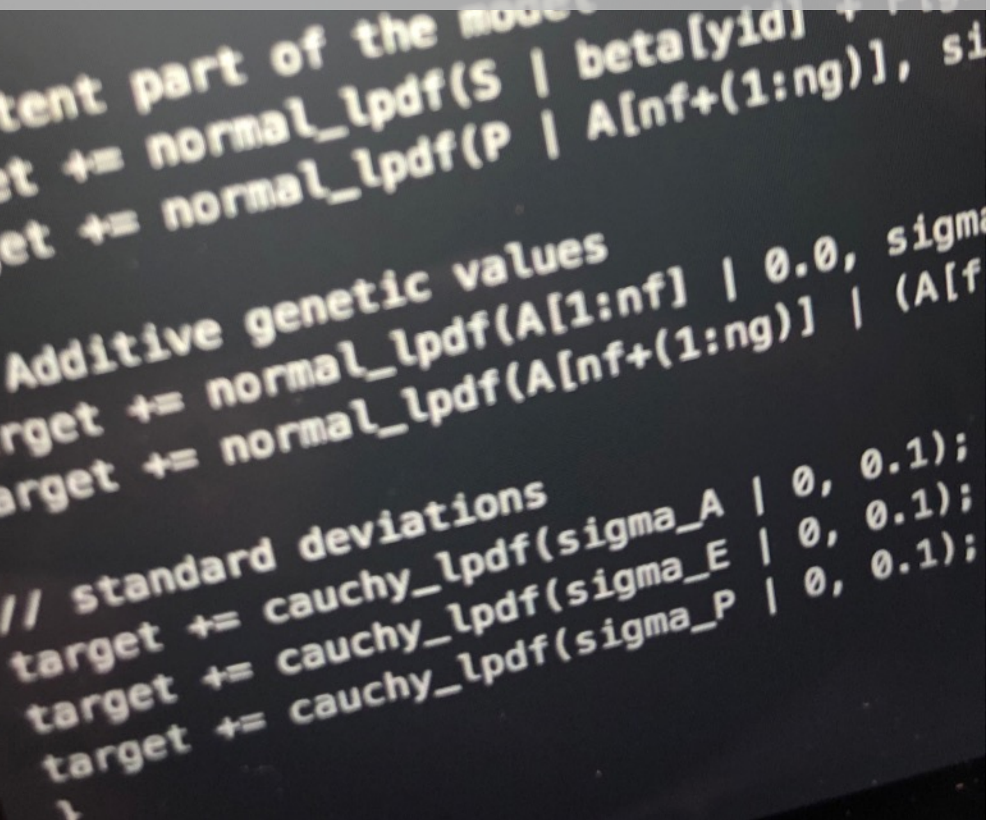
Inference in ecology and evolution beyond generalised linear mixed models



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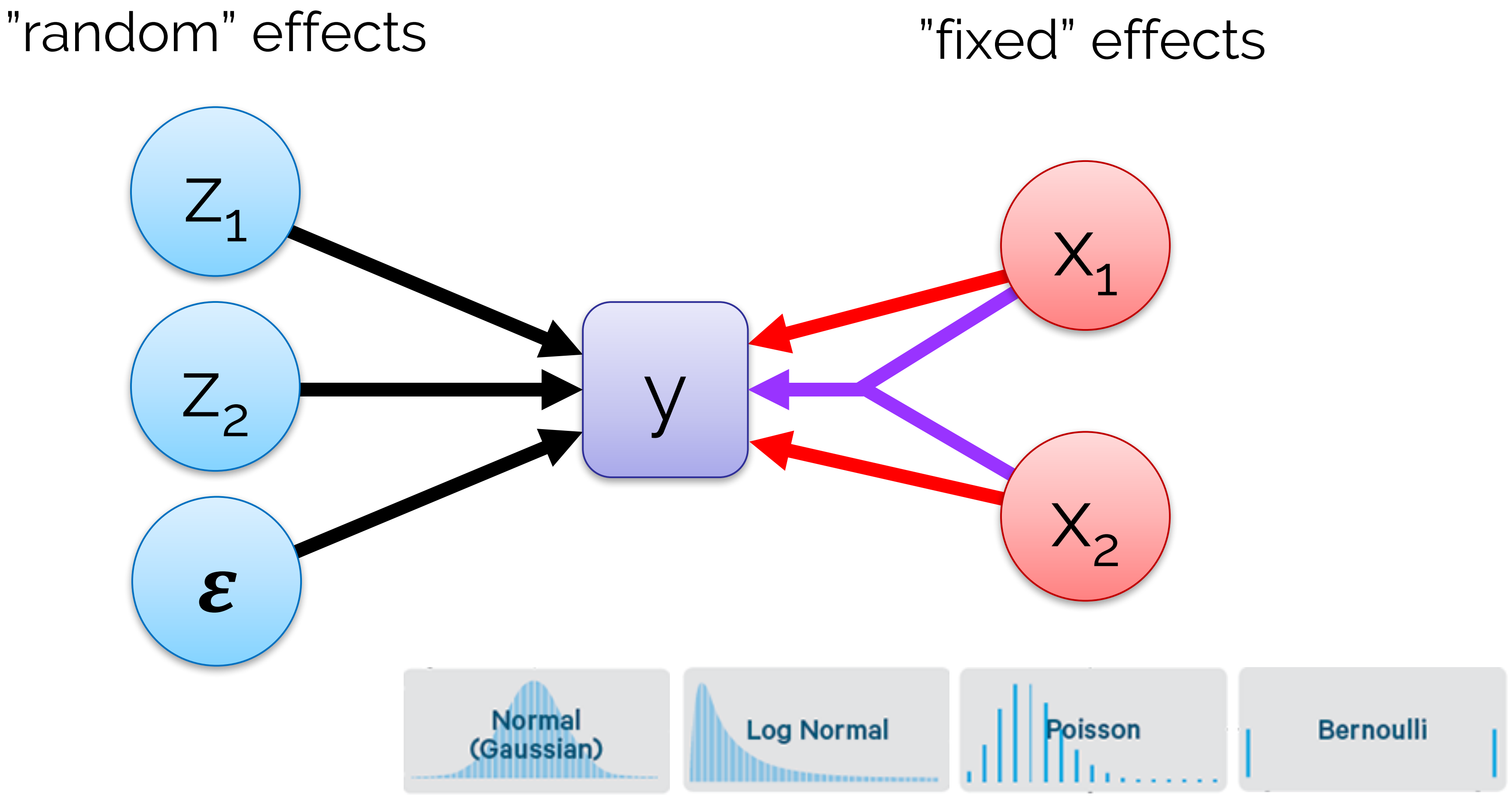
Structure of GLMMs



