Another multi-level credit-assignment problem

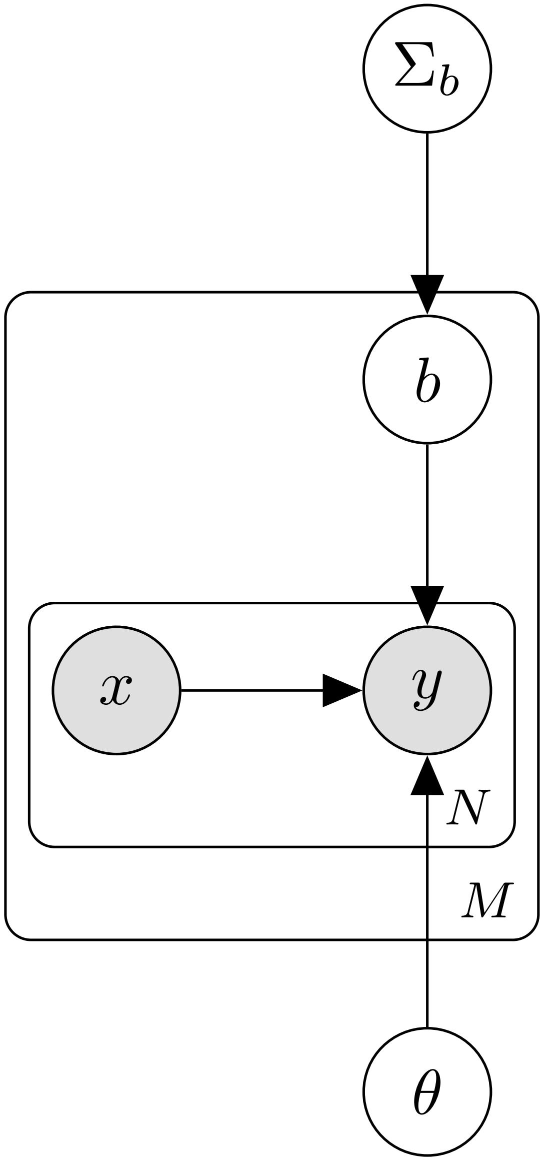
- Scenario: a new tutoring method is being compared with an older tutoring method
- Experiment design:
  - 6 tutoring sites
  - 4 tutored students at each site
  - No repeated measures from either students or tutors
  - Student:tutor pairs randomly assigned to tutoring method
  - Dependent variable: does the student pass a test?

R implementation of experiment design

```r
library(dplyr) # Load necessary libraries

set.seed(10) # Set seed for reproducibility

# Number of sites and students per site
n_sites <- 6   # Small number of sites to induce variance uncertainty
n_students_per_site <- 4  # Each student is assigned to ONE teaching method

# Generate student-level data
dat <- expand.grid(site_id = 1:n_sites, student_id = 1:n_students_per_site)

# Assign each student to a teaching method (ensuring between-subjects design)
dat <- dat %>%
  group_by(site_id) %>%
  mutate(method = sample(0:1, size = n(), replace = TRUE)) %>%
  ungroup()
```

```
> head(dat,n=8)
# A tibble: 8 × 7
  site_id student_id method
    <int>      <int>  <int>
1       1          1      0
2       2          1      1
3       3          1      0
4       4          1      0
5       5          1      1
6       6          1      0
7       1          2      0
8       2          2      0
```

