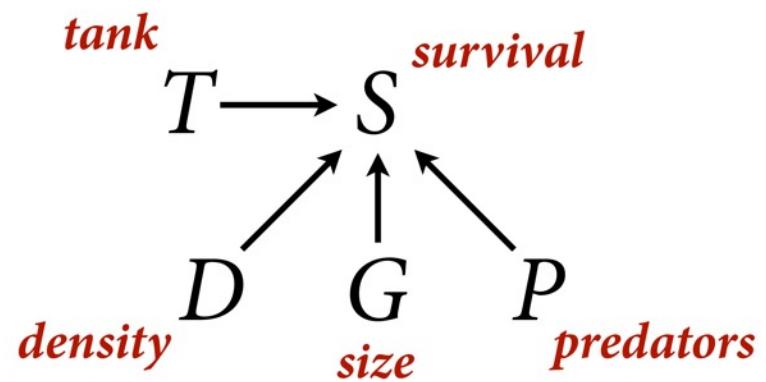
# Reedfrogs in peril

data(reedfrogs)

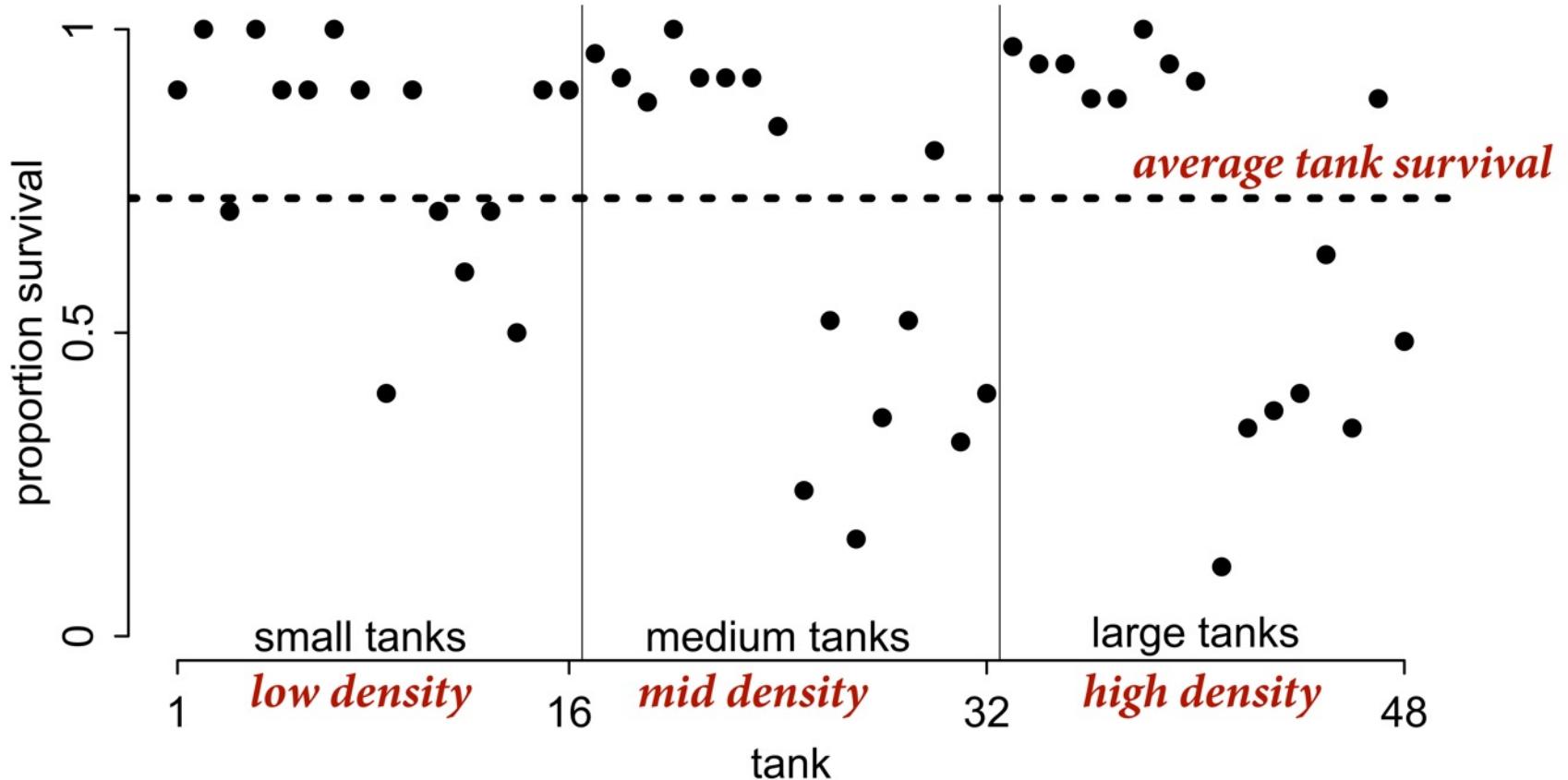
48 groups (“tanks”) of tadpoles

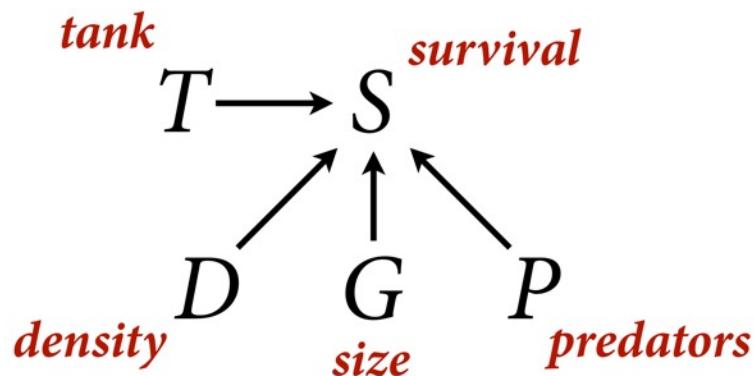
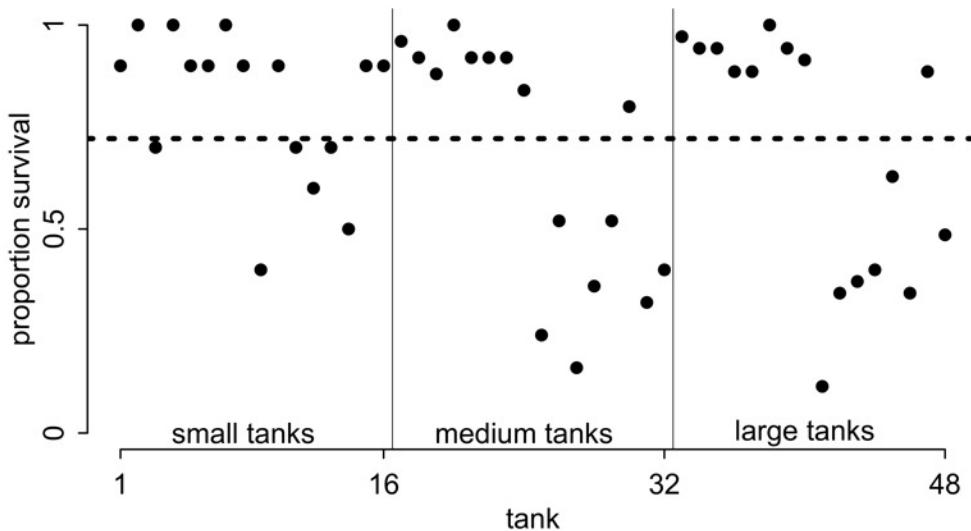
Treatments: density, size, predation

Outcome: survival



Vonesh & Bolker (2005) Compensatory larval responses shift trade-offs associated with predator-induced hatching plasticity