Stan, a flexible language and powerful inference library

```
brm(angle ~ recipe * temperature + (1 | recipe:replicate), data = cake)
```

```
data {
  int<lower=0> N; // number of data items
  int<lower=0> K; // number of predictors
  matrix[N, K] x; // predictor matrix
  vector[N] y; // outcome vector
  }

parameters {
  real alpha; // intercept
  vector[K] beta; // coefficients for predictors
  real<lower=0> sigma; // error scale
  }

model {
  y ~ normal(x * beta + alpha, sigma); // likelihood
  }
```

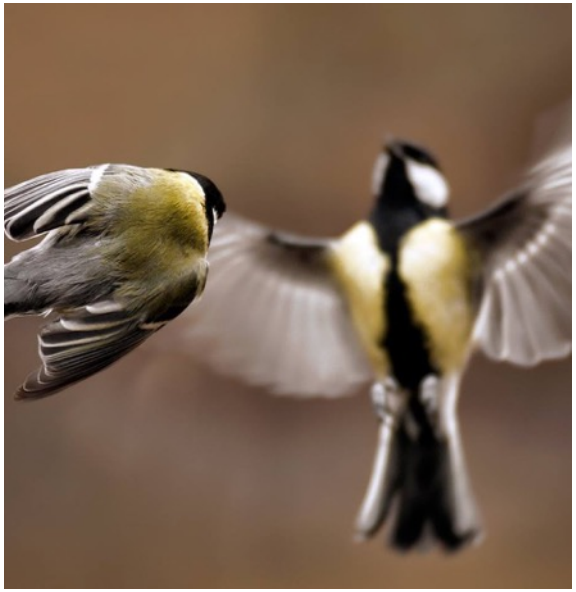
```
data {
  int<lower=2> K;                       // capture events
  int<lower=0> I;                       // number of individuals
  int<lower=0> Is;                      // index of last female
  int<lower=0> max_age;                 // number of age classes
  int<lower=0,upper=1> X[I,K];          // X[i,k]: individual i captured at k
  int<lower=0> age[I];                  // individual age
  int<lower=0> last[I];                 // last observation
  vector[I] cov;                        // individual covariate
  int<lower=1> N;                       // sum of all last observations
  }

parameters {
  matrix<lower=-10,upper=10> [max_age,2] phi_f;  // survival women
  vector<lower=-10,upper=10> [max_age] p_f;    // survival men
  matrix<lower=-10,upper=10> [max_age,2] phi_m;  // visibility women
  vector<lower=-10,upper=10> [max_age] p_m;    // visibility men
  }

transformed parameters {
  real<lower=0,upper=1>chi[I,K+1]; // probability that an individual is never
                                   // recaptured after its last capture

  {
  int k;
  // FEMALES
  for (i in 1:Is) {
    chi[i,K+1] = 1.0;
    k = K;
    while (k > 0) {
      chi[i,k] = (1 -inv_logit(phi_f[age[i],1]+phi_f[age[i],2]*cov[i])) +
        inv_logit(phi_f[age[i],1]+phi_f[age[i],2]*cov[i]) *
        (1 - inv_logit(p_f[age[i]])) * chi[i,k+1];
         k = k - 1;
      }
    }

  // MALES
  for (i in (Is+1):I) {
    chi[i,K+1] = 1.0;
    k = K;
    while (k > 0) {
      chi[i,k] = (1 -inv_logit(phi_m[age[i],1]+phi_m[age[i],2]*cov[i])) +
        inv_logit(phi_m[age[i],1]+phi_m[age[i],2]*cov[i]) *
        (1 - inv_logit(p_m[age[i]])) * chi[i,k+1];
        k = k - 1;
      }
    }
    }
  }

model {

  // FEMALES
  for (i in 1:Is) {
    if(last[i]>0){
      for (k in 1:last[i]) {
        target += log_inv_logit(phi_f[age[i],1]+phi_f[age[i],2]*cov[i]);
        if (X[i,k] == 1)
          target += log_inv_logit(p_f[age[i]]);
        else
          target += log1m_inv_logit(p_f[age[i]]);
        }
      }
      target += log(chi[i,last[i]+1]);
    }

  // MALES
  for (i in (Is+1):I) {
    if(last[i]>0){
      for (k in 1:last[i]) {
        target += log_inv_logit(phi_m[age[i],1]+phi_m[age[i],2]*cov[i]);
        if (X[i,k] == 1)
          target += log_inv_logit(p_m[age[i]]);
        else
          target += log1m_inv_logit(p_m[age[i]]);
        }
      }
    target += log(chi[i,last[i]+1]);
    }

  phi_f[,1] ~ normal(0,1);
  phi_f[,2] ~ normal(0,1);
  p_f   ~ normal(0,1);
  phi_m[,1] ~ normal(0,1);
  phi_m[,2] ~ normal(0,1);
  p_m   ~ normal(0,1);
  }

generated quantities {
  int n;
  vector[N] log_lik;
  n = 1;

  // FEMALES
  for (i in 1:Is) {
    for (k in 1:last[i]) {
      log_lik[n] = bernoulli_logit_lpmf(X[i,k]|inv_logit(phi_f[age[i],1]+
        phi_f[age[i],2]*cov[i])*inv_logit(p_f[age[i]]));
        n = n + 1;
      }
    }

  // MALES
  for (i in (Is+1):I) {
    for (k in 1:last[i]) {
      log_lik[n] = bernoulli_logit_lpmf(X[i,k]|inv_logit(phi_m[age[i],1]+
        phi_m[age[i],2]*cov[i])*inv_logit(p_m[age[i]]));
        n = n + 1;
      }
    }
  }
```

http://mc-stan.org

Carpenter, *et al*. 2017. Stan: A probabilistic programming language. *J Stat Soft* 76. DOI 10.18637/jss.v076.i01