Mixed logit model assumption



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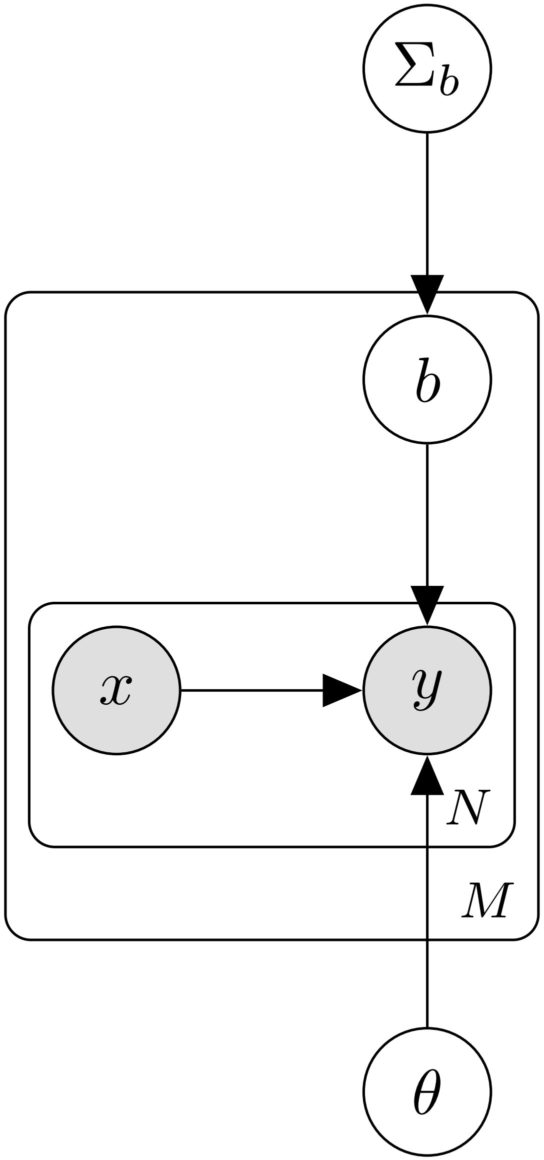

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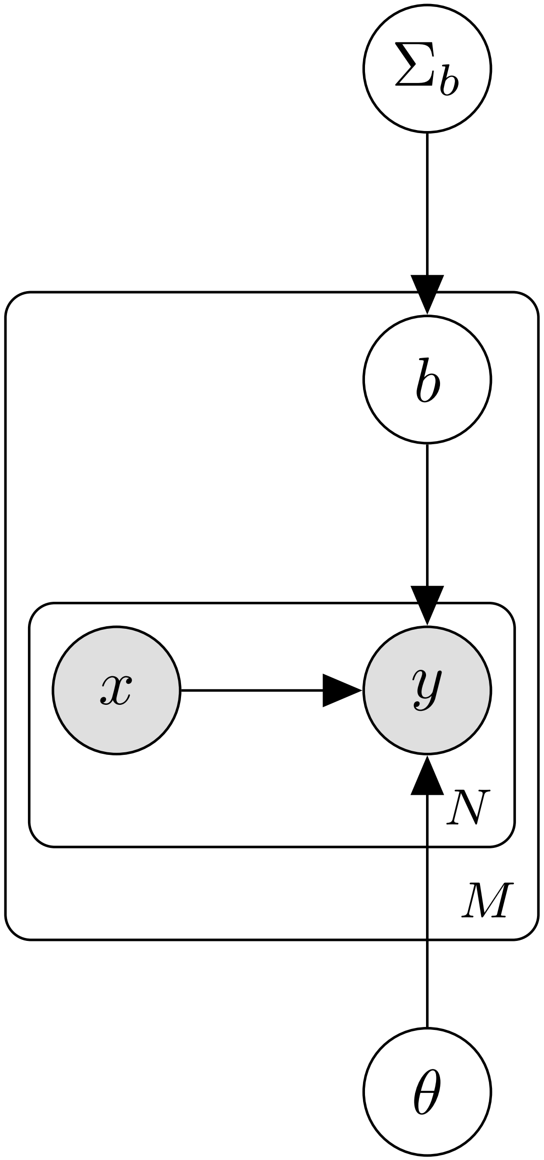

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$$\eta = \left(\beta + b\right) x$$