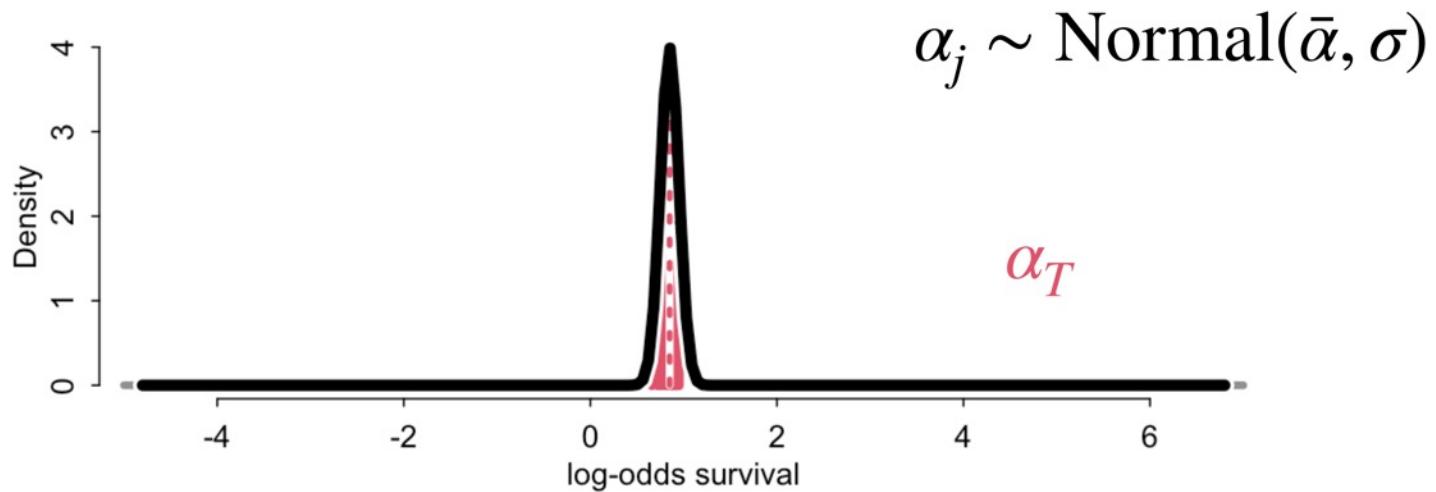
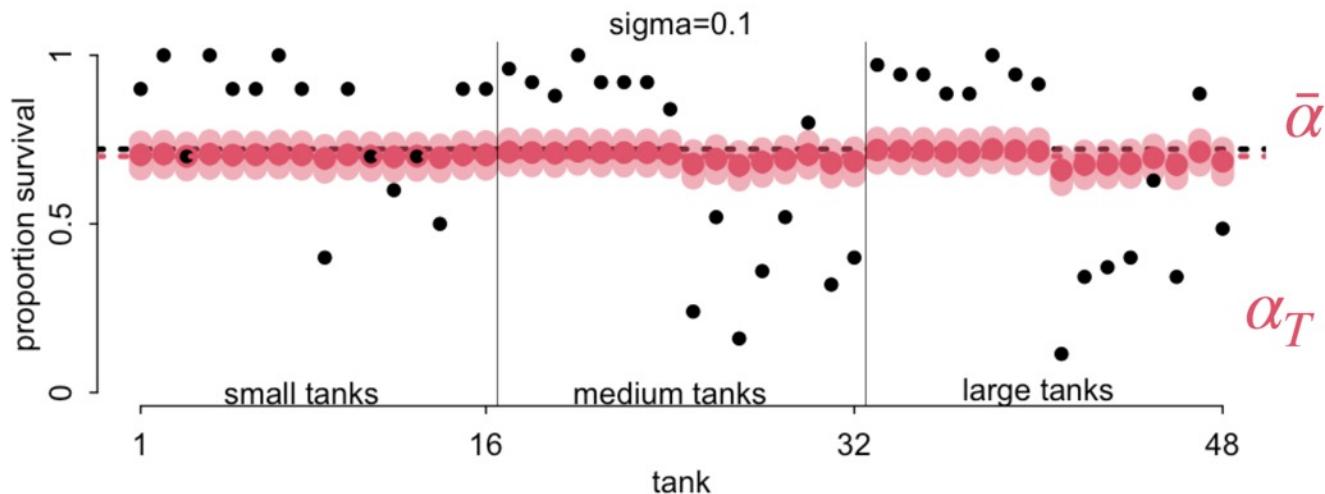


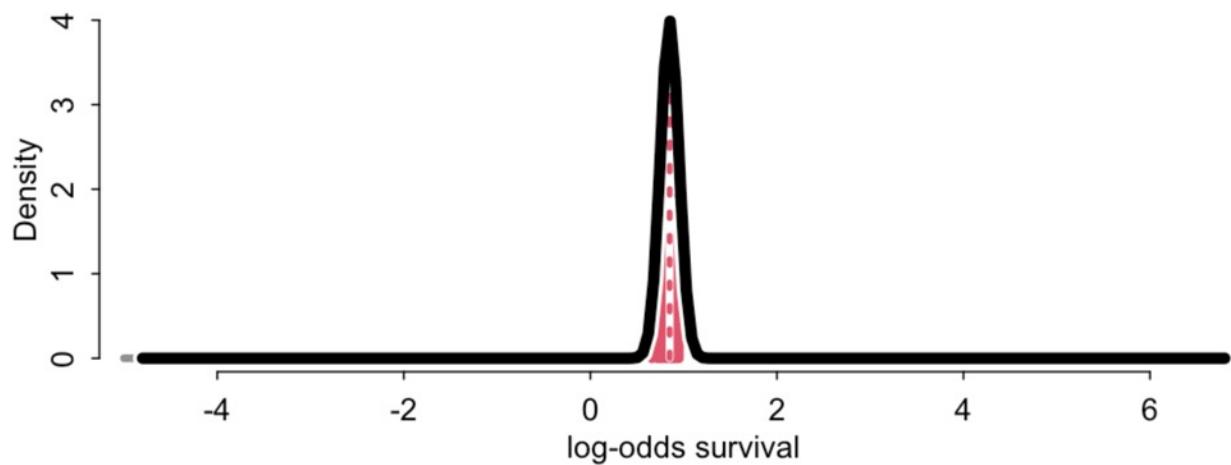
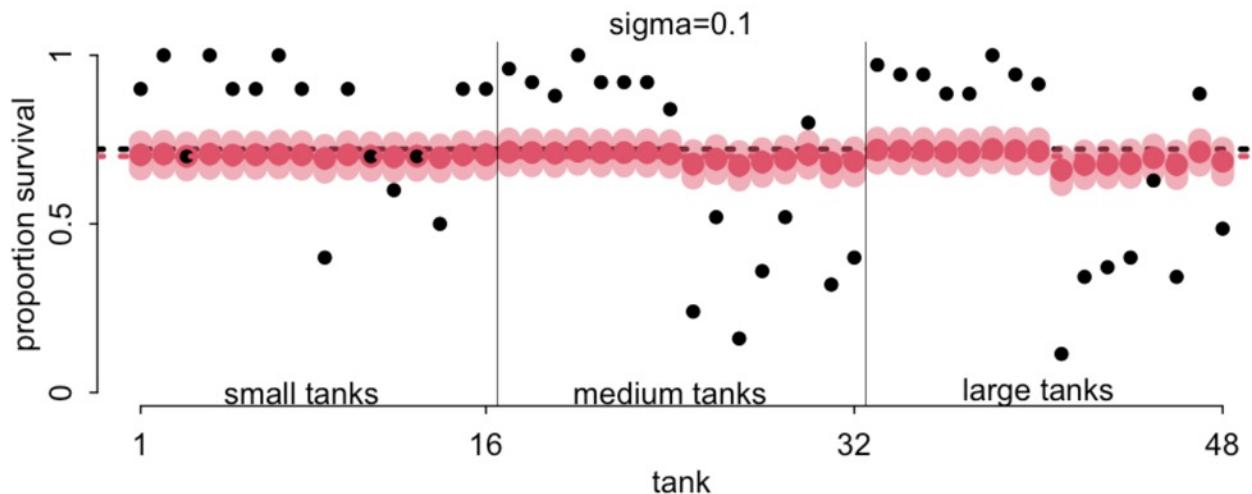
$$S_i \sim \text{Binomial}(D_i, p_i)$$

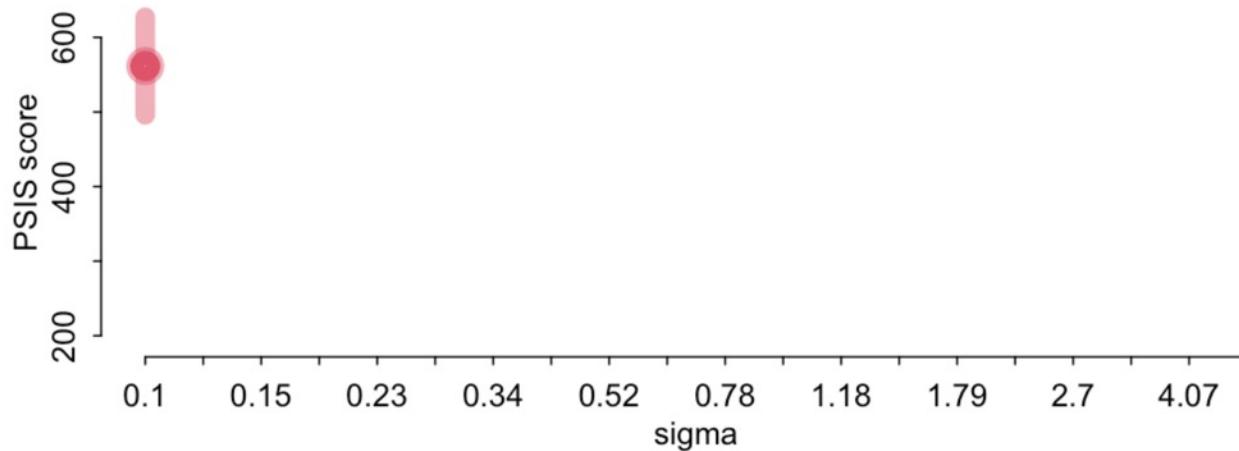
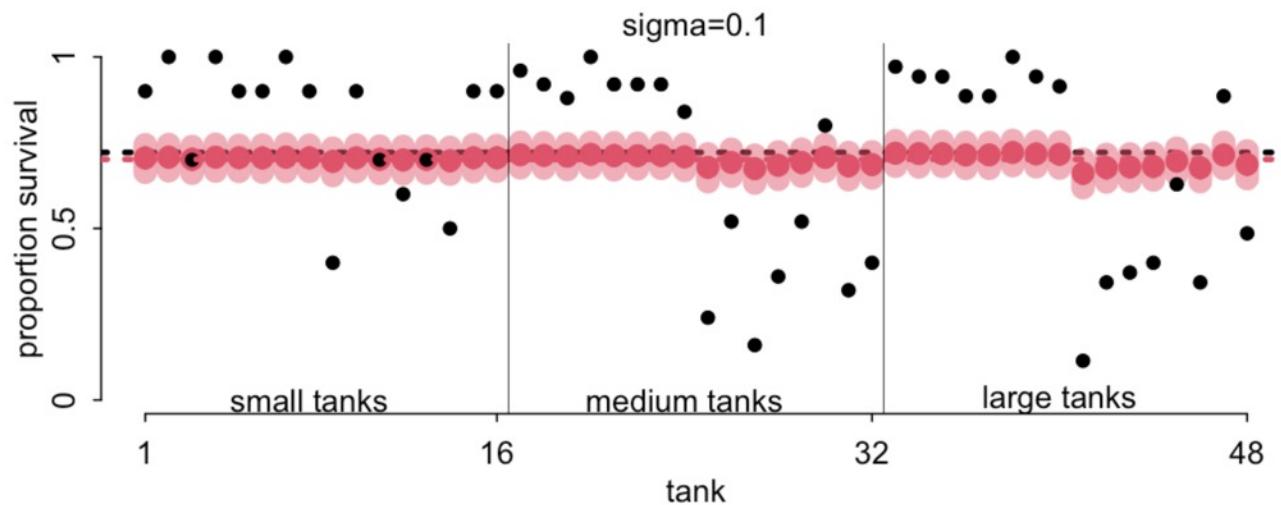
$$\text{logit}(p_i) = \alpha_{T[i]}$$

