# Bayesian Model Selection

Globular cluster mass profiles

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# Testing lowered isothermal models with direct N-body simulations of globular clusters

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#### LIMPEY

## Data:

- 3D Position  $(x,y,z \rightarrow r)$
- 3D Velocity (xy, xz, yz -> v)

# Model parameters:

- m (mass)r (half light radius)
- g (truncation energy) | shape | phi (potential) | shape | gravitational | notential
- r a (anisotropy radius can -> infinity, become isotropic)

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Assume we have the <u>complete</u> dataset of the cluster's dynamic information (position and velocity)

**Goal:** Get the estimated of true parameters, posterior distribution And, Which model we should choose?



#### **Model Selection**

- 1. fit isotropic data with the correct isotropic model
- 2. fit isotropic data with a more expansive anisotropic model
- 3. fit anisotropic data with the incorrect isotropic model
- 4. fit anisotropic data with the correct anisotropic model (the anisotropy does not go to 0)

### Data X: true parameter {m5r3g1.5phi3.0}

## Steps:

1. Assume the models

Model1: isotropic (expected to prefer)

Model2: anisotropic

# 2. Set up Bayes Method (Why not p-value?)

$$\begin{aligned} \text{Posterior Prob} &= P(\Theta|X) = \frac{P(\Theta)P(X|\Theta)}{P(X)} = \frac{\text{Prior \cdot Likelihood}}{\text{Evidence}} \\ P(X|\Theta) &= \prod_{i}^{N_*} \Lambda_i(X_i|\Theta) & \text{N \#of stars} \\ \Lambda_i &= \frac{f(X_i|\Theta)}{\text{Normalizing term}} & f(E,J^2) = A \exp\left(-\frac{J^2}{2r_{\text{a}}^2 s^2}\right) E_{\gamma}\left(g,\frac{\phi(r_{\text{t}}) - E}{s^2}\right) \end{aligned}$$

For Model Comparison, We evaluate K = 
$$\frac{P(M1|X)}{P(M2|X)} = \frac{P(X|M1)}{P(X|M2)} \frac{P(M1)}{P(M2)}$$

A value of logK > 1 means that M1 is more strongly supported by the data than M2

# 3. Calculate Likelihood/ Choice of Sampling Methods

Marginal likelihood= 
$$P(X|M) = \int P(X|\theta, M)P(\theta|M)d\theta = E_{prior}[P(X|M)]$$

Naive Monte Carlo Estimator

$$\hat{p}(X|\theta) = \frac{1}{N} \sum_{i=1}^{N} p(X|\hat{\theta_i}), \text{ where } \hat{\theta_i} \sim p(\theta) \text{ prior distribution}$$

## - Importance Sampling

$$\begin{split} \int p(X|\theta)p(\theta)d\theta &= \int p(X|\theta)p(\theta)\frac{g(\theta)}{g(\theta)}d\theta = E_g(\frac{p(X|\theta)p(\theta)}{g(\theta)}) \\ \hat{p} &= \frac{1}{N}\sum_i \frac{p(X|\hat{\theta})p(\hat{\theta})}{g(\hat{\theta})} & \text{drawing sample from proposal $g$ instead of prior} \end{split}$$

importance weight = posterior/ proposal

#### Application: Estimation of Euler's constant

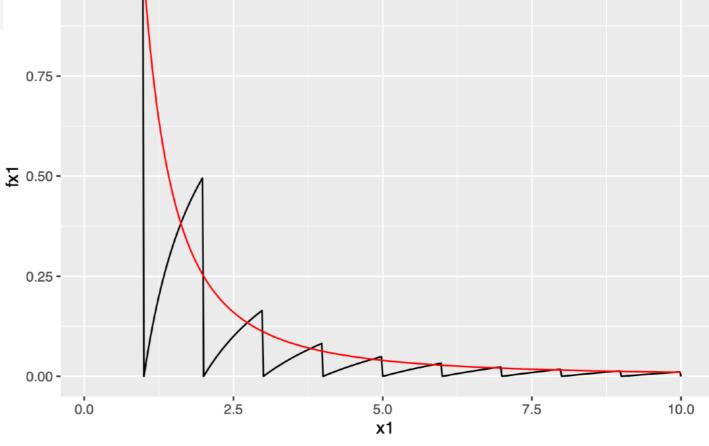
Let importance density 
$$g(x)=x^{-2}$$
 
$$=\int_1^\infty (\frac{1}{\lfloor x\rfloor}-\frac{1}{x})dx$$
 
$$=\int_1^\infty x^2(\frac{1}{\lfloor x\rfloor}-\frac{1}{x})x^{-2}dx$$
 
$$=\int_1^\infty x^2(\frac{1}{\vert x\vert}-\frac{1}{x})g(x)dx$$

1.00 -

```
N=10000000
gammalist = c(rep(0,N))
for (i in 1:N){
   unif = runif(1)
   x <- 1/(1-unif)
   gammalist[i] = (x^2)*(1/floor(x)-1/x)
}
mean(gammalist)</pre>
```

#### ## [1] 0.5769798

The true value of Euler constant is 0.57721566...