Extending GLMMs

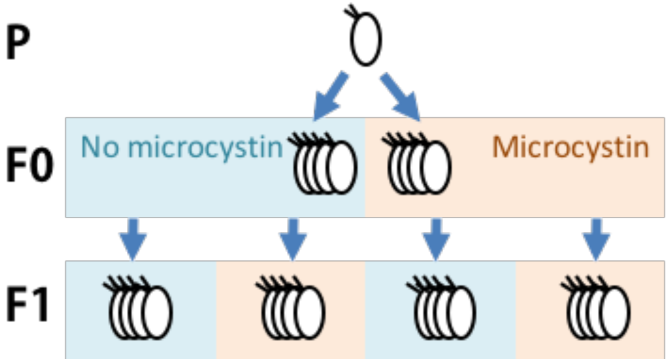
2 GLMMs
with shared
“random” effects

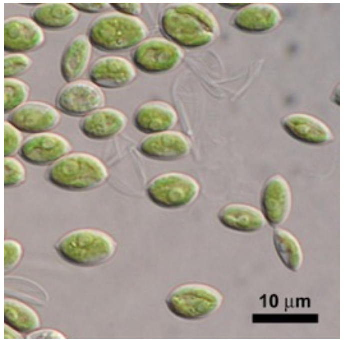


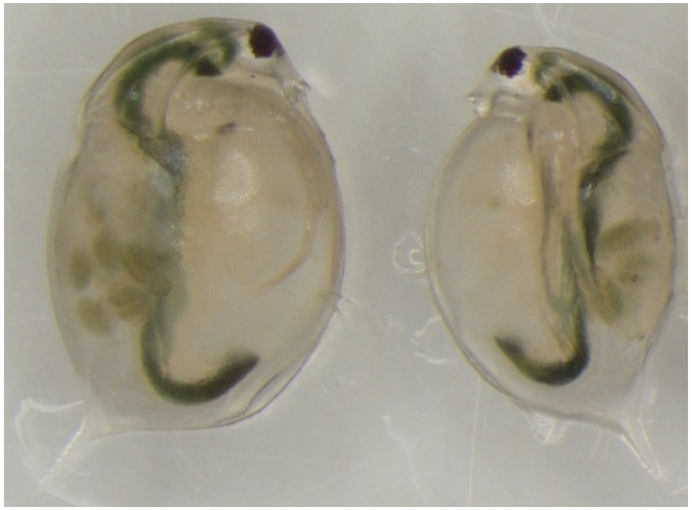
Latent variable
modeling

Survival analysis
with imperfect
detection

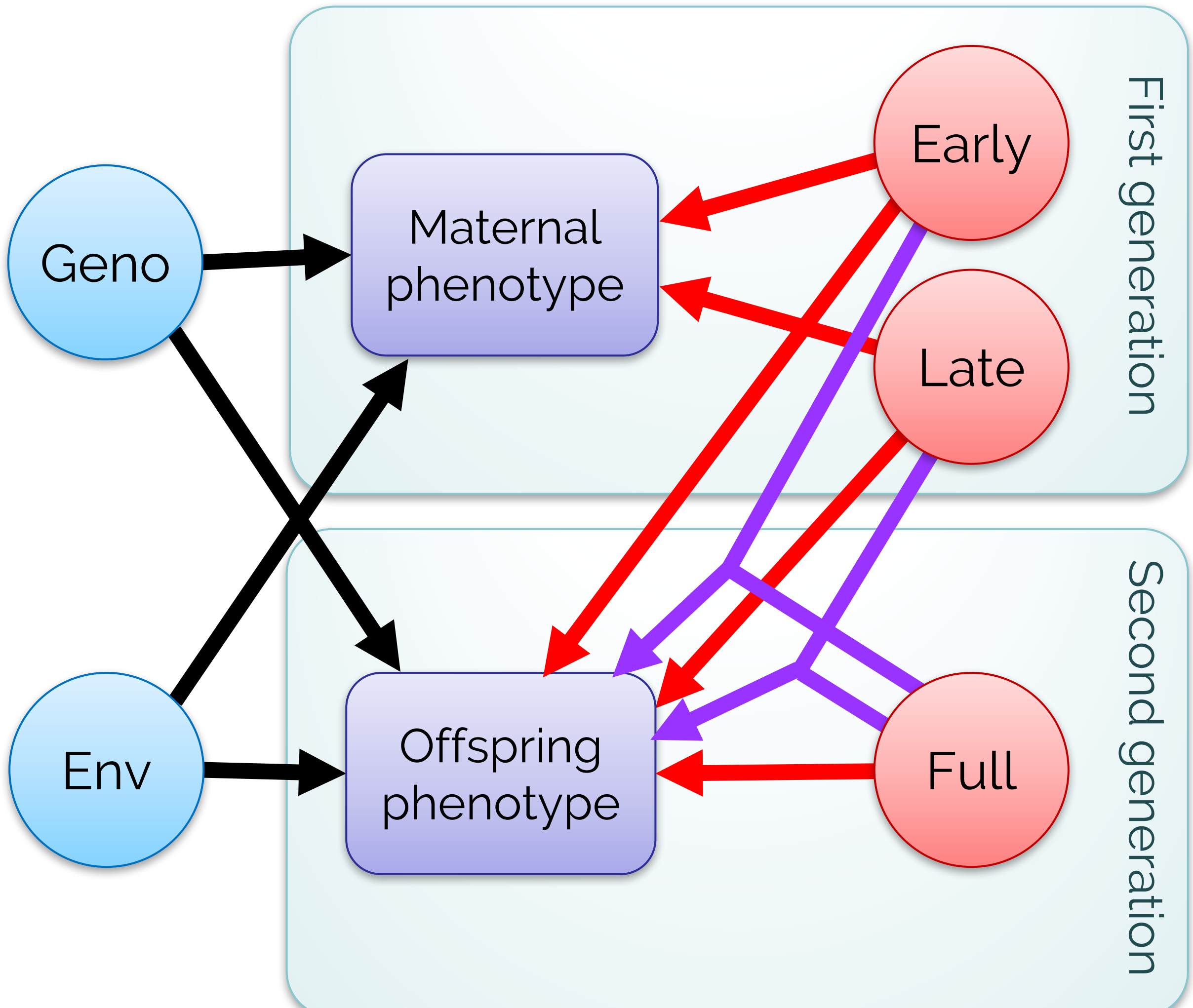
Daphnia as model for adaptive maternal effects