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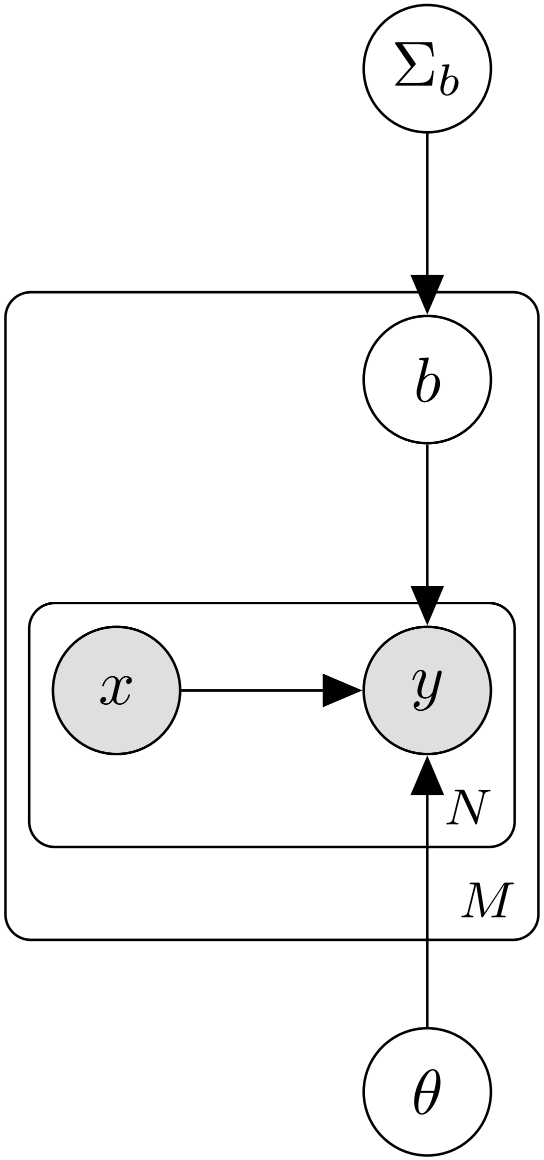

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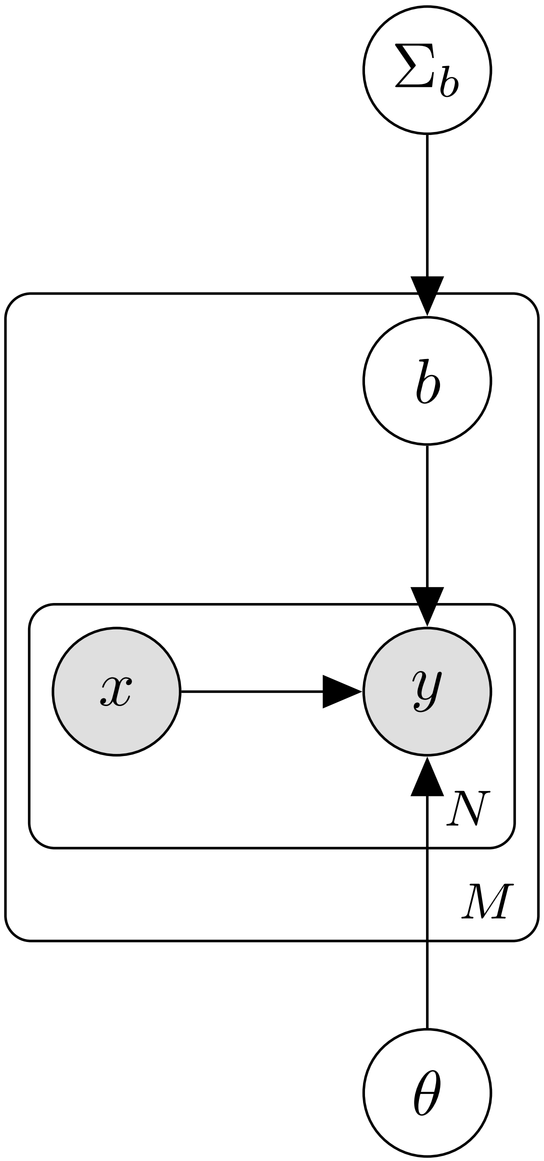