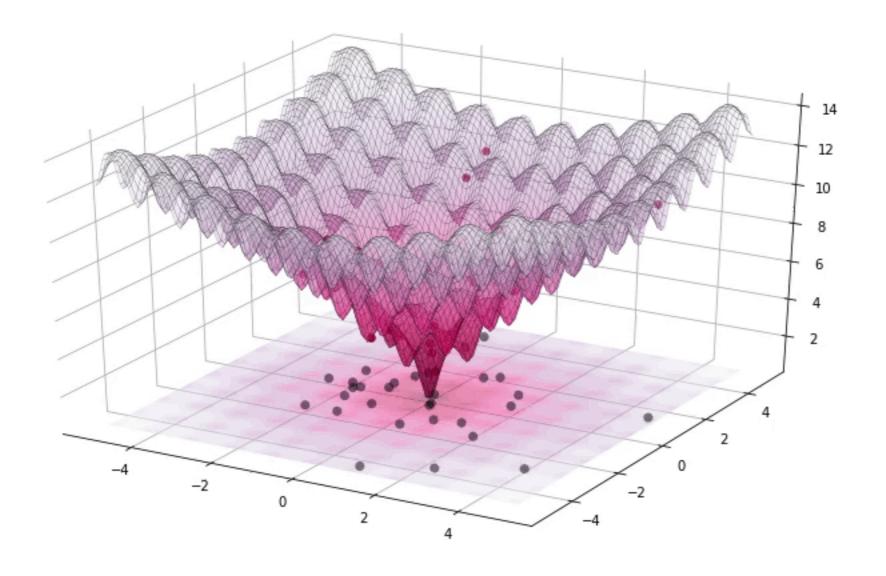
# Optimization, get parameter estimates

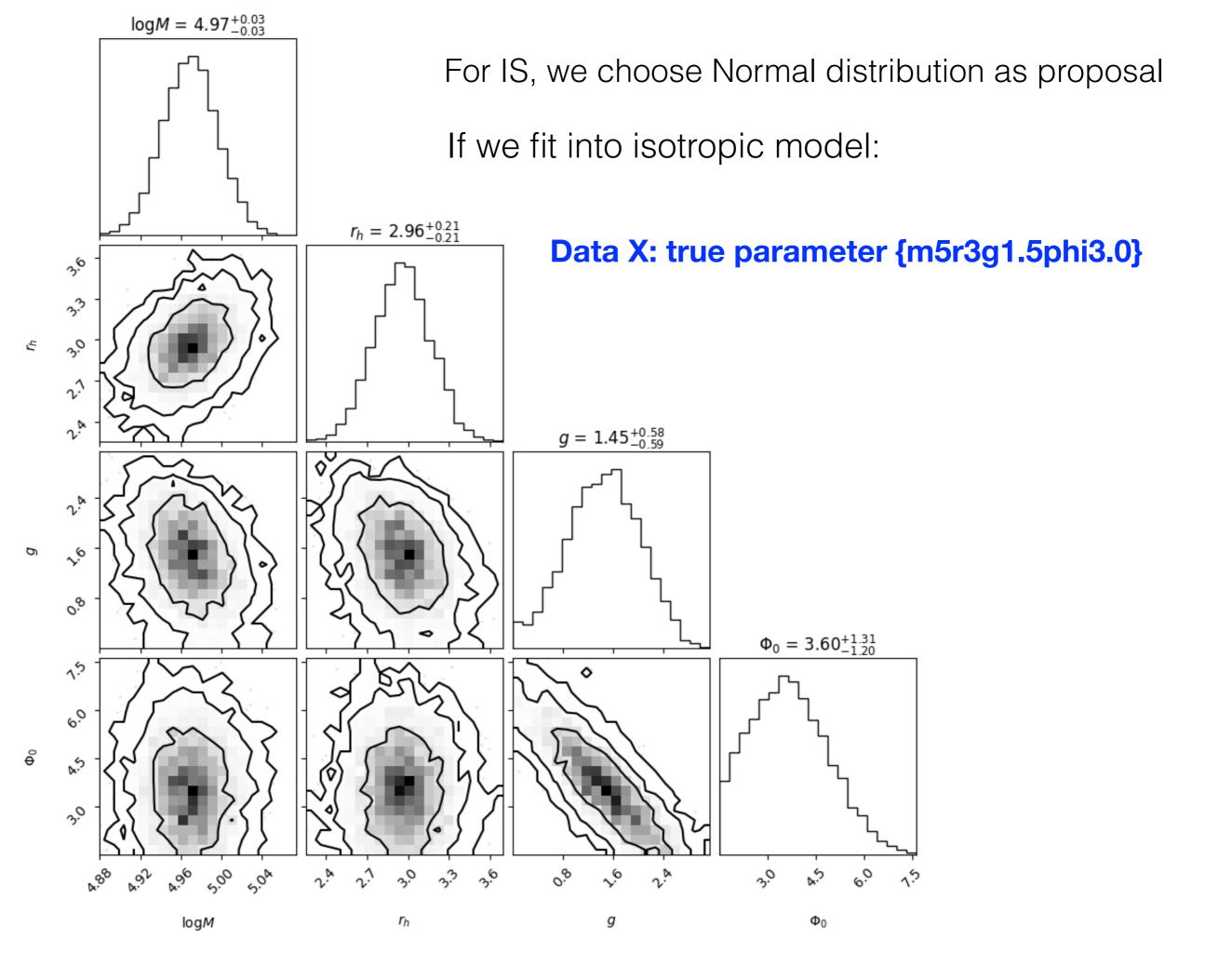
Max posterior =

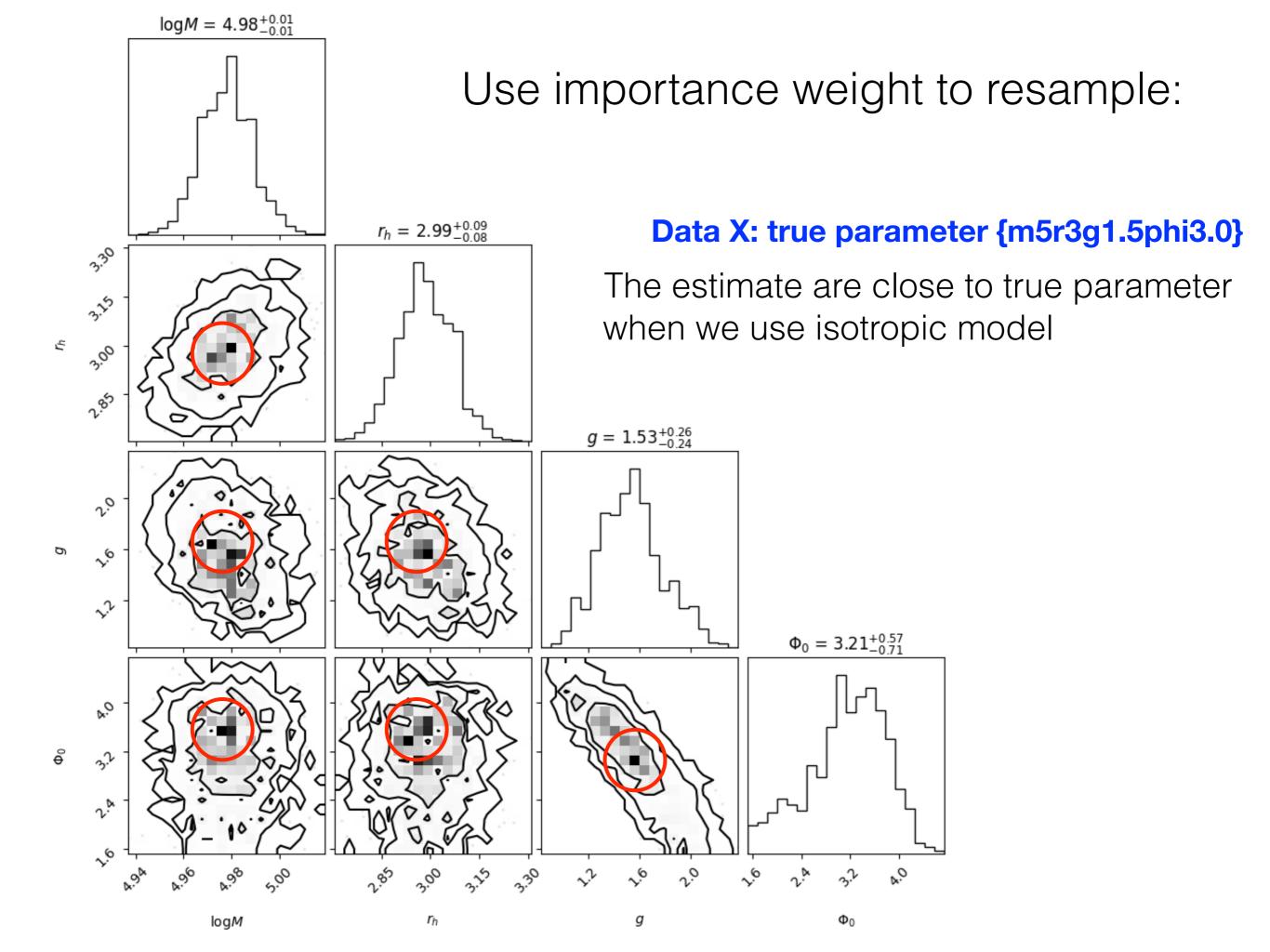
Min {Negative of the log-posterior function of the input parameters}