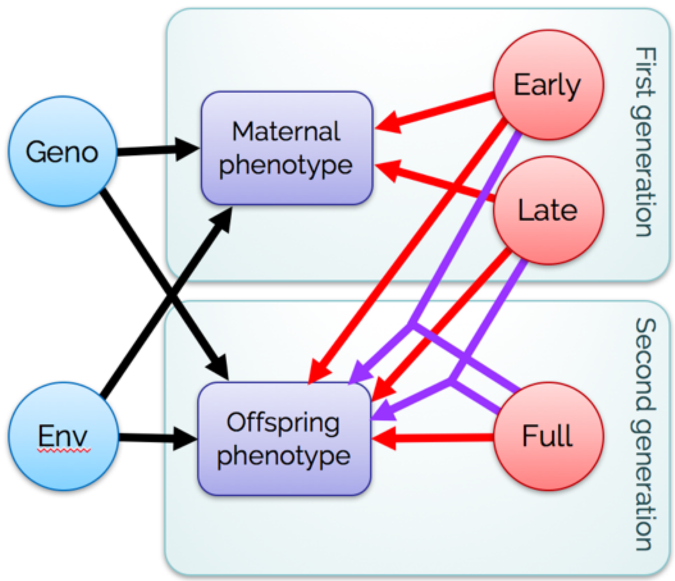


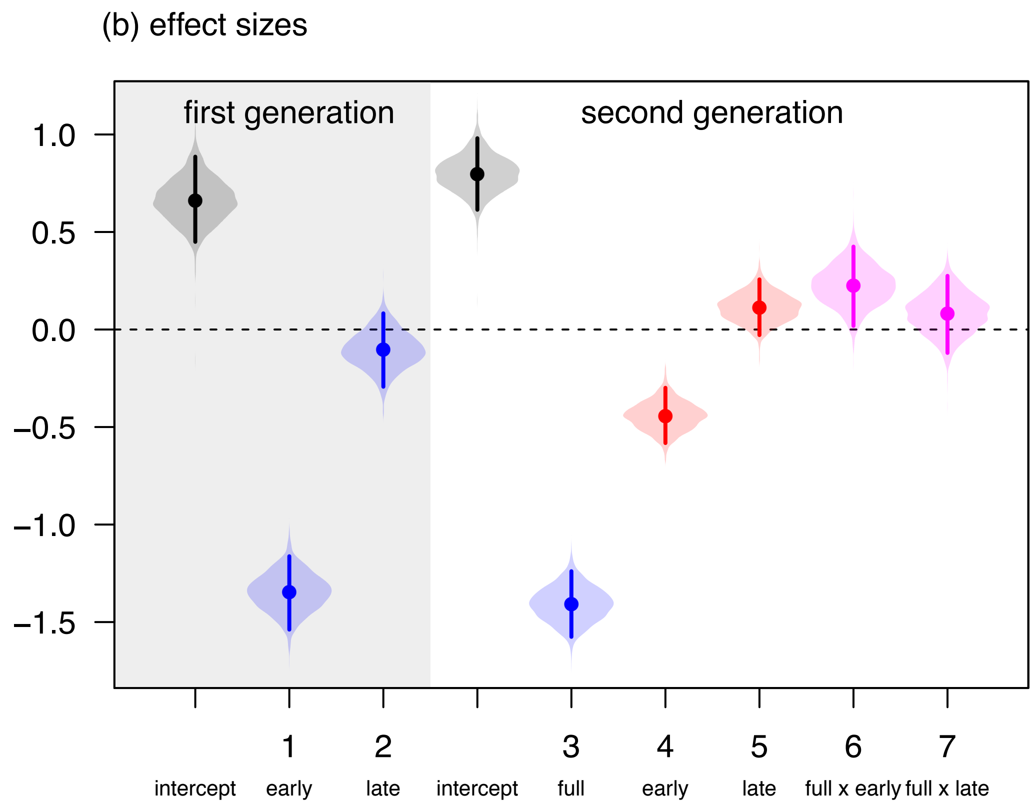
2 GLMMs, shared "random" effects



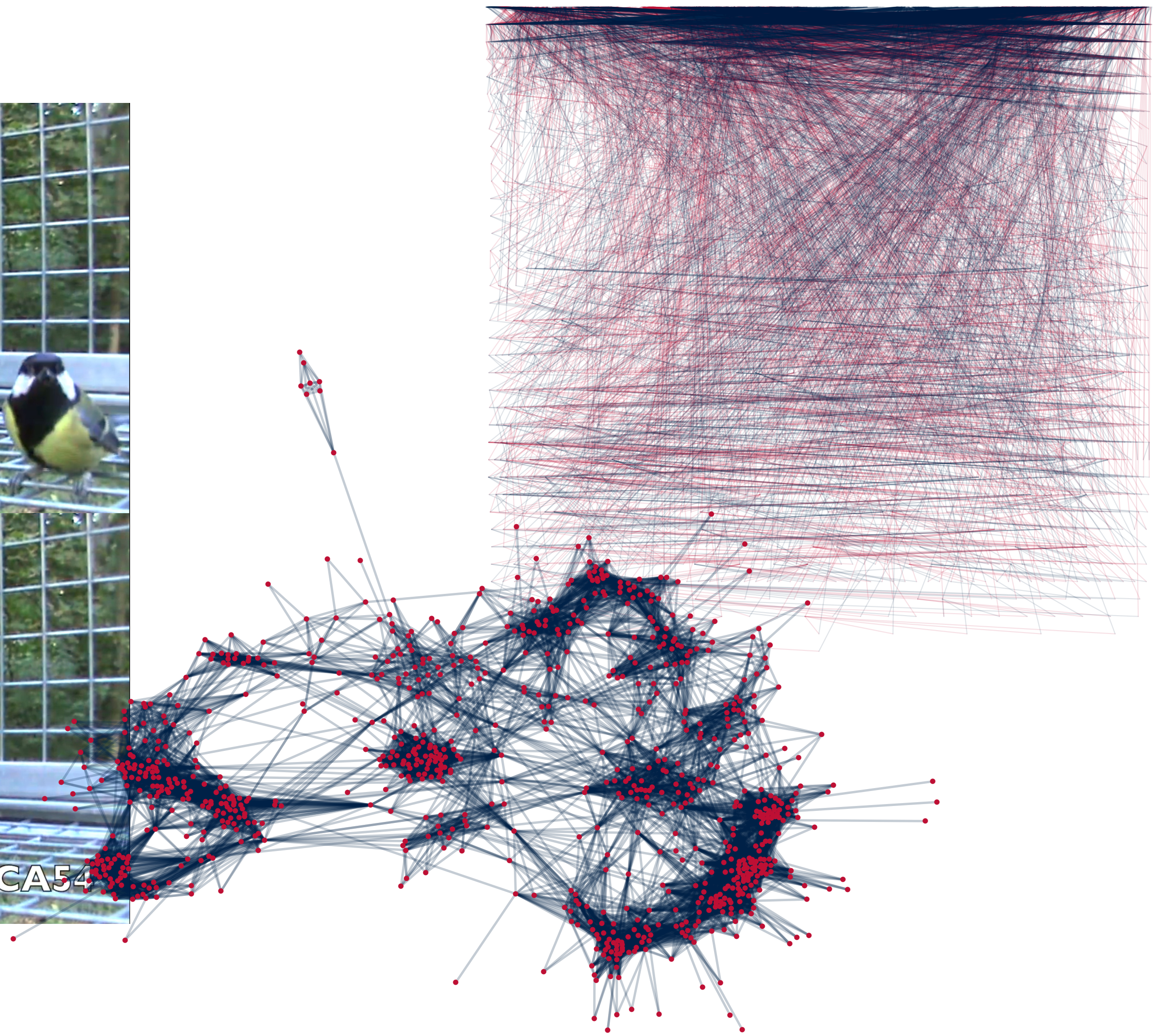
$N_{mothers}$ = 233
$N_{offspring}$ = 804
$N_{genotypes}$ = 7