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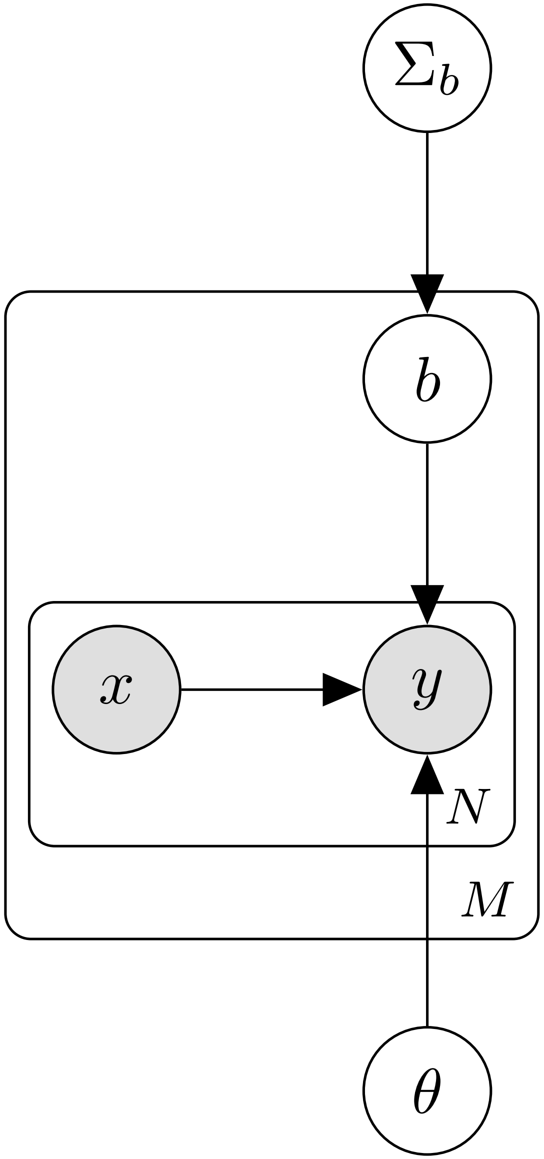

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For our case, $\eta = \alpha + \beta X + b$, where X is a {0,1} dummy variable

R implementation of data generation

```r
# True parameters
beta_0 <-      [redacted]# Intercept (baseline pass probability)
beta_method <- [redacted]# Positive effect of the new teaching method
sigma_site <-  [redacted]# Variance of site random effects

# Generate site-level random intercepts
sites <- data.frame(site_id = 1:n_sites,
                    u = rnorm(n_sites, mean = 0, sd = sigma_site))

# Merge with site random effects
dat <- left_join(dat, sites, by = "site_id")

# Compute log-odds of passing
dat$logit_p <- beta_0 + beta_method * dat$method + dat$u
dat$p <- exp(dat$logit_p) / (1 + exp(dat$logit_p))  # Log-odds -> probability

# Simulate pass/fail outcome
dat$passed <- rbinom(nrow(data), 1, dat$p)
```

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```
> head(dat,n=8)
# A tibble: 8 × 7
  site_id student_id method      u logit_p     p passed
    <int>      <int>  <int>  <dbl>   <dbl> <dbl>  <int>
1       1          1      0 -0.476 -0.176  0.456      1
2       2          1      1  1.97   2.27   0.907      0
3       3          1      0  1.48   1.78   0.856      1
4       4          1      0  0.179  0.479  0.617      1
5       5          1      1 -1.91  -1.61   0.167      0
6       6          1      0 -0.390 -0.0903 0.477     0
7       1          2      0 -0.476 -0.176  0.456      0
8       2          2      0  1.97   2.27   0.907      1
```

Some summary statistics

The *"raw statistics"* suggest that the new teaching method ($X = 1$) leads to a lower pass rate:

```
> dat %>%
+   group_by(method) %>%
+   summarize(mean_passed=mean(passed))
# A tibble: 2 × 2
  method mean_passed
   <int>       <dbl>
1      0       0.667
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But there is also site-level variation in both rate of use of the new teaching method and pass rate:

```
> dat1 <- dat %>%
+   group_by(site_id) %>%
+   summarize(mean_new_method=mean(method),mean_passed=mean(passed))
> print(dat1)
# A tibble: 6 × 3
  site_id mean_new_method mean_passed
    <int>           <dbl>       <dbl>
1       1            0.5         0.25
2       2            0.75        0.75
3       3            0.25        1
4       4            0.25        0.75
5       5            0.75        0
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```

This is *exactly* the case where we want to fit a multi-level model to work out credit assignment

MLE fitting the mixed-logit model

```r
# Fit mixed logit model (random intercept for site)
library(lme4)
model <- glmer(passed ~ method + (1 | site_id), data = dat, family = binomial)
```

```
> summary(model)
Generalized linear mixed model fit by maximum likelihood (Laplace Approximation) ['glmerMod']
 Family: binomial  ( logit )
Formula: passed ~ method + (1 | site_id)
   Data: dat

     AIC      BIC   logLik deviance df.resid
    28.6     32.2    -11.3     22.6       21

Scaled residuals:
     Min       1Q   Median       3Q      Max
-1.18452 -0.25342 -0.08034  0.35771  0.97355

Random effects:
 Groups  Name        Variance Std.Dev.
 site_id (Intercept) 9.343    3.057
Number of obs: 24, groups:  site_id, 6

Fixed effects:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)    1.031      1.689    0.61    0.542
method        -3.261      2.039   -1.60    0.110

Correlation of Fixed Effects:
       (Intr)
method -0.427
```

Problem with interpretation of ML fit!

```
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- The Wald Z is $\widehat{\beta}/\mathrm{SE}(\widehat{\beta})$, and this is computed **using a point estimate of the random effects covariance matrix** $\widehat{\Sigma}_b$**!**
- The data leave us uncertain about not only β but also Σ_b, but this uncertainty is not taken into account by the Wald Z statistic
- This motivates the use of inferential methods that **take into account the collective uncertainty about all model parameters**
- One powerful technique to do this is **Bayesian inference**

Unnormalizable posteriors

*For now, θ denotes **all** model parameters, not just the fixed effects*

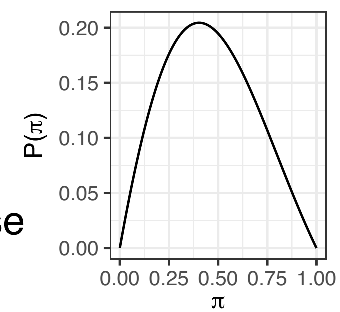
- Our motivation: Bayesian posterior inference

$$P(\theta \mid \mathbf{y}, I) = \frac{P(\mathbf{y} \mid \theta, I) P(\theta \mid I)}{P(\mathbf{y} \mid I)}$$

- Sometimes $P(\mathbf{y} \mid I)$ can't be calculated exactly. Example

Bernoulli data with non-conjugate prior:

$$P(\pi) \propto \begin{cases} \pi(1-\pi)e^{-\pi^2} & \pi \in [0,1] \\ 0 & \text{otherwise} \end{cases}$$



Posterior after observing 2 heads, 2 tails:

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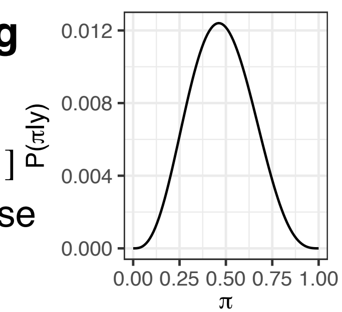
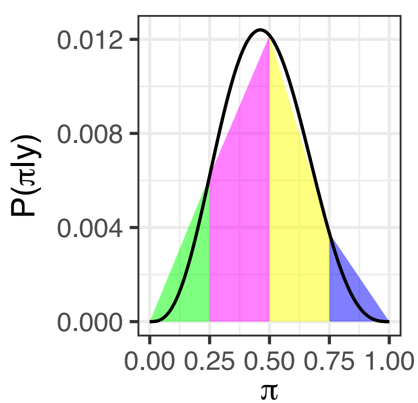


- In simple cases like this, we can numerically approximate the integral:



- But in high dimension and/or unbounded ranges, difficult or even impossible!