There are many optimization methods like gradient/coordinate descent Here we use **Differential Evolution** 

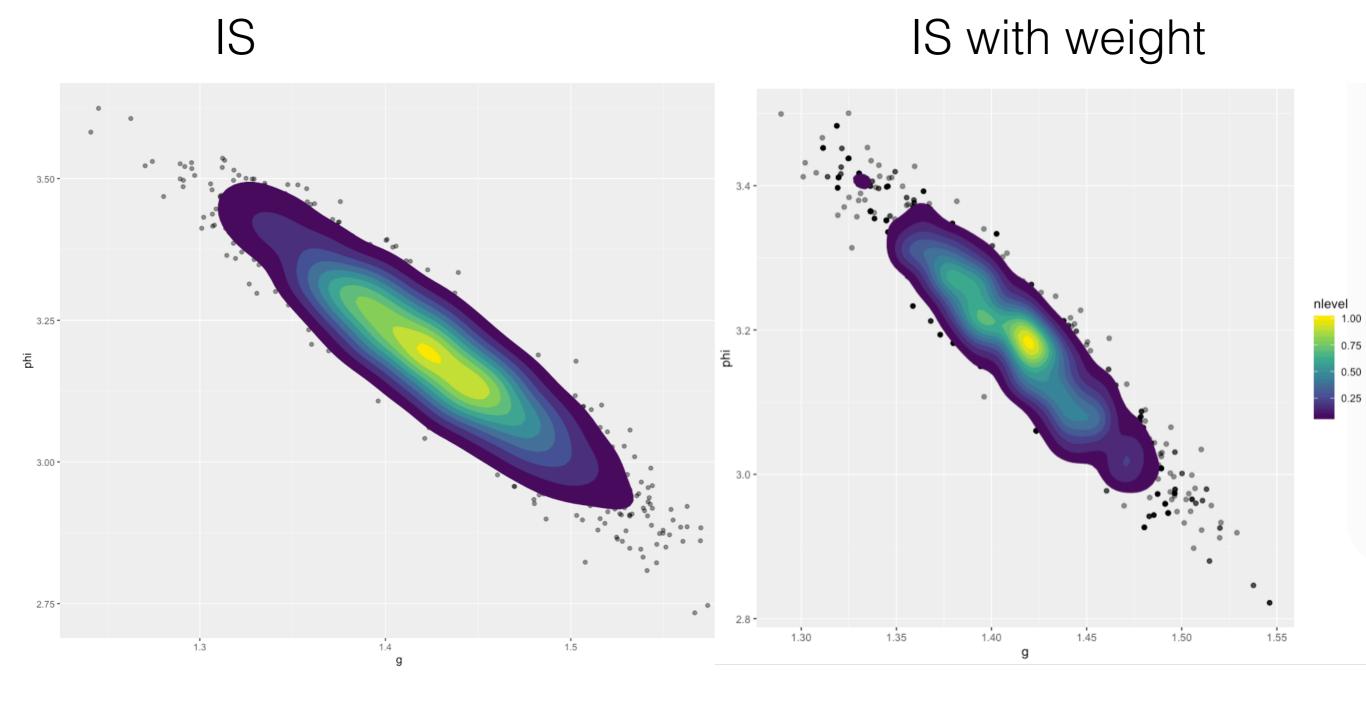
Target function not required to be differential (not even continuous)