Adaptive maternal effects present, though small and accumulative

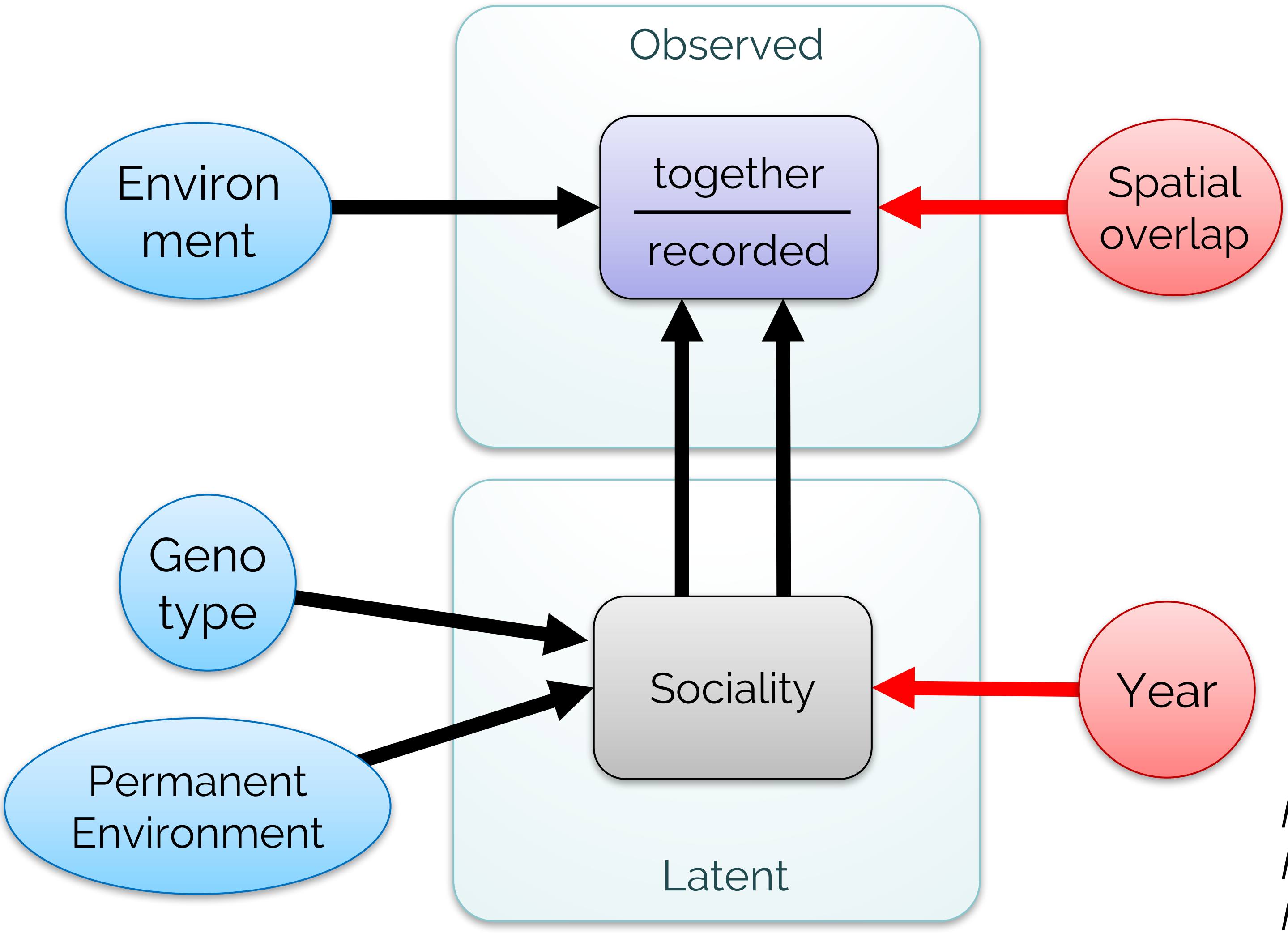




Heritability of social behaviour

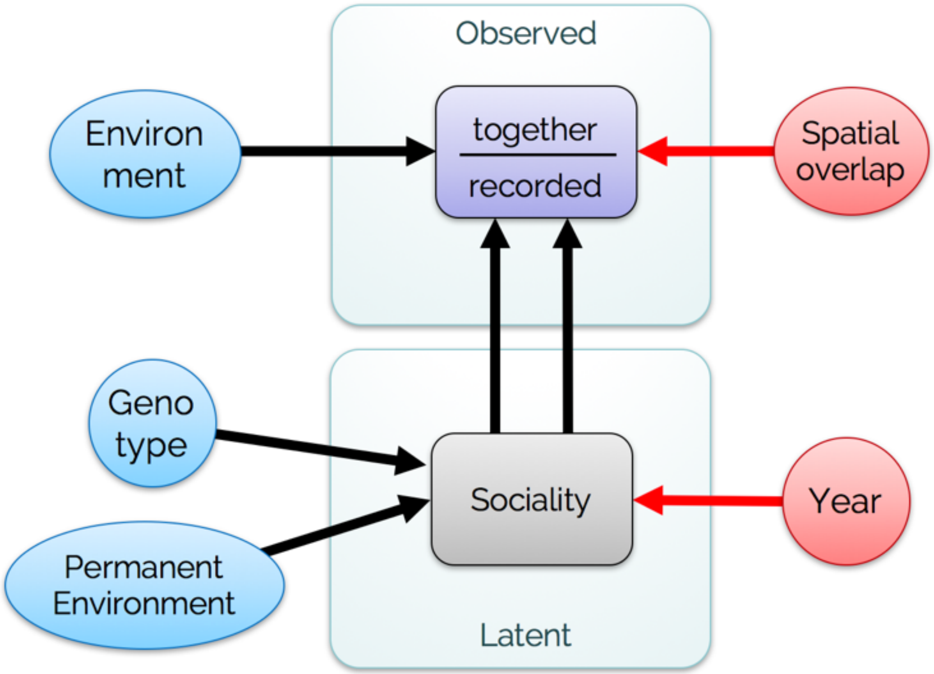