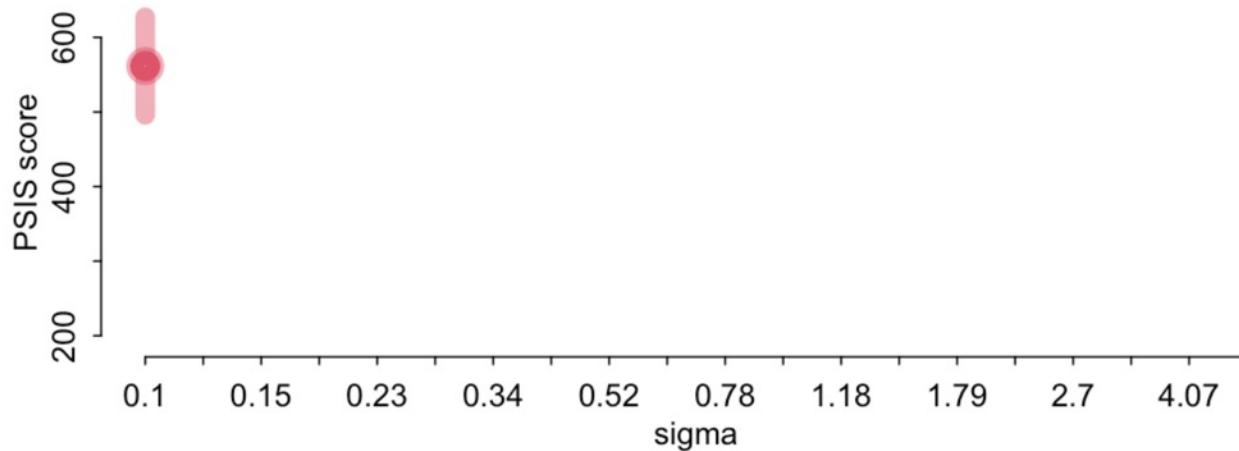
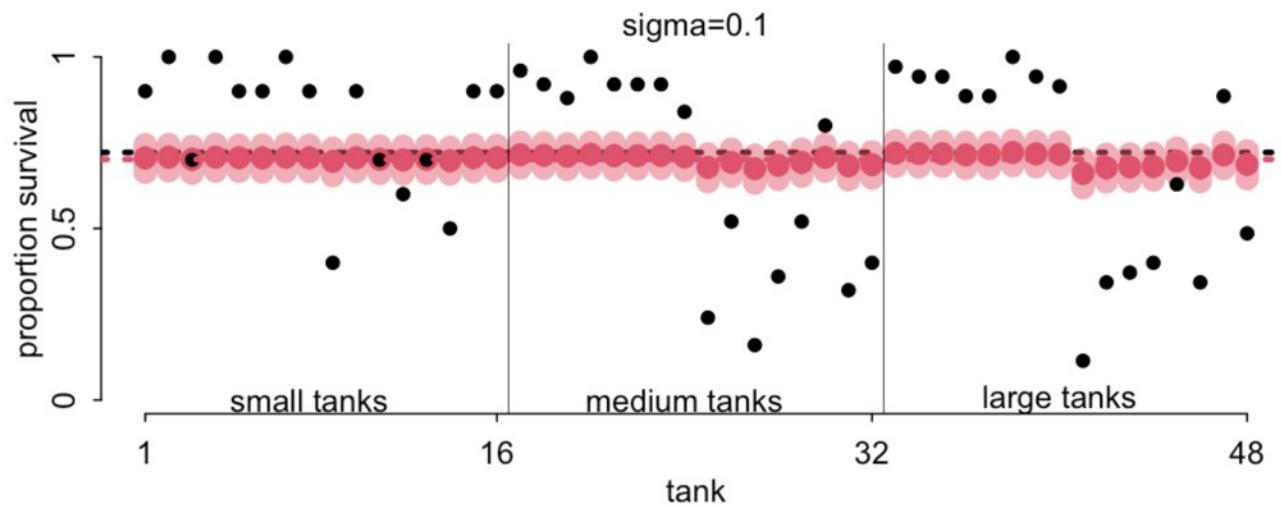
$$\alpha_j \sim \text{Normal}(\bar{\alpha}, ?)$$

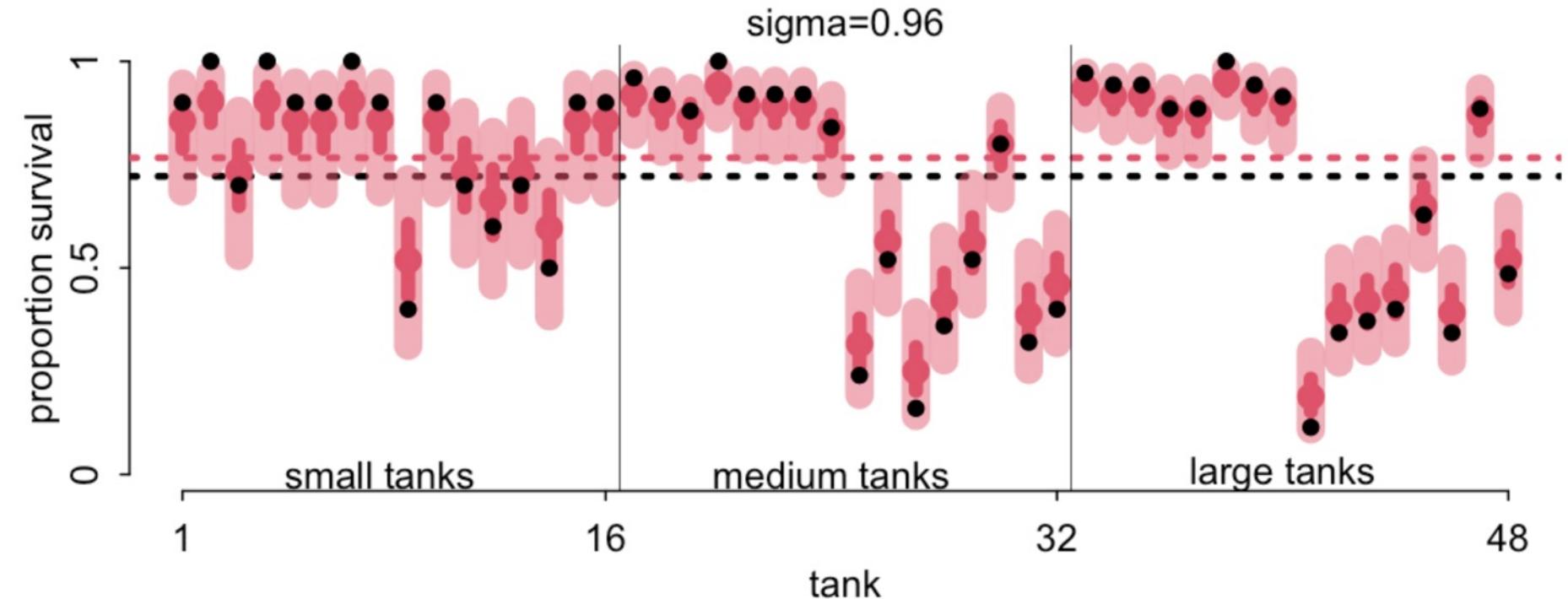
$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$







