Approximate Bayesian computation (ABC)

Reporter

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- **Population genetics** is a subfield of genetics that deals with genetic differences within and between populations.

- ABC is a group of methods, that is suitable to solve the problems, arise in population genetics along with other fields.

- **ABC** constitutes a class of computational methods rooted in Bayesian statistics.

- **Bayesian statistics** is a theory in the field of statistics, in which the evidence about the true state of the world is expressed in terms of *degrees of belief* , as known as Bayesian probabilities.

- Instead of frequency or propensity of some phenomenon

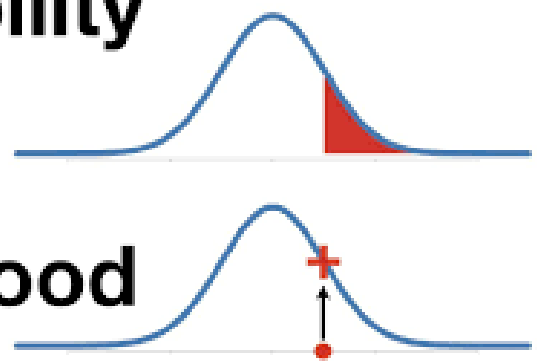
History

- The term *Bayesian* derives from the name of Thomas Bayes.
- He was a great mathematician, philosopher and theologian of 18 th century.
- The term ABC was established by Mark Beaumont *et al*.
- Bayesian phylogenetic methods were introduced in the 1990s.

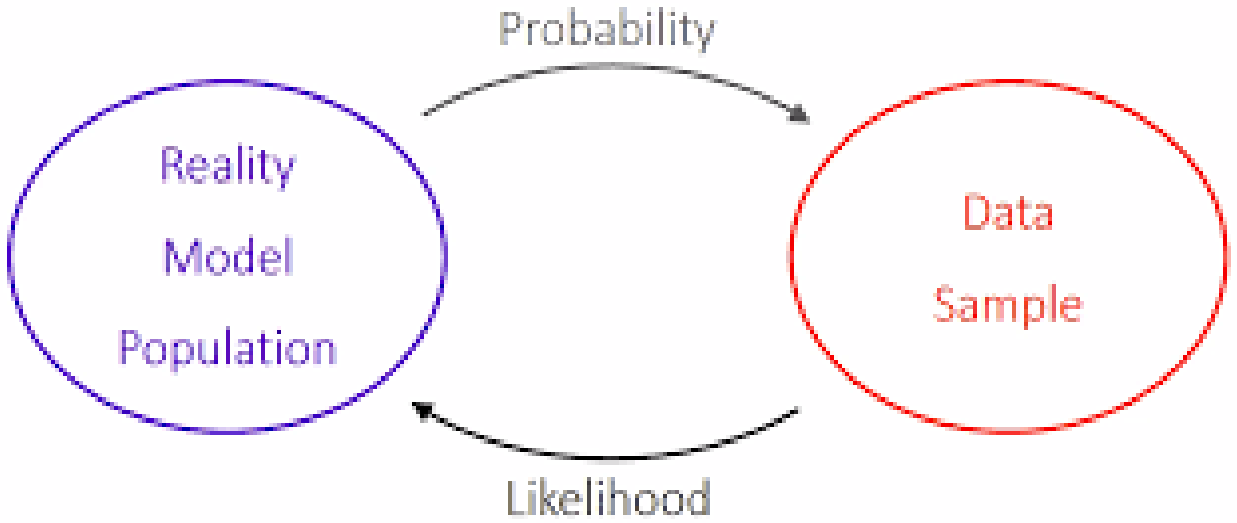
- The estimation of demographic parameters from genetic data often requires the computation of likelihoods.

- But the situation changed recently with the advent of ABC algorithms allowing one to obtain parameter posterior distributions based on simulations not requiring likelihood computations.