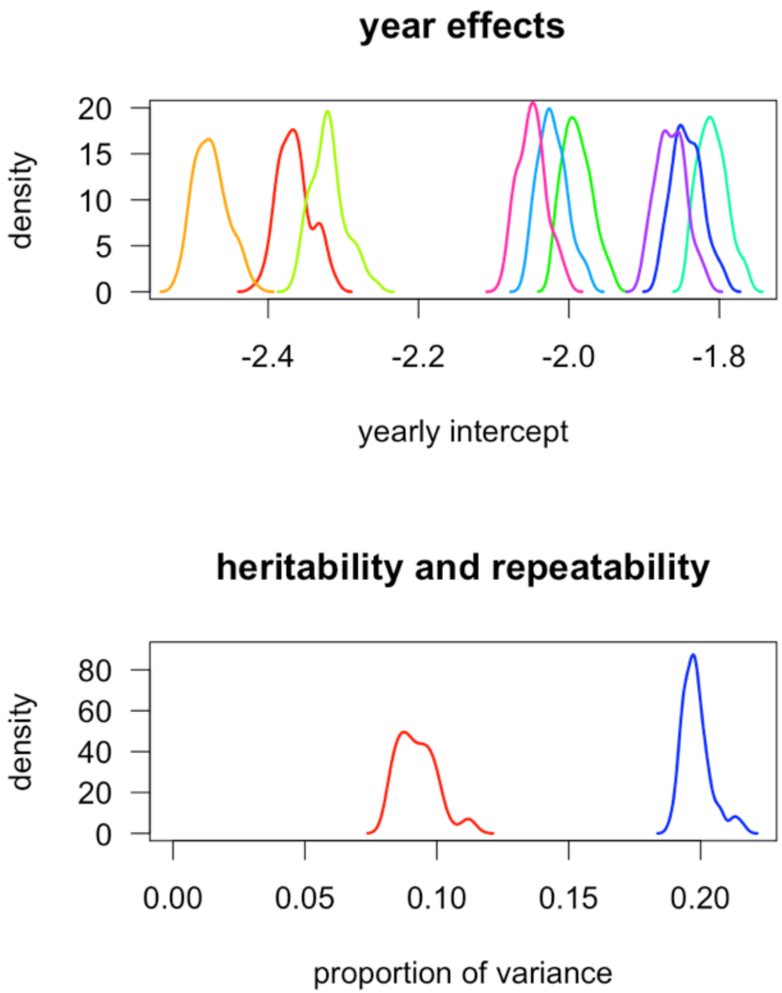
Latent variable model



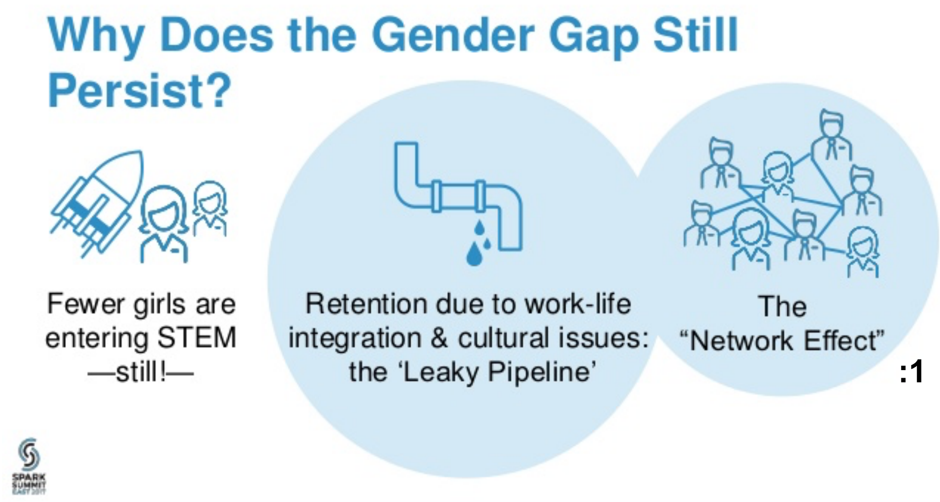
$N_{individuals}$ = 6,844
N_{pairs} = 295,327
N_{years} = 9