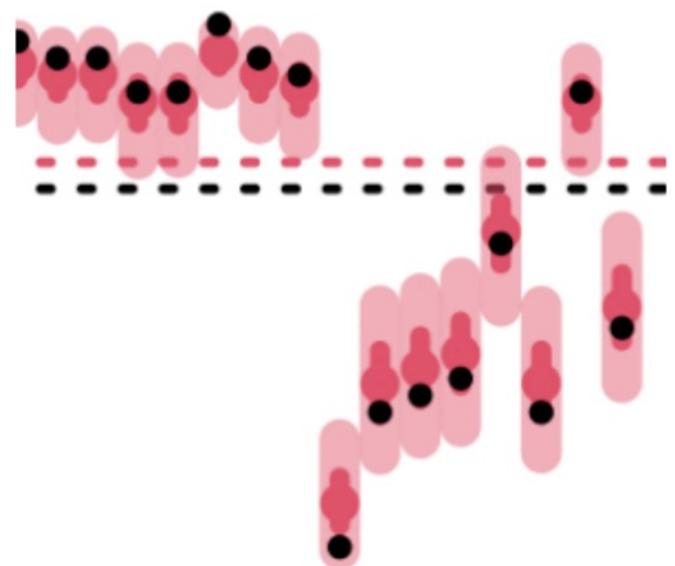


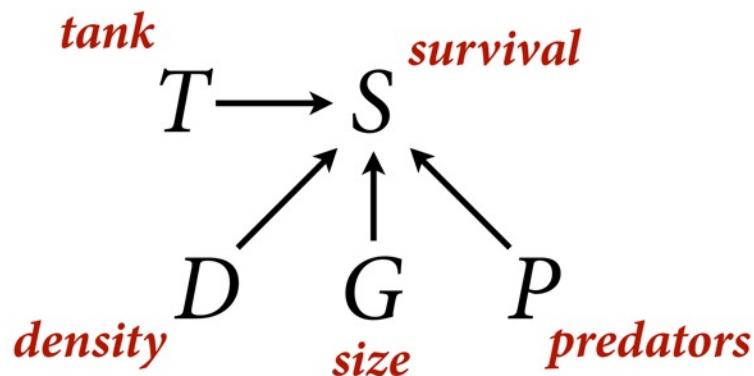
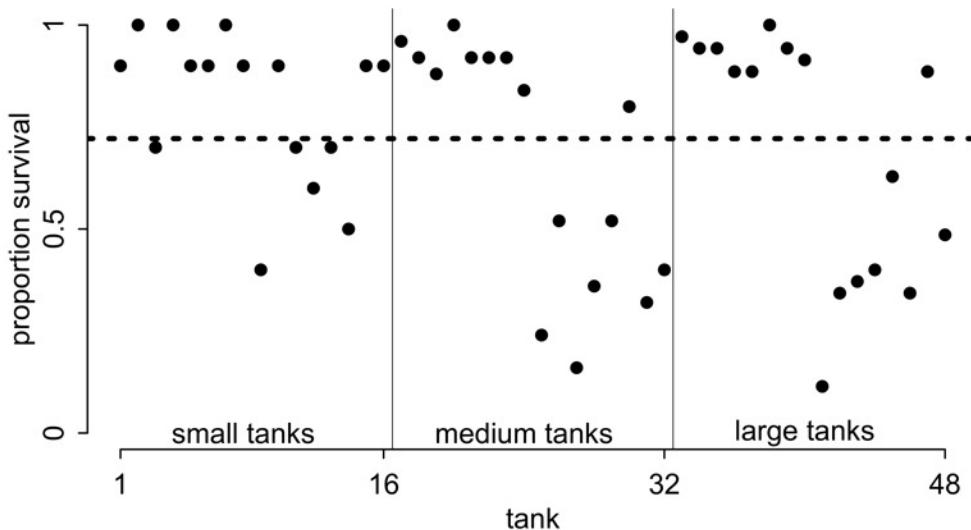


# Automatic regularization

Wouldn't it be nice if we could find a good sigma without running so many models?

Maybe we could learn it from the data?





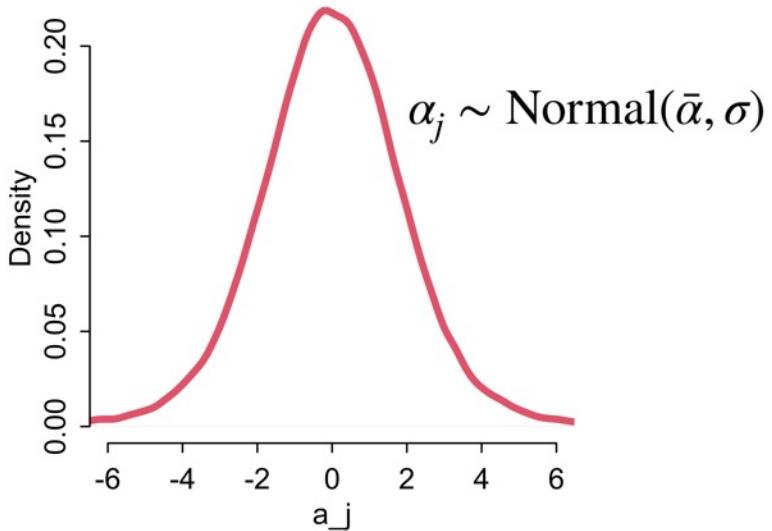
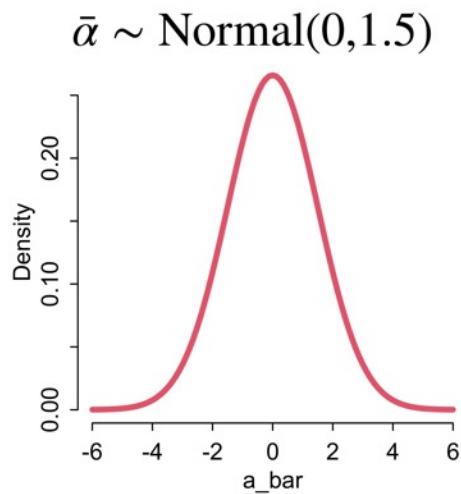
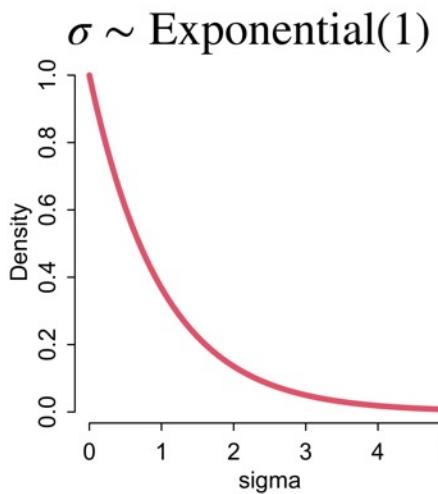
$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\text{logit}(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$


$$S_i \sim \text{Binomial}(D_i, p_i)$$
$$\text{logit}(p_i) = \alpha_{T[i]}$$
$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$
$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$
$$\sigma \sim \text{Exponential}(1)$$

```

library(rethinking)
data(reedfrogs)
d <- reedfrogs
d$tank <- 1:nrow(d)
dat <- list(
  S = d$surv,
  D = d$density,
  T = d$tank )

mST <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 ) )
  ), data=dat , chains=4 , log_lik=TRUE )

```

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\text{logit}(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$

```

library(rethinking)
data(reedfrogs)
d <- reedfrogs
d$tank <- 1:nrow(d)
dat <- list(
  S = d$surv,
  D = d$density,
  T = d$tank )

mST <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )

  ), data=dat , chains=4 , log_lik=TRUE )

```

	> precis(mST,depth=2)	mean	sd	5.5%	94.5%	n_eff	Rhat
a[1]	2.13	0.85	0.89	3.54	2992	1	
a[2]	3.06	1.04	1.57	4.82	2716	1	
a[3]	1.01	0.67	-0.01	2.11	5635	1	
a[4]	3.08	1.07	1.53	4.88	2441	1	
a[5]	2.14	0.87	0.85	3.61	3460	1	
a[6]	2.11	0.85	0.88	3.61	3628	1	
a[7]	3.05	1.08	1.54	4.90	3603	1	
a[8]	2.14	0.89	0.83	3.69	3190	1	
a[9]	-0.17	0.64	-1.20	0.88	5424	1	
a[10]	2.15	0.90	0.83	3.72	2559	1	
a[11]	1.00	0.66	-0.03	2.09	3265	1	
a[12]	0.57	0.63	-0.44	1.60	6602	1	
a[13]	1.01	0.67	-0.02	2.13	3618	1	
a[14]	0.21	0.62	-0.75	1.21	4147	1	
a[15]	2.18	0.85	0.84	3.51	4563	1	
a[16]	2.12	0.85	0.89	3.58	3030	1	
a[17]	2.88	0.77	1.82	4.22	3888	1	
a[18]	2.38	0.65	1.42	3.46	3645	1	
a[19]	2.01	0.58	1.16	2.95	4029	1	
a[20]	3.65	1.04	2.17	5.47	2750	1	
a[21]	2.39	0.65	1.43	3.47	3585	1	
a[22]	2.39	0.66	1.41	3.51	3607	1	
a[23]	2.40	0.66	1.45	3.49	3312	1	
a[24]	1.71	0.53	0.92	2.58	3395	1	
a[25]	-0.99	0.43	-1.69	-0.32	3187	1	
a[26]	0.16	0.39	-0.47	0.80	4611	1	
a[27]	-1.43	0.49	-2.23	-0.69	3289	1	
a[28]	-0.47	0.41	-1.15	0.15	5525	1	
a[29]	0.17	0.40	-0.46	0.82	5628	1	
a[30]	1.44	0.50	0.68	2.26	4925	1	
a[31]	-0.62	0.41	-1.29	0.03	5449	1	
a[32]	-0.30	0.39	-0.95	0.32	4039	1	
a[33]	3.19	0.80	2.06	4.60	2357	1	
a[34]	2.71	0.63	1.79	3.80	3117	1	
a[35]	2.71	0.62	1.82	3.71	3185	1	
a[36]	2.07	0.53	1.28	2.95	3616	1	
a[37]	2.05	0.47	1.34	2.82	4705	1	
a[38]	3.87	0.91	2.56	5.42	3022	1	
a[39]	2.71	0.66	1.76	3.80	3479	1	
a[40]	2.37	0.59	1.47	3.38	2981	1	
a[41]	-1.79	0.45	-2.54	-1.13	4340	1	
a[42]	-0.58	0.35	-1.14	0.00	4354	1	
a[43]	-0.45	0.36	-1.01	0.10	5360	1	
a[44]	-0.33	0.34	-0.89	0.22	4541	1	
a[45]	0.58	0.35	0.02	1.15	5803	1	
a[46]	-0.56	0.37	-1.14	0.02	4696	1	
a[47]	2.06	0.51	1.27	2.91	3955	1	
a[48]	0.01	0.35	-0.55	0.56	5353	1	
a_bar	1.35	0.26	0.93	1.78	2746	1	
sigma	1.61	0.21	1.32	1.96	1557	1	