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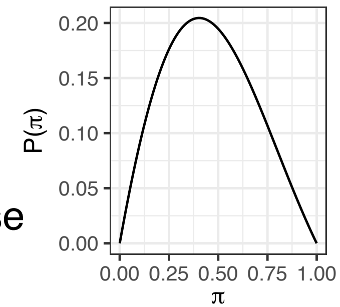

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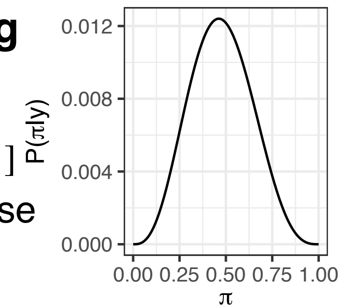

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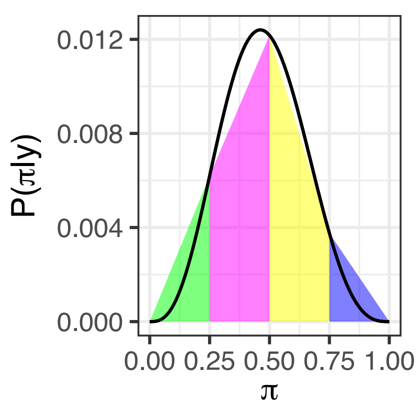

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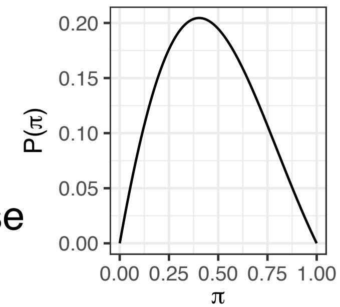

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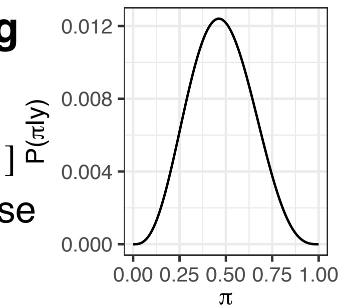

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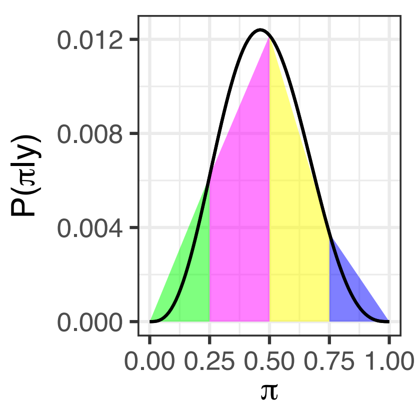

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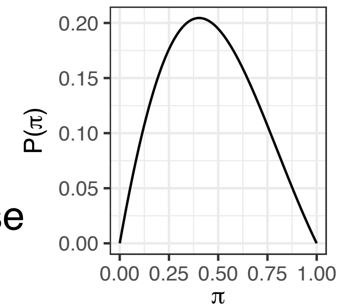

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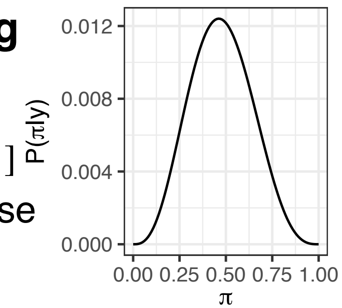

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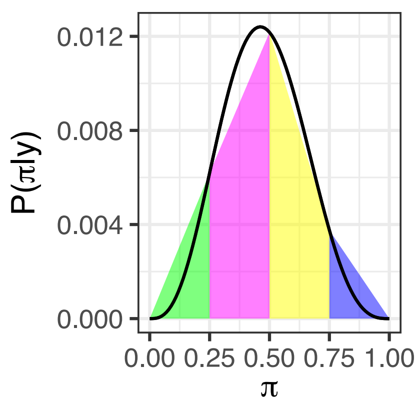