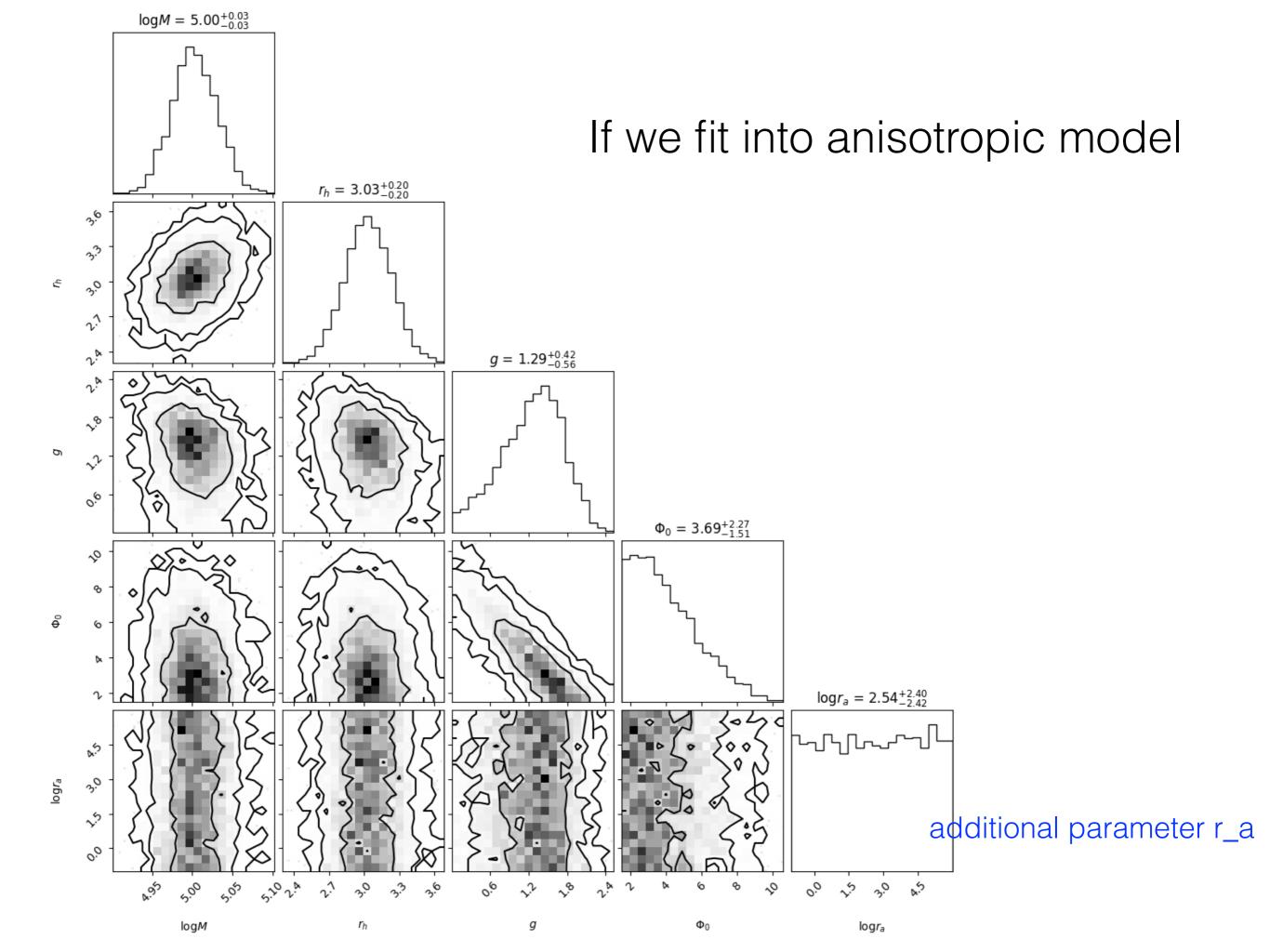


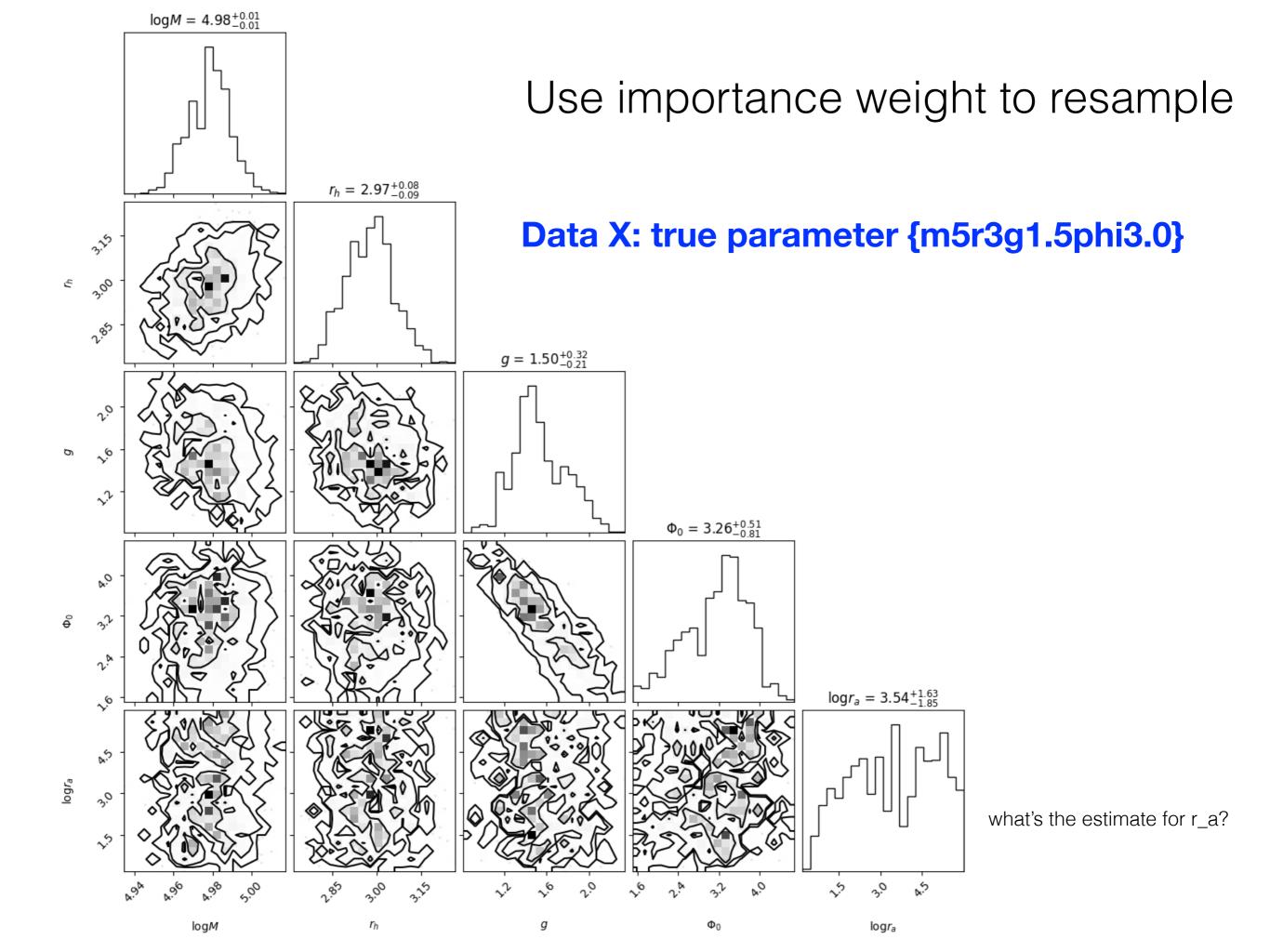




g vs phi







#Effective sample size

("exchange rate"

btw dependent &independent samples)

$$n_{\text{eff}} \equiv \frac{\left(\sum_{i=1}^{n} w_i\right)^2}{\sum_{i=1}^{n} w_i^2}$$

Model 1: 305.5455

Total 2500 samples

Model 2: 113.3407 (prop

(proposal distribution not good enough)

Bayes Factor logK = 
$$\frac{P(M1|X)}{P(M2|X)} = \frac{P(X|M1)}{P(X|M2)} \frac{P(M1)}{P(M2)}$$
 = 2.41

log <sub>10</sub> K	K	Strength of evidence
0 to 1/2	1 to 3.2	Not worth more than a bare mention