$\alpha_{T[i]}$

$\text{Normal}(\bar{\alpha}, \sigma)$

$\text{Normal}(0, 1.5)$

$\text{Exponential}(1)$

```

library(rethinking)
data(reedfrogs)
d <- reedfrogs
d$tank <- 1:nrow(d)
dat <- list(
  S = d$surv,
  D = d$density,
  T = d$tank )

mST <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )

  ), data=dat , chains=4 , log_lik=TRUE )

```

```

> precis(mST, depth=2)
      mean   sd  5.5% 94.5% n_eff Rhat4
a[1]  2.13 0.85  0.89  3.54  2992    1
a[2]  3.06 1.04  1.57  4.82  2716    1
a[3]  1.01 0.67 -0.01  2.11  5635    1
a[4]  3.08 1.07  1.53  4.88  2441    1
a[5]  2.14 0.87  0.85  3.61  3460    1
a[6]  2.11 0.85  0.88  3.61  3628    1
a[7]  3.05 1.08  1.54  4.90  3603    1
a[8]  2.14 0.89  0.83  3.69  3190    1
a[9] -0.17 0.64 -1.20  0.88  5424    1
a[10] 2.15 0.90  0.83  3.72  2559    1
a[11] 1.00 0.66 -0.03  2.09  3265    1
a[12] 0.57 0.63 -0.44  1.60  6602    1
a[13] 1.01 0.67 -0.02  2.13  3618    1
a[14] 0.21 0.62 -0.75  1.21  4147    1
a[15] 2.18 0.85  0.84  3.51  4563    1
a[16] 2.12 0.85  0.89  3.58  3030    1
a[17] 2.88 0.77  1.82  4.22  3888    1
a[18] 2.38 0.65  1.42  3.46  3645    1
a[19] 2.01 0.58  1.16  2.95  4029    1
a[20] 3.65 1.04  2.17  5.47  2750    1

```

$\text{Binomial}(D_i, p_i)$

$\alpha_{T[i]}$

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a_bar	1.35	0.26	0.93	1.78	2746	1
sigma	1.61	0.21	1.32	1.96	1557	1

$\bar{x}, \sigma$ )

$\text{Normal}(0, 1.5)$

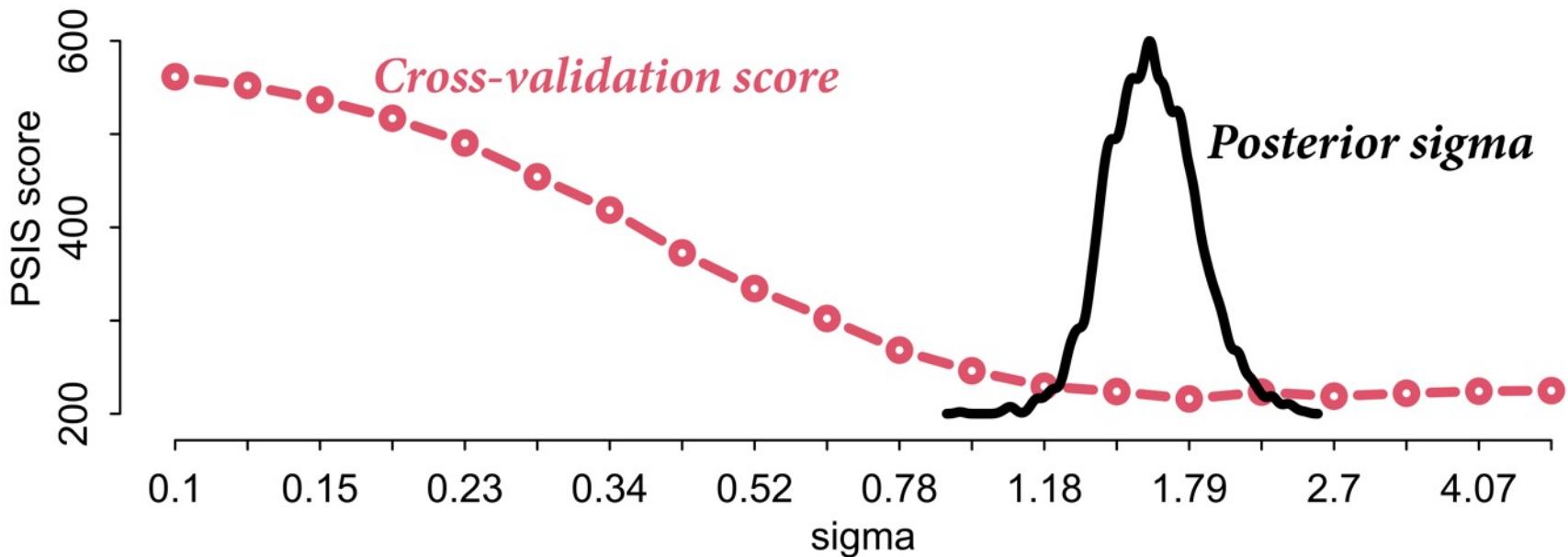
$\text{Exponential}(1)$

```

a[29] 0.17 0.40 -0.46  0.82  5628    1
a[30] 1.44 0.50  0.68  2.26  4925    1
a[31] -0.62 0.41 -1.29  0.03  5449    1
a[32] -0.30 0.39 -0.95  0.32  4039    1
a[33] 3.19 0.80  2.06  4.60  2357    1
a[34] 2.71 0.63  1.79  3.80  3117    1
a[35] 2.71 0.62  1.82  3.71  3185    1
a[36] 2.07 0.53  1.28  2.95  3616    1
a[37] 2.05 0.47  1.34  2.82  4705    1
a[38] 3.87 0.91  2.56  5.42  3022    1
a[39] 2.71 0.66  1.76  3.80  3479    1
a[40] 2.37 0.59  1.47  3.38  2981    1
a[41] -1.79 0.45 -2.54 -1.13  4340    1
a[42] -0.58 0.35 -1.14  0.00  4354    1
a[43] -0.45 0.36 -1.01  0.10  5360    1
a[44] -0.33 0.34 -0.89  0.22  4541    1
a[45] 0.58 0.35  0.02  1.15  5803    1
a[46] -0.56 0.37 -1.14  0.02  4696    1
a[47] 2.06 0.51  1.27  2.91  3955    1
a[48] 0.01 0.35 -0.55  0.56  5353    1
a_bar 1.35 0.26  0.93  1.78  2746    1
sigma 1.61 0.21  1.32  1.96  1557    1

```

	mean	sd	5.5%	94.5%	n_eff	Rhat4
a_bar	1.35	0.26	0.93	1.78	2746	1
sigma	1.61	0.21	1.32	1.96	1557	1



```
mST <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )
  ), data=dat , chains=4 , log_lik=TRUE )
```

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\text{logit}(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$

```
mSTnomem <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , 1 ) ,
    a_bar ~ dnorm( 0 , 1.5 )
  ), data=dat , chains=4 , log_lik=TRUE )

compare( mST , mSTnomem , func=WAIC )
```

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\text{logit}(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, 1)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

```

mST <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )
  ), data=dat , chains=4 , log_lik=TRUE )
compare( mST , mSTnomem , func=WAIC )

```

```

mSTnomem <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , 1 ) ,
    a_bar ~ dnorm( 0 , 1.5 )
  ), data=dat , chains=4 , log_lik=TRUE )
compare( mST , mSTnomem , func=WAIC )

```

	WAIC	SE	dWAIC	dSE	pWAIC	weight
mST	200.6	7.52	0.0	NA	21.1	1
mSTnomem	217.4	7.80	16.8	4.35	25.6	0

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\logit(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\logit(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, 1)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

```
mST <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )
  ), data=dat , cld
```

```
mSTnomem <- ulam(
  alist(
```

	WAIC	SE	dWAIC	dSE	pWAIC	weight
mST	200.6	7.52	0.0	NA	21.1	1
mSTnomem	217.4	7.80	16.8	4.35	25.6	0

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\logit(p_i) = \alpha_{T[i]}$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha} \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$