Probability Vs Likelihood



- *Probability* describes the plausibility of observed data assumed to be described by a statistical model, without reference to any observed data.
- whereas *likelihood* describes the plausibility of a paramet
describe



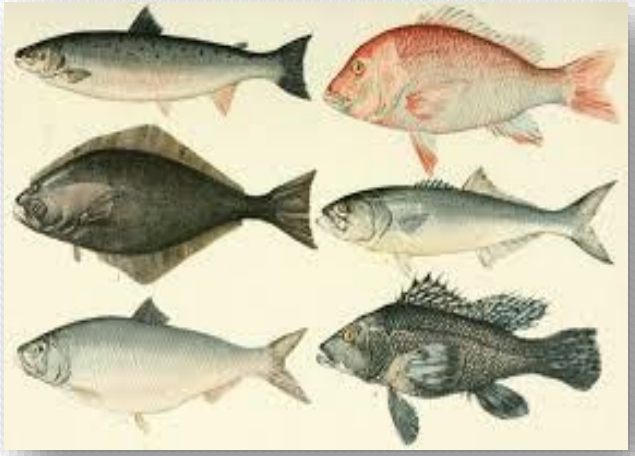
Applications

- Analysis of ecology or systems biology
- Phylogeographic analysis of virus spread in humans
- Inference of phylogeographic history and migration between species
- Analysis of species diversification rates
- Inference of phylogenetic relationships among species or populations.
- Analysis of complex problems arising in biological sciences, e.g. in population genetics and systems biology.