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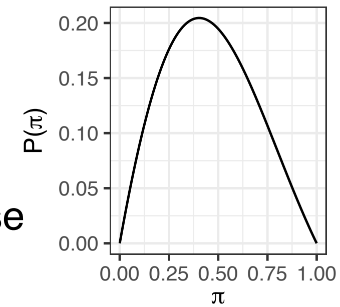

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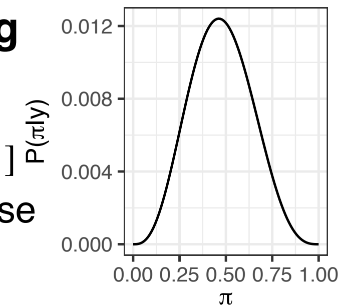
No closed form!



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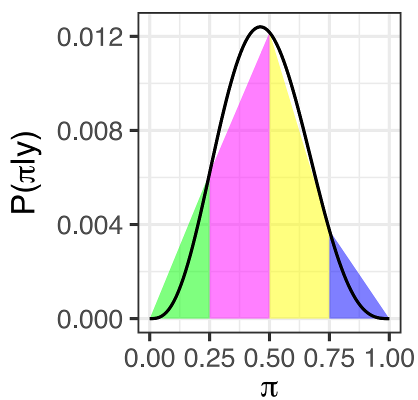

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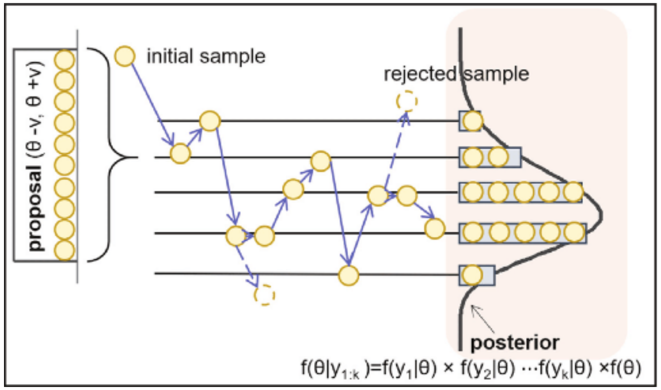
Markov chain Monte Carlo

- However, we can often **take samples from the posterior** even when we can't compute normalized probabilities
- One general and widely used approach: **Markov chain Monte Carlo (MCMC)**
- MCMC is a mathematically principled random walk on a non-negative function, directed toward regions where the function takes on a larger value



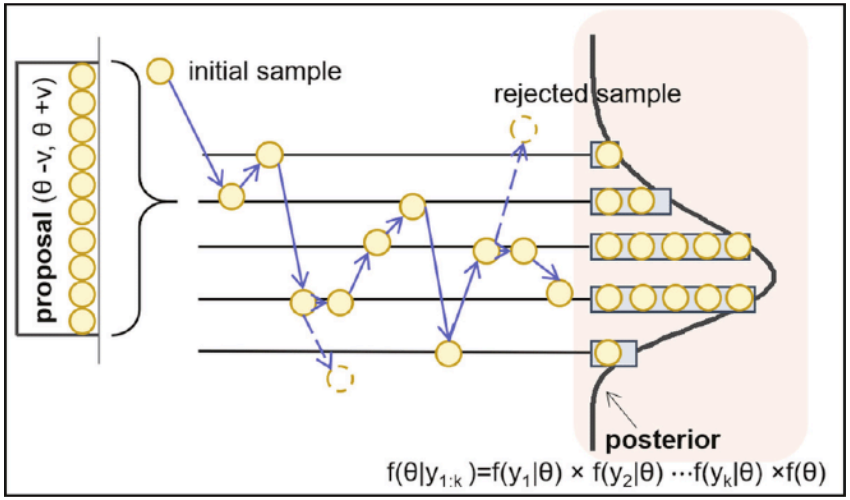
- Asymptotically, the random walk gives us samples from in proportion to the height of the function