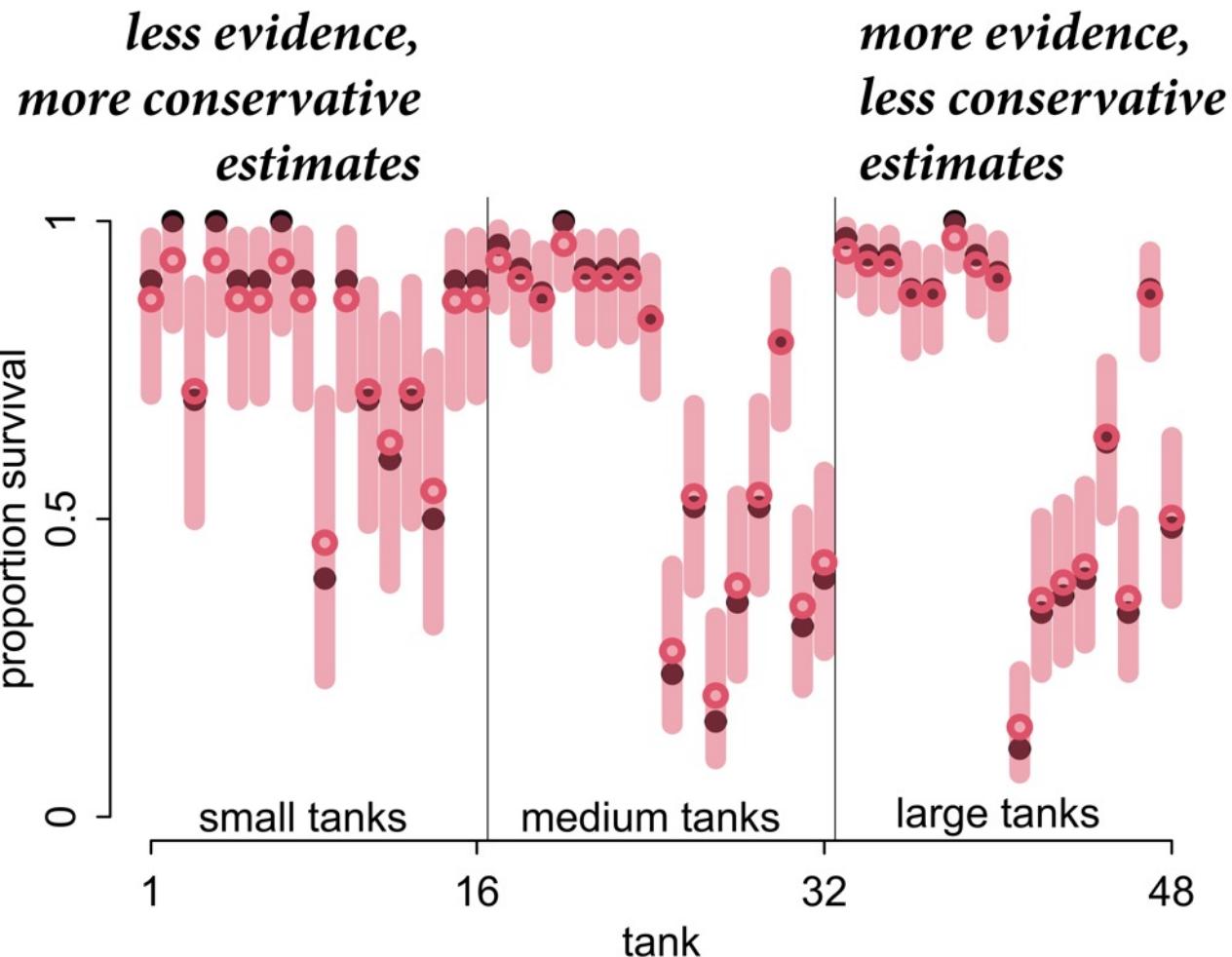
$$S_i \sim \text{Binomial}(D_i, p_i)$$

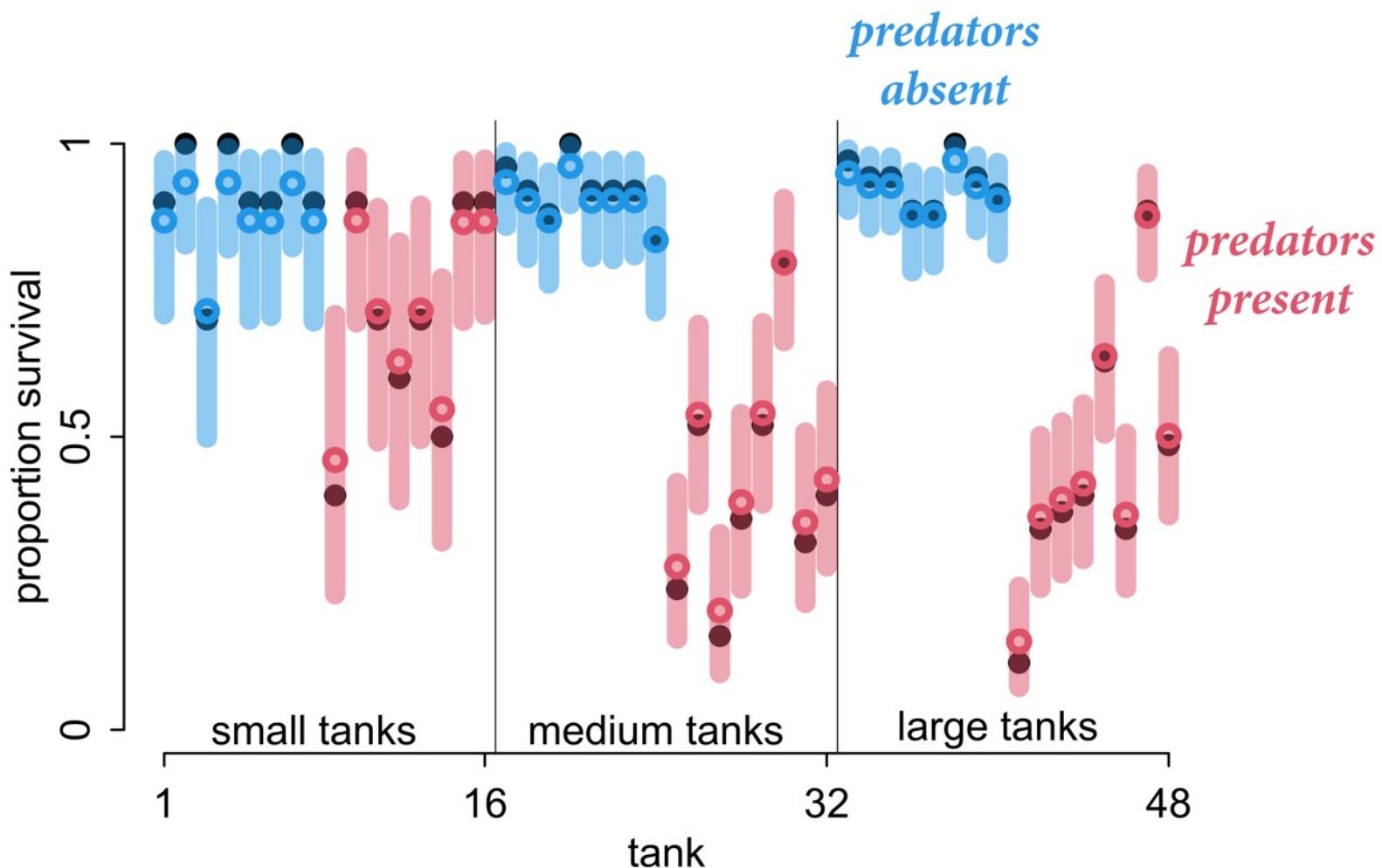
$$\logit(p_i) = \alpha_{T[i]}$$

*Adding parameters can reduce overfitting*

```
a_bar ~ dnorm( 0 , 1.5 )
alpha ~ Normal(0,1.5)
sigma ~ dexp( 1 )
), d
compare(mST , mSTnomem , func=WAIC )
```

*What matters is structure, not number*





## Stratify mean by predators

$$S_i \sim \text{Binomial}(D_i, p_i)$$

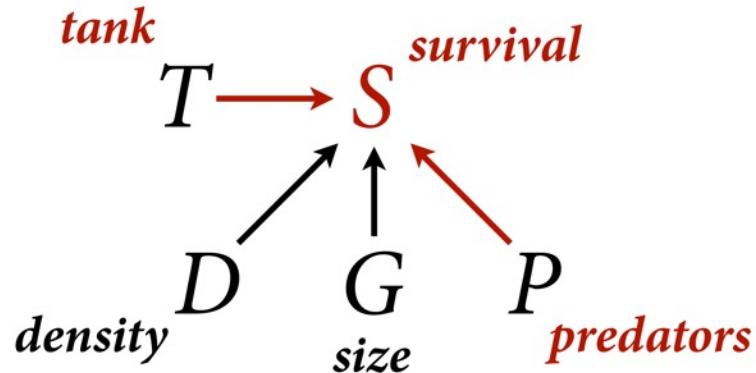
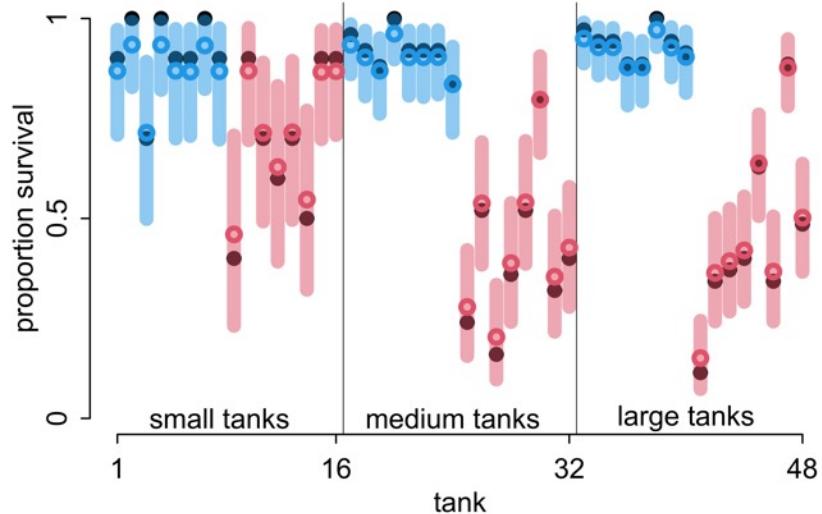
$$\text{logit}(p_i) = \alpha_{T[i]} + \beta_P P_i$$

$$\beta_P \sim \text{Normal}(0, 0.5)$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha}_j \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$