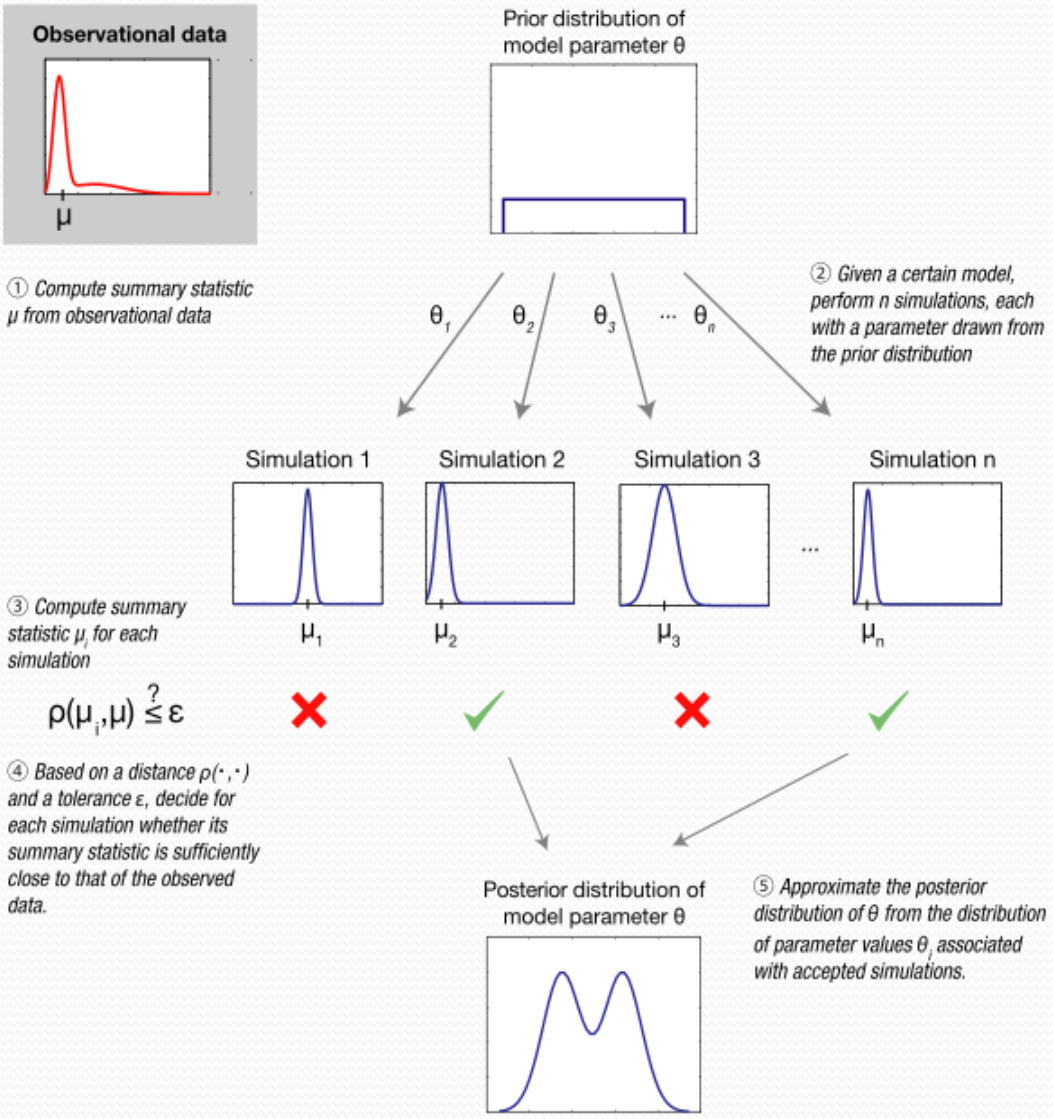
What type of data we can use

- DNA and amino acid sequence alignments

- Morphological characters



Conceptual overview

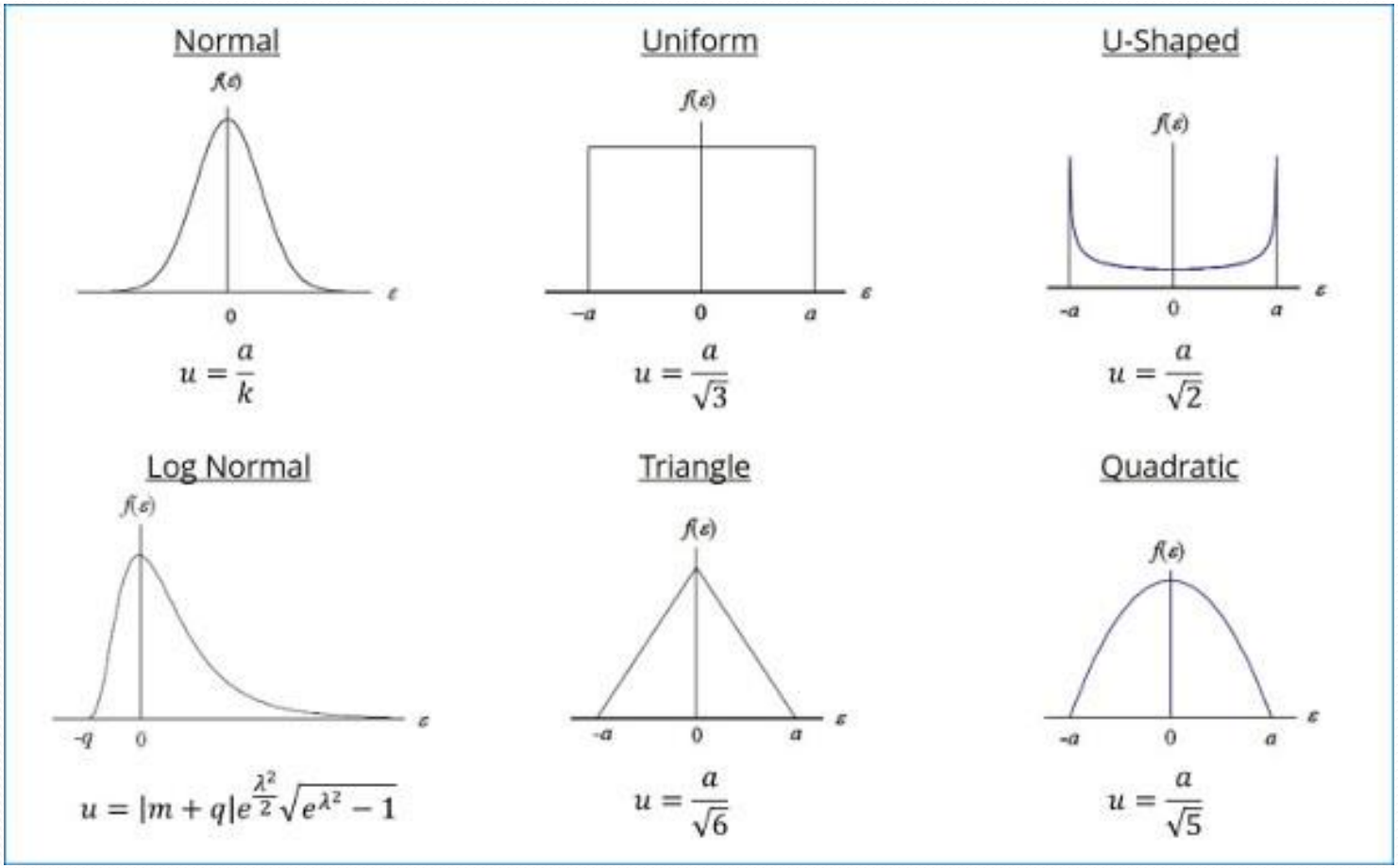


Summary statistics

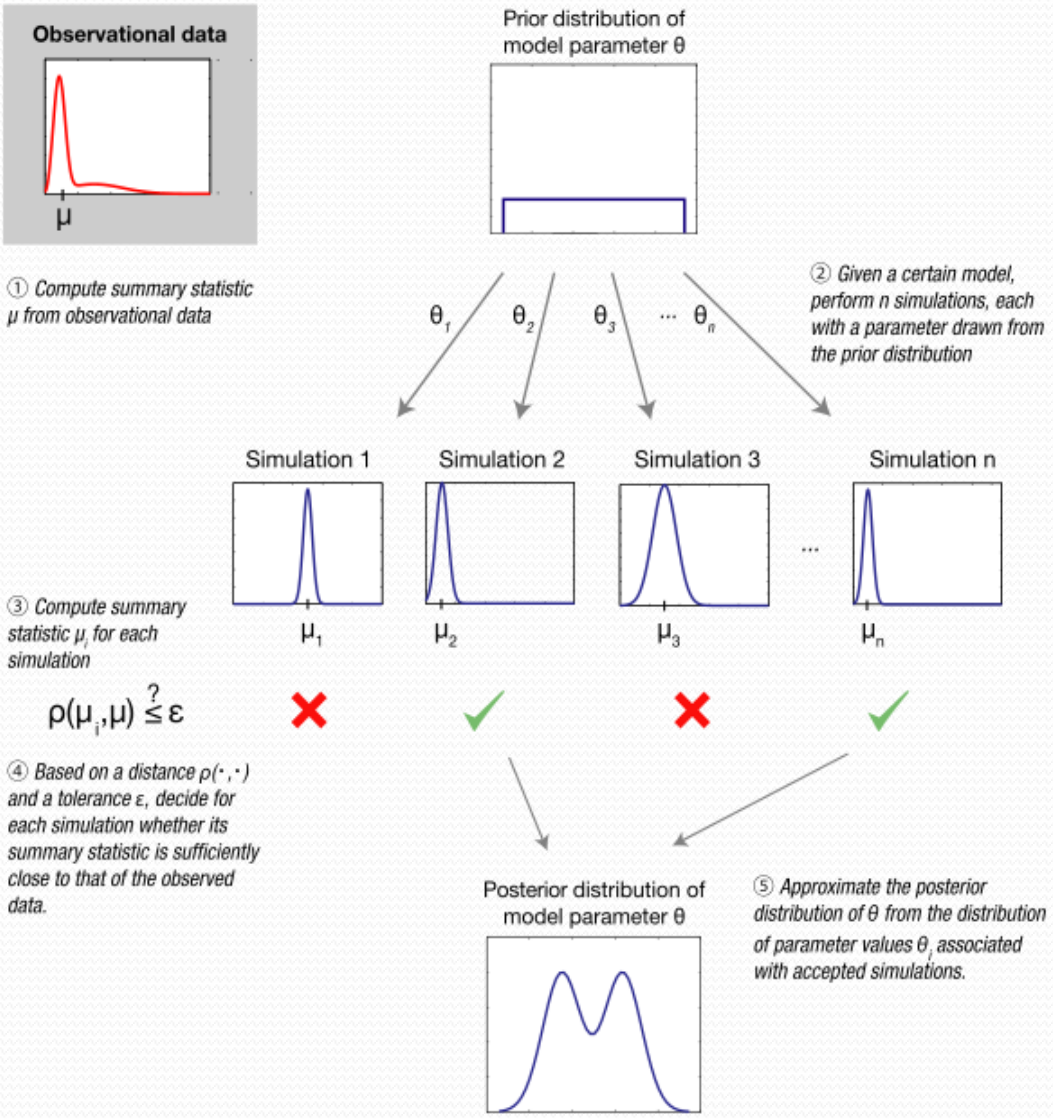
- In order to evaluate the distance between the simulated data and the observed data, the data needs to be summarized in a quantitative form.
- The choice of summary statistics, however, is a tough one.
- Too few summary statistics may not capture the characteristics of the model, which leads to overall low power for parameter estimation.
- Too many summary statistics, on the other hand, may introduce random noise.

- Observed data: AABAAAAABBABBBBBBBBA
- Summary statistic value: 6

Prior probability distribution



Conceptual overview



Example of ABC rejection algorithm

i		Simulated datasets (step 2)	Summary statistic (step 3)	Distance (step 4)	Outcome (step 4)
1	0.08	AABAAAABAAB AAABAAAAA	8	2	accepted
2	0.68	AABBABABAAAB BABABBAB			
3	0.87	BBBABBABBBBA BABBBBBA			
4	0.43	AABAAAAABBA BBBBBBBBA			
5	0.53	ABBBBBAABBAB BABAABBB			

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