Genes play a role, albeit effect is small





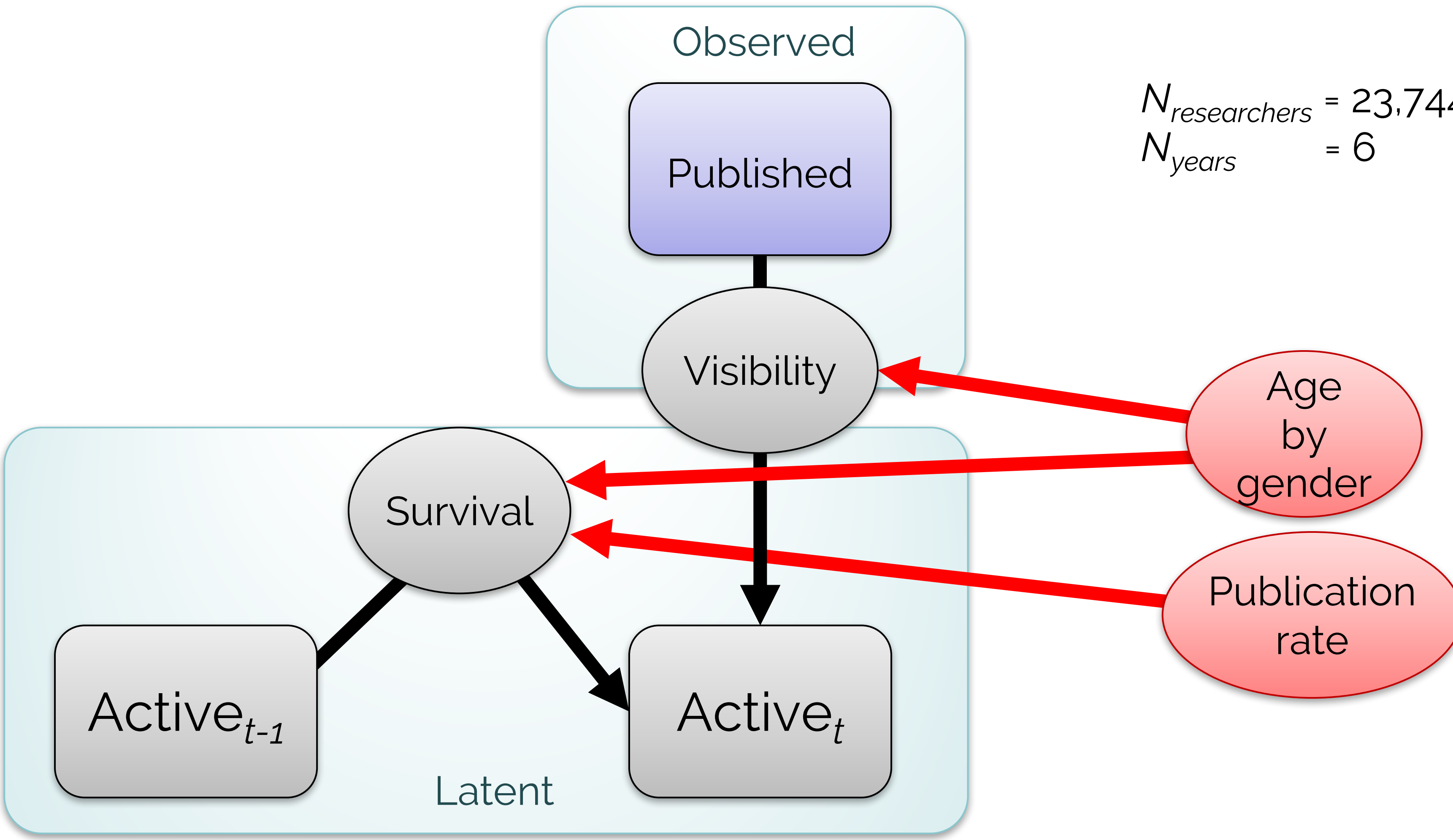
Gender bias in science



WEB OF SCIENCE™

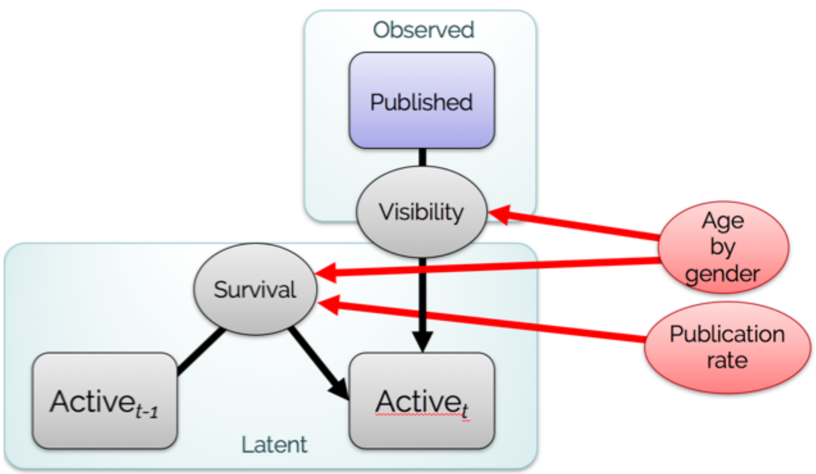
	A	B	C	D	E	F	G	[illegible]	[illegible]	J
1	gender	age	first.y.pub	last.y.pub	pub.y.08	pub.y.09	p[illegible].y.10	pub.y.11	pub.y.12	[illegible]b.y.13
2	F	1	2007	2012	2	1	1	0	1	0
3	F	1	2007	2010	2	2	1	0	[illegible]	0
4	F	1	2007	2010	0	3	1	[illegible]	0	0
5	F	1	2007	2012	1	0	4	0	1	0
6	F	1	2007	2013	2	2	3	0	0	1
7	F	1	2007	2010	0	0	1	0	0	0
8	F	1	2007	2012	0	0	0	1	1	0
9	F	1	2007	2013	5	11	15	9	12	11
10	F	1	2007	2013	1	1	2	2	3	1
11	F	1	2007	2013	2	2	4	1	3	4
12	F	1	2007	2011	0	1	0	1	0	0
13	F	1	2007	2011	1	1	0	3	0	0
14	F	1	2007	2013	1	0	1	0	0	1