# Stratify mean by predators

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\text{logit}(p_i) = \alpha_{T[i]} + \beta_P P_i$$

$$\beta_P \sim \text{Normal}(0, 0.5)$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

$$\bar{\alpha}_j \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$

```
dat$P <- ifelse(d$pred=="pred",1,0)
mSTP <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] + bP★P ,
    bP ~ dnorm( 0 , 0.5 ) ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )
  ), data=dat , chains=4 , log_lik=TRUE )
```

# Stratify mean by predators

$$S_i \sim \text{Binomial}(D_i, p_i)$$

$$\text{logit}(p_i) = \alpha_{T[i]} + \beta_P P_i$$

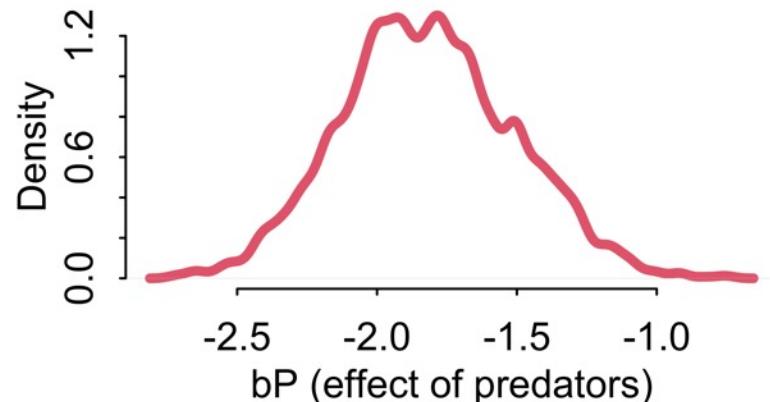
$$\beta_P \sim \text{Normal}(0, 0.5)$$

$$\alpha_j \sim \text{Normal}(\bar{\alpha}, \sigma)$$

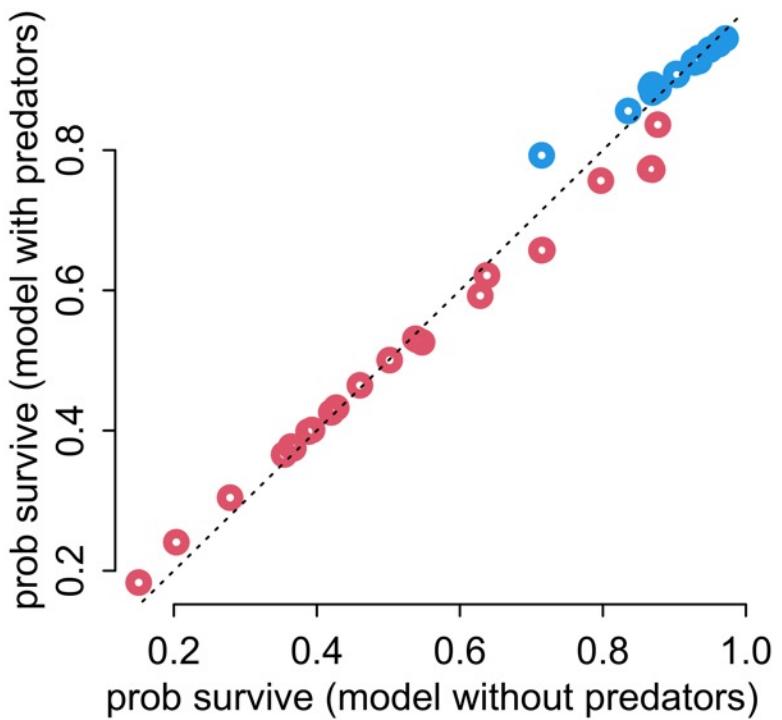
$$\bar{\alpha}_j \sim \text{Normal}(0, 1.5)$$

$$\sigma \sim \text{Exponential}(1)$$

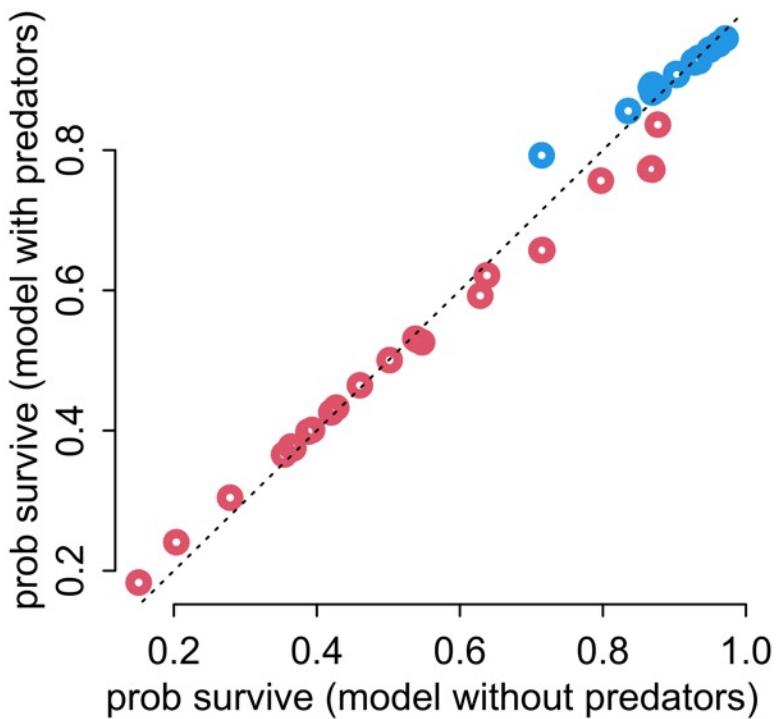
```
dat$P <- ifelse(d$pred=="pred",1,0)
mSTP <- ulam(
  alist(
    S ~ dbinom( D , p ) ,
    logit(p) <- a[T] + bP★P ,
    bP ~ dnorm( 0 , 0.5 ) ,
    a[T] ~ dnorm( a_bar , sigma ) ,
    a_bar ~ dnorm( 0 , 1.5 ) ,
    sigma ~ dexp( 1 )
  ), data=dat , chains=4 , log_lik=TRUE )
```



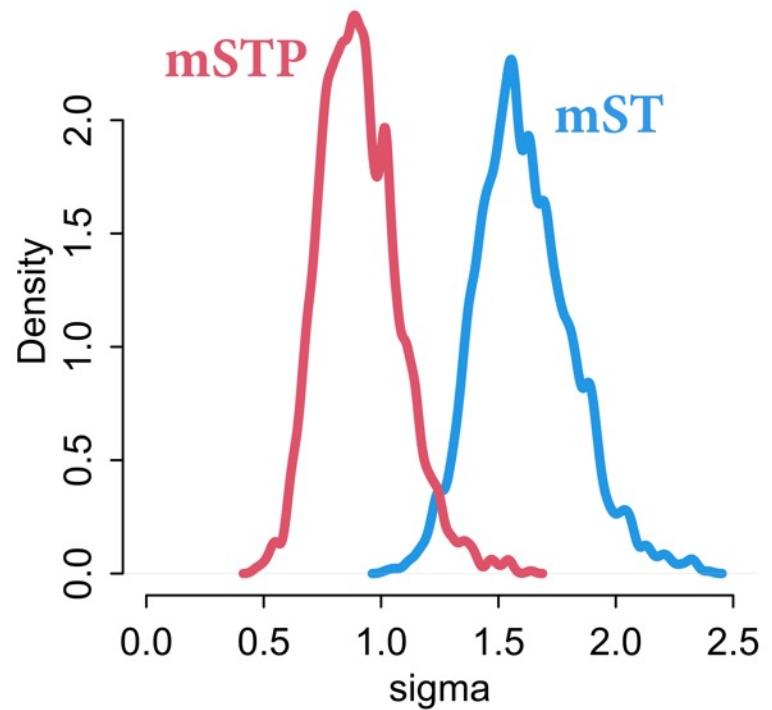
## Extremely similar predictions



## Extremely similar predictions



## Very different sigma values



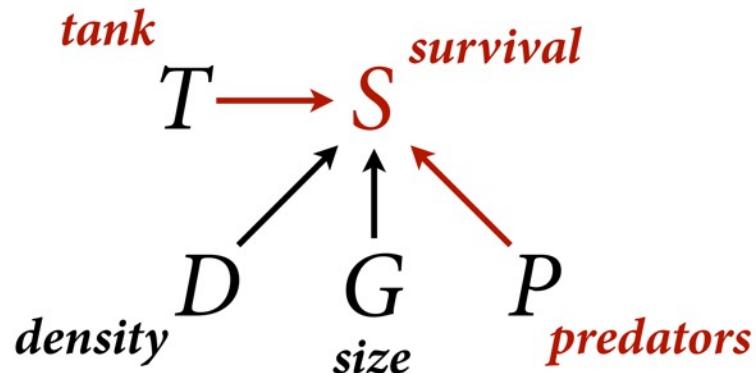
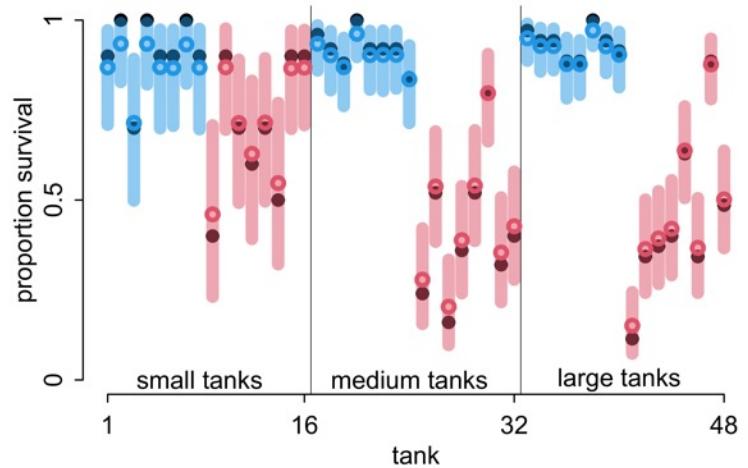
# Multilevel Tadpoles