Image credit: Dong et al., 2019, http://dx.doi.org/10.5772/intechopen.82781

MCMC for posterior sampling

- We use the *unnormalized* form of the posterior:

$$P(\theta \,|\, \mathbf{y}, I) \propto P(\mathbf{y} \,|\, \theta, I) P(\theta \,|\, I)$$

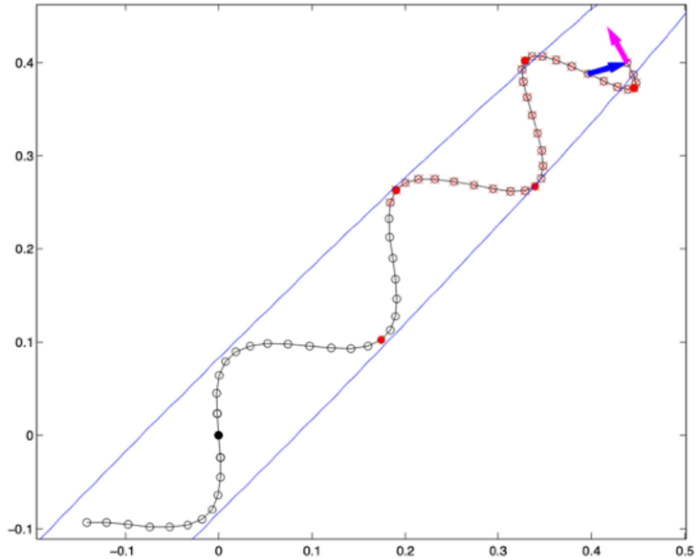


- We run MCMC and then treat the chain of values as samples from the posterior
- The full set of samples is not iid (nearby values on the chain are correlated), but methods exist for estimating "effectively" how many independent samples we have

Image credit: Dong et al., 2019, http://dx.doi.org/10.5772/intechopen.82781

Stan, HMC, and NUTS

- There are many different MCMC algorithms (e.g., Metropolis, Gibbs Sampling)
- We will use the probabilistic programming language **Stan** for Bayesian inference about model parameters
- Stan uses an algorithm called **Hamiltonian Monte Carlo** (**HMC**) with the **No U-Turn Sampler (NUTS)**



(Hoffman & Gelman, 2014)

- This algorithm tends to be particularly efficient for many problems we'll face

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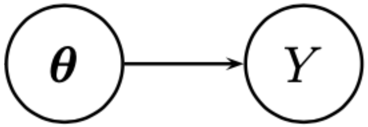

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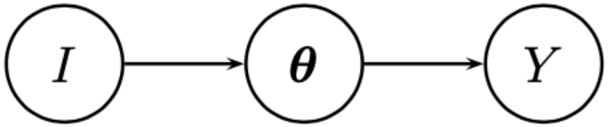

A Stan model

```
data {
  int<lower = 0> n;  // Total number of trials
  int<lower = 0> r;  // number of successes
}
parameters {
  real<lower = 0, upper = 1> p;
}
model {
  // Prior:
  p ~ beta(1,1);
  // Likelihood
  r ~ binomial(n,p);
}
```

Likelihood ratio test more robust than Wald Z

```
> model <- glmer(passed ~ method + (1 | site_id), data = dat, family = binomial)
> m0 <- glmer(passed ~ 1 + (1 | site_id), data = dat, family = binomial)
> anova(m0,model)
Data: dat
Models:
m0: passed ~ 1 + (1 | site_id)
model: passed ~ method + (1 | site_id)
      npar    AIC    BIC  logLik deviance  Chisq Df Pr(>Chisq)
m0       2 31.482 33.838 -13.741   27.482
model    3 28.636 32.170 -11.318   22.636 4.8455  1    0.02772 *
---
Signif. codes:  0 ‘***’ 0.001 ‘**’ 0.01 ‘*’ 0.05 ‘.’ 0.1 ‘ ’ 1
```