15	F	1	2007	2013	2	3	2	6	0	4
16	F	1	2007	2011	0	0	0	1	0	0
17	F	1	2007	2012	3	3	6	3	2	0
18	F	1	2007	2013	0	0	0	0	0	2
19	F	1	2007	2013	10	13	12	8	14	7
20	F	1	2007	2013	1	1	3	2	1	1
21	F	1	2007	2013	2	3	4	9	6	1
22	F	1	2007	2013	0	0	0	0	0	1
23	F	1	2007	2008	1	0	0	0	0	0
24	F	1	2007	2011	0	0	1	3	0	0
25	F	1	2007	2009	2	2	0	0	0	0
26	F	1	2007	2010	0	0	1	0	0	0

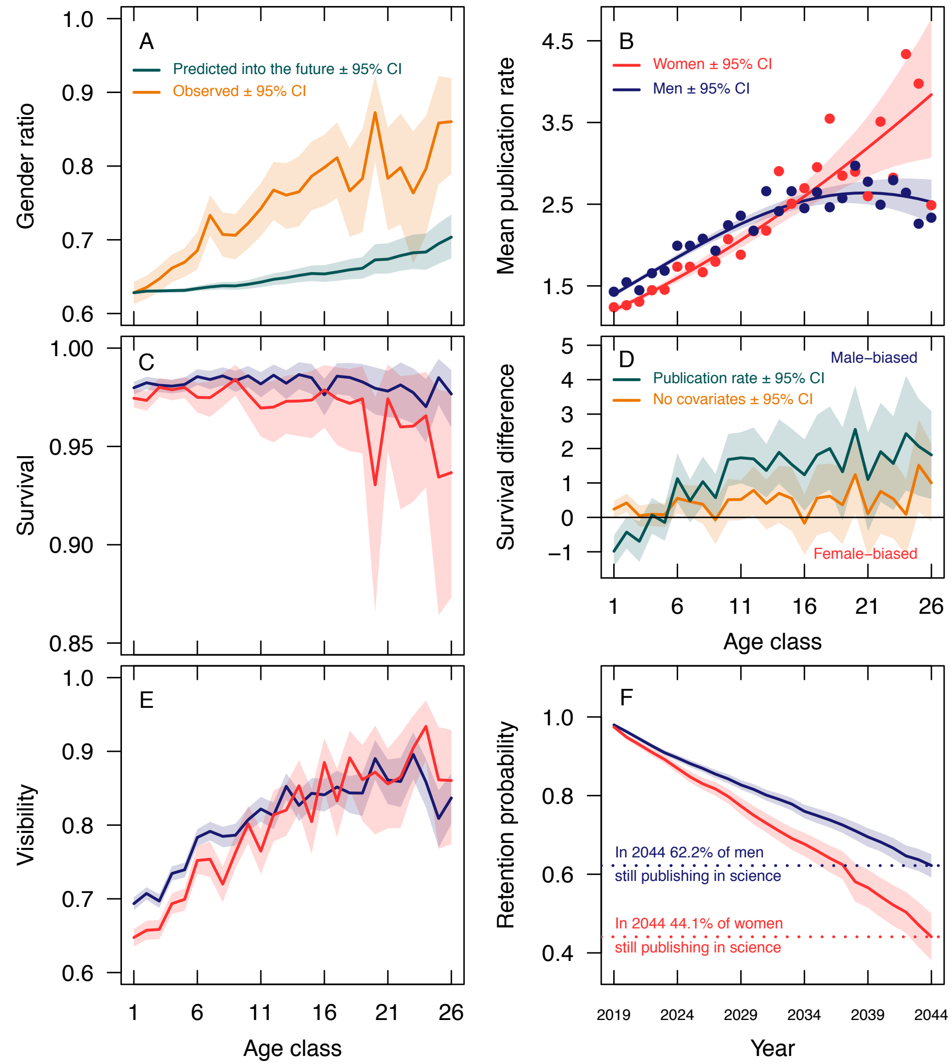
Survival model with imperfect detection



$N_{researchers}$ = 23,744
N_{years} = 6

Gap is closing, but increment of small differences adds up





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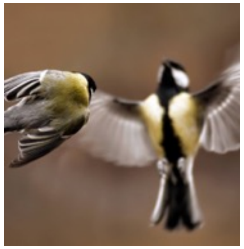

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