Model of unobserved population helps learn about observed units

Use data efficiently, reduce overfitting

**Varying effects:** Unit-specific partially pooled estimates

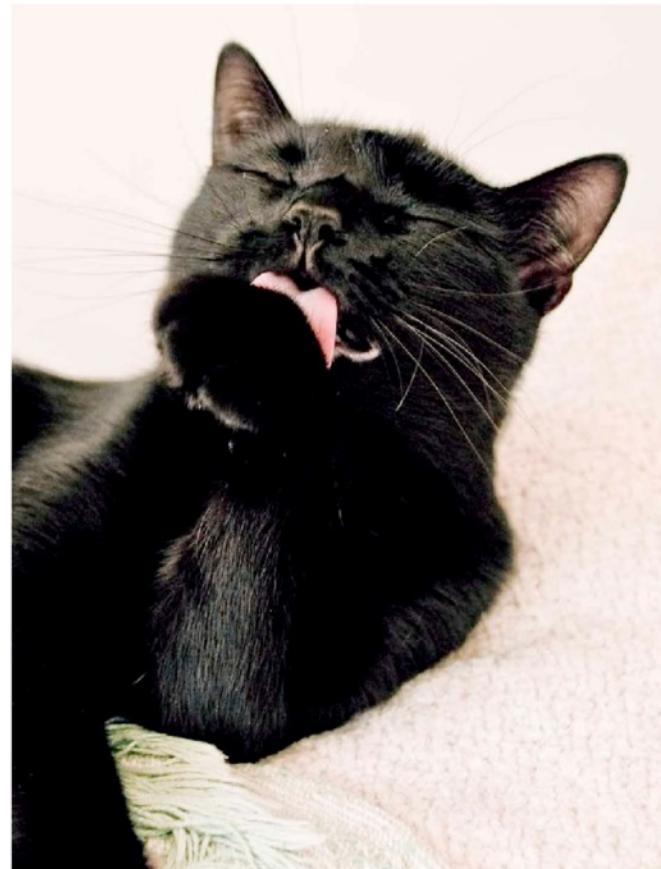
What about  $D$  and  $G$ ? Homework



# Varying Effect Superstitions

Varying effect models are plagued by superstition

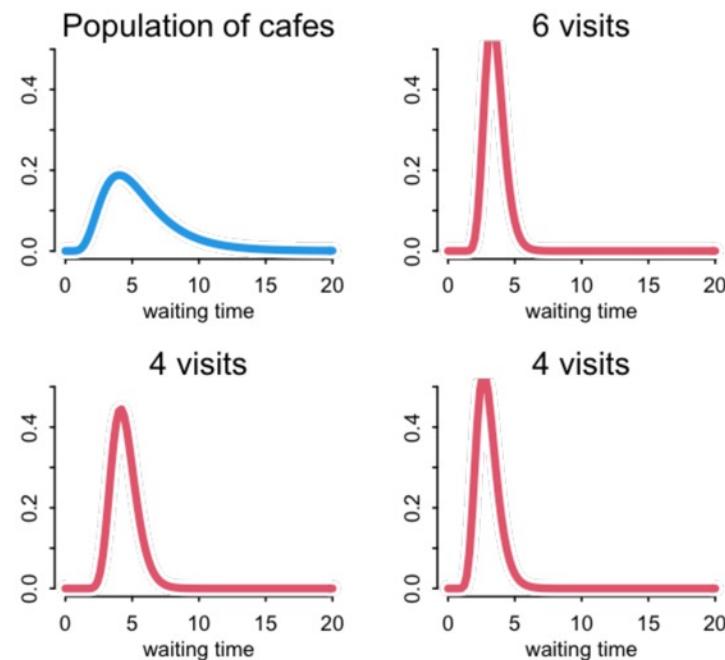
- (1) Units must be sampled at random
- (2) Number of units must be large
- (3) Assumes Gaussian variation



# Varying Effect Superstitions

Varying effect models are plagued by superstition

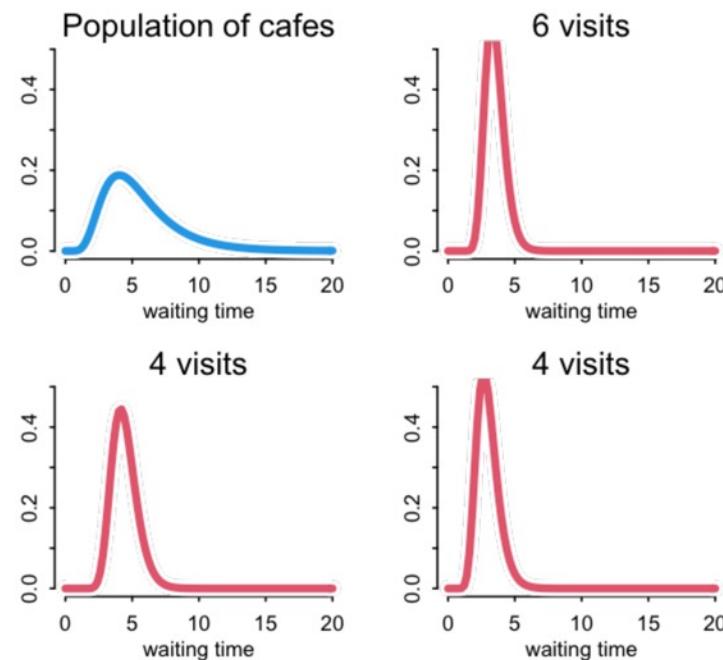
- (1) Units must be sampled at random
- (2) Number of units must be large
- (3) Assumes Gaussian variation



# Varying Effect Superstitions

Varying effect models are plagued by superstition

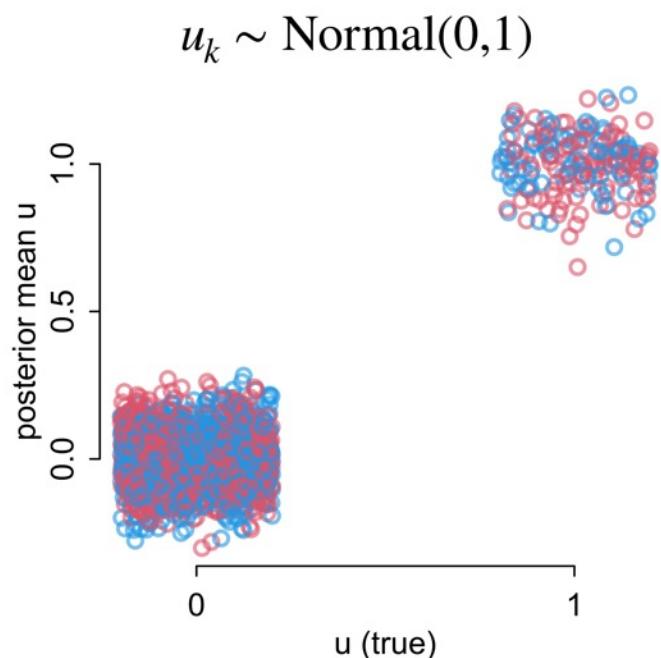
- (1) ~~Units must be sampled at random~~
- (2) Number of units must be large
- (3) Assumes Gaussian variation



# Varying Effect Superstitions

Varying effect models are plagued by superstition

- (1) ~~Units must be sampled at random~~
- (2) ~~Number of units must be large~~
- (3) Assumes Gaussian variation

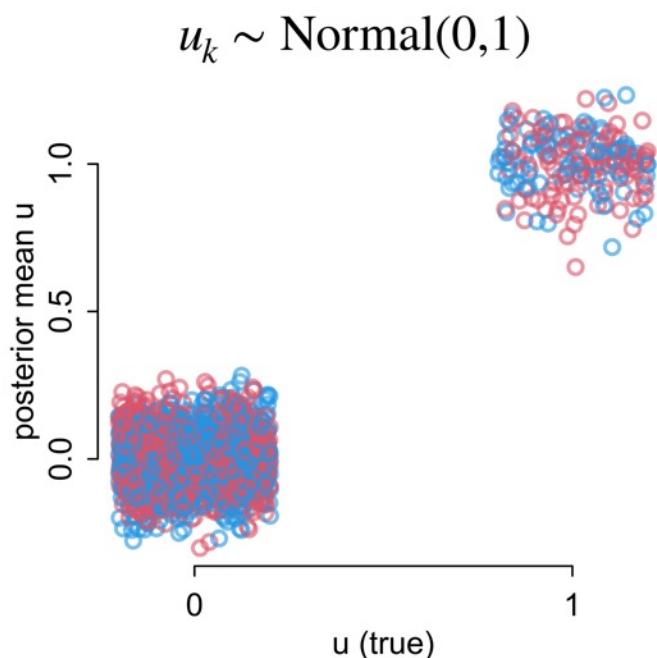


Lecture 10

# Varying Effect Superstitions

Varying effect models are plagued by superstition

- (1) ~~Units must be sampled at random~~
- (2) ~~Number of units must be large~~
- (3) ~~Assumes Gaussian variation~~



Lecture 10

# Practical Difficulties

Varying effects are a good default, but...

- (1) How to use **more than one** cluster type at the same time? For example **stories** and **participants**
- (2) How to sample efficiently