1/2 to 1	3.2 to 10	Substantial
1 to 2	10 to 100	Strong
> 2	> 100	Decisive

As expected, we prefer Model 1

# Markov Chain Monte Carlo (MCMC)

Markov Chain: Time homogenous property

$$\Pr(X_{n+1} = x \mid X_1 = x_1, X_2 = x_2, \dots, X_n = x_n) = \Pr(X_{n+1} = x \mid X_n = x_n)$$

MCMC: By constructing a Markov Chain such that it will converge to its desired stationary distribution

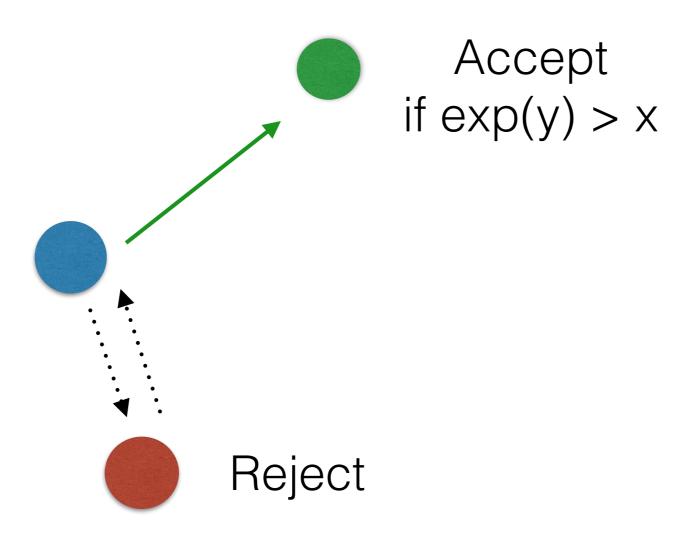
Ex: Metropolis Hasting Algorithm

In Bayesian, the samples generated by MCMC can be used to evaluate the integral over high dimensional variable

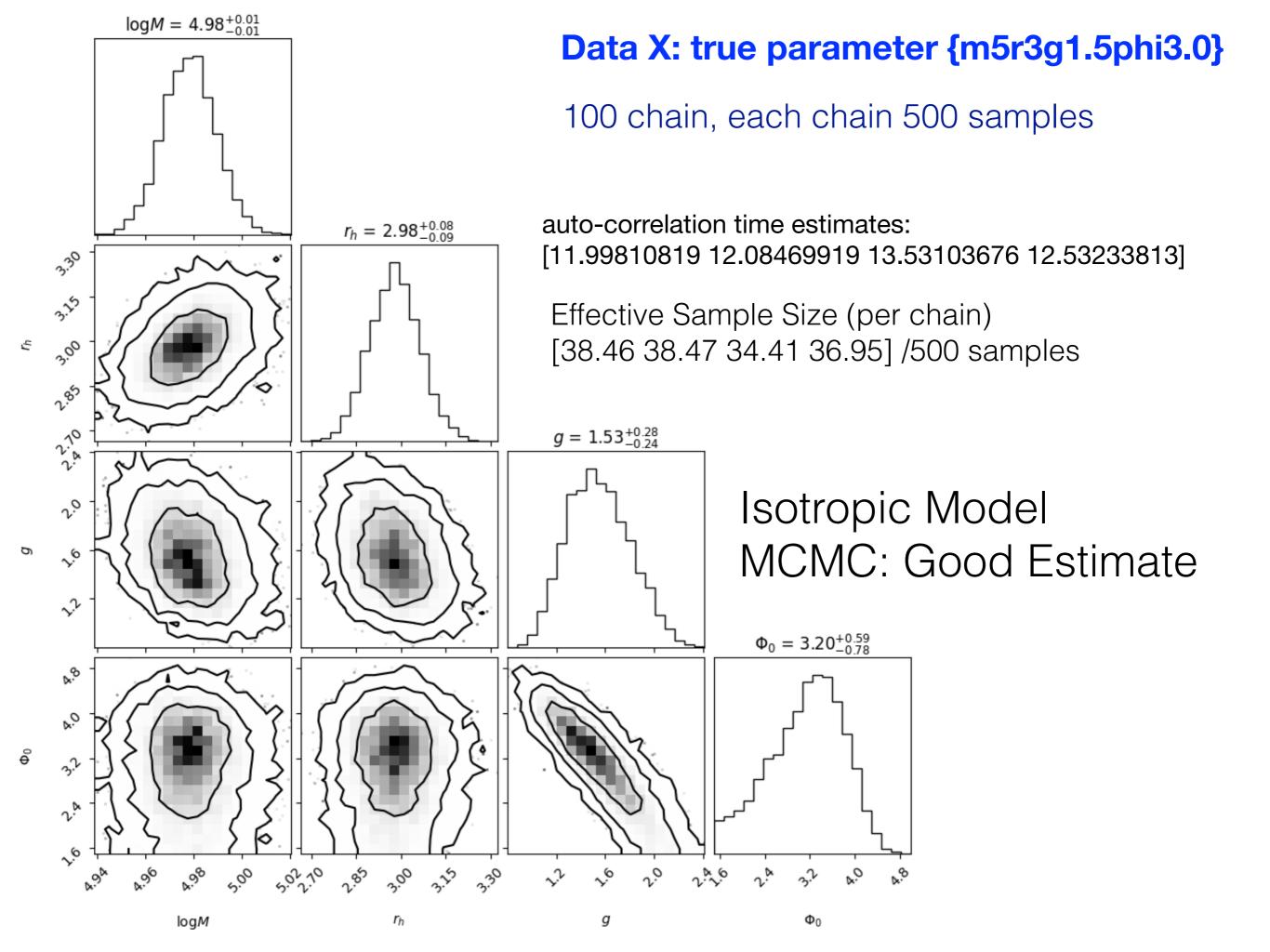
Same Goal: Calculate the likelihood

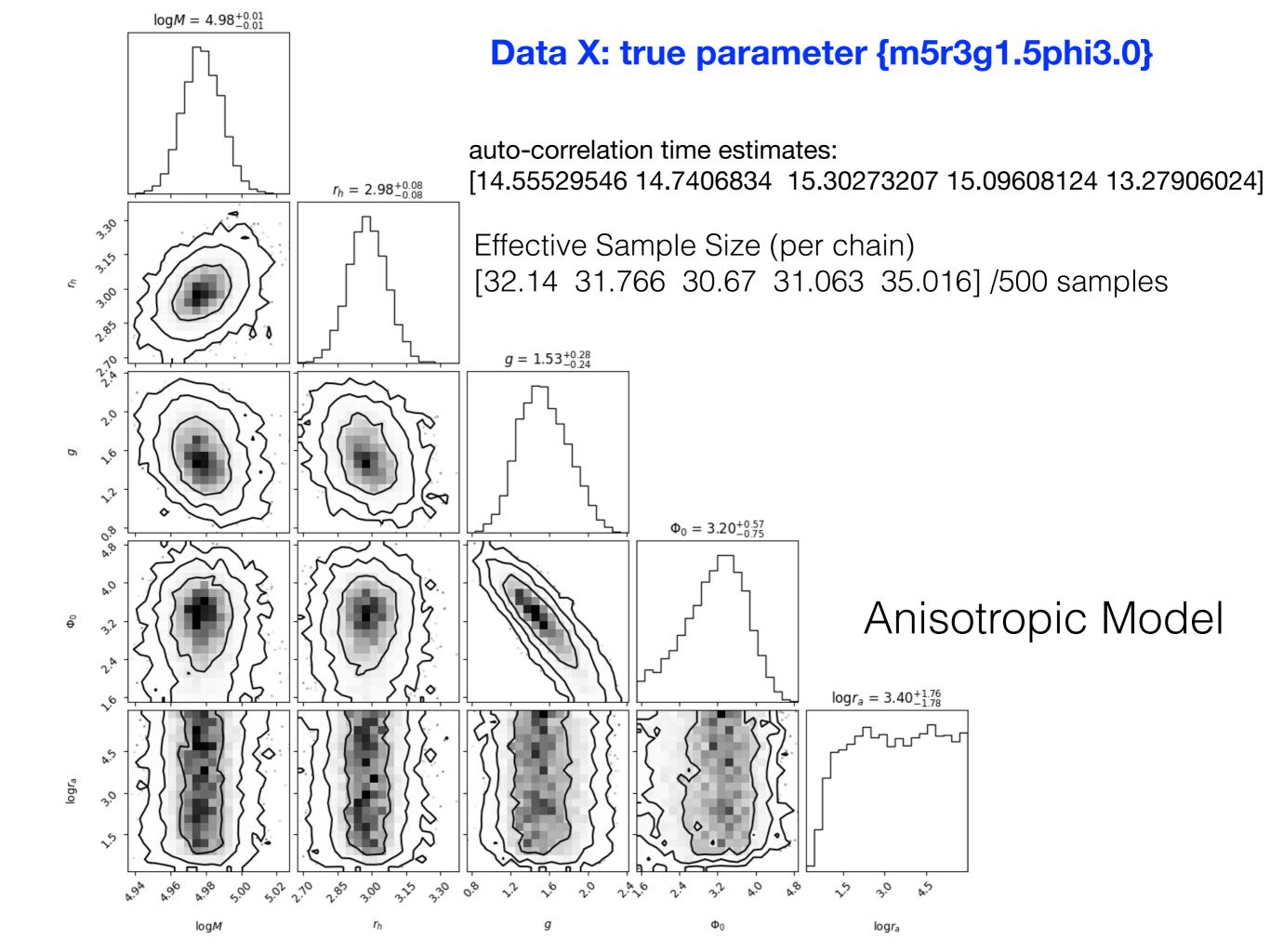
- 1. Calculate difference of logs of likelihood\*prior between current and new proposed points = y
- 2. Generate X~ Unif[0,1] independently

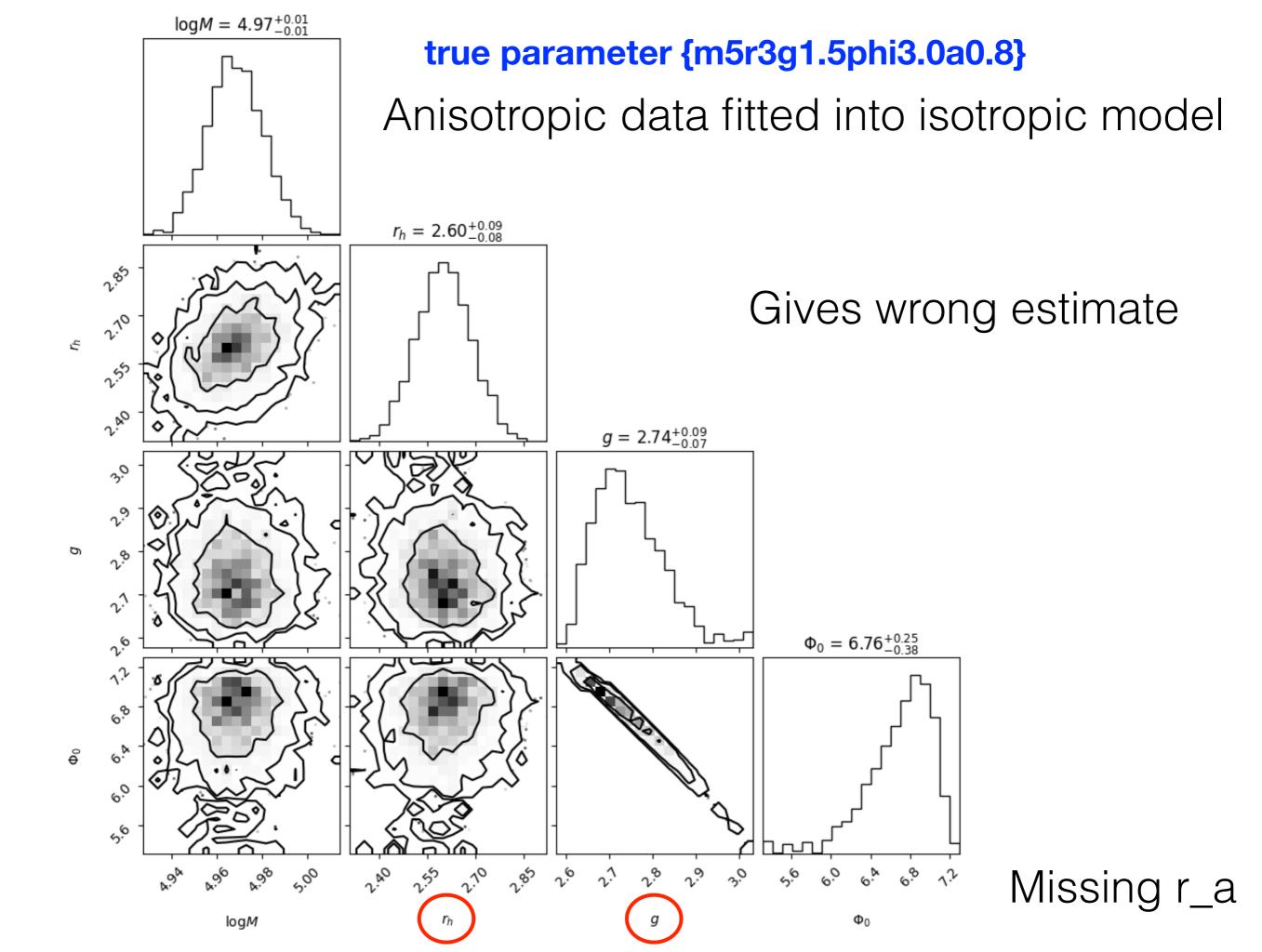
Detailed Options:
Thinning
Finite Adaptive MCMC

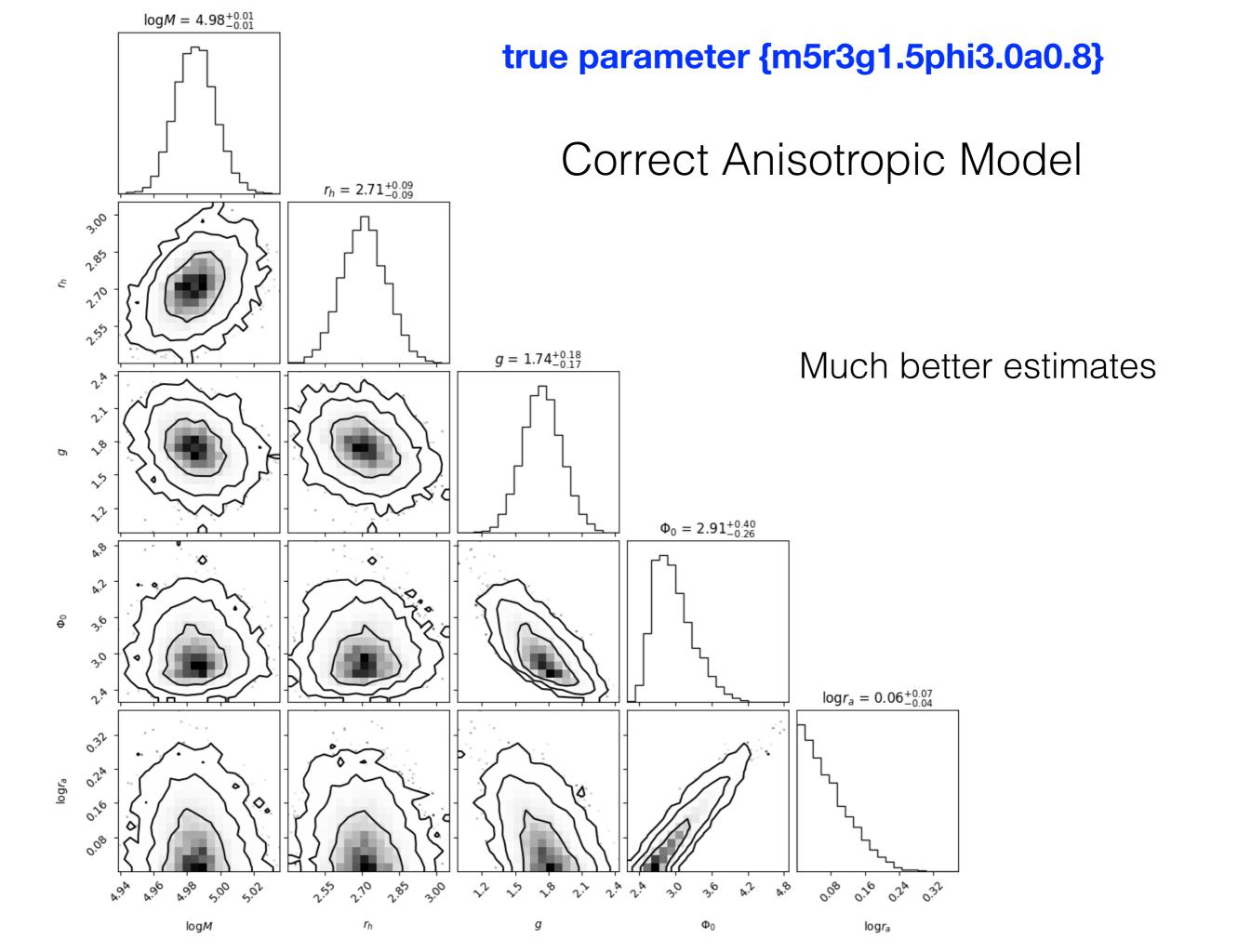


if return 0 probability from prior if return -Inf from the log likelihood if exp(y) < x









# **Next Step:**

- Try other sampling methods, such as Bridge Sampling, Nested Sampling
- 2. Consider the case when we don't have complete dataset (Projection/ missing positions)
- 3. Error Measurements/ Uncertainty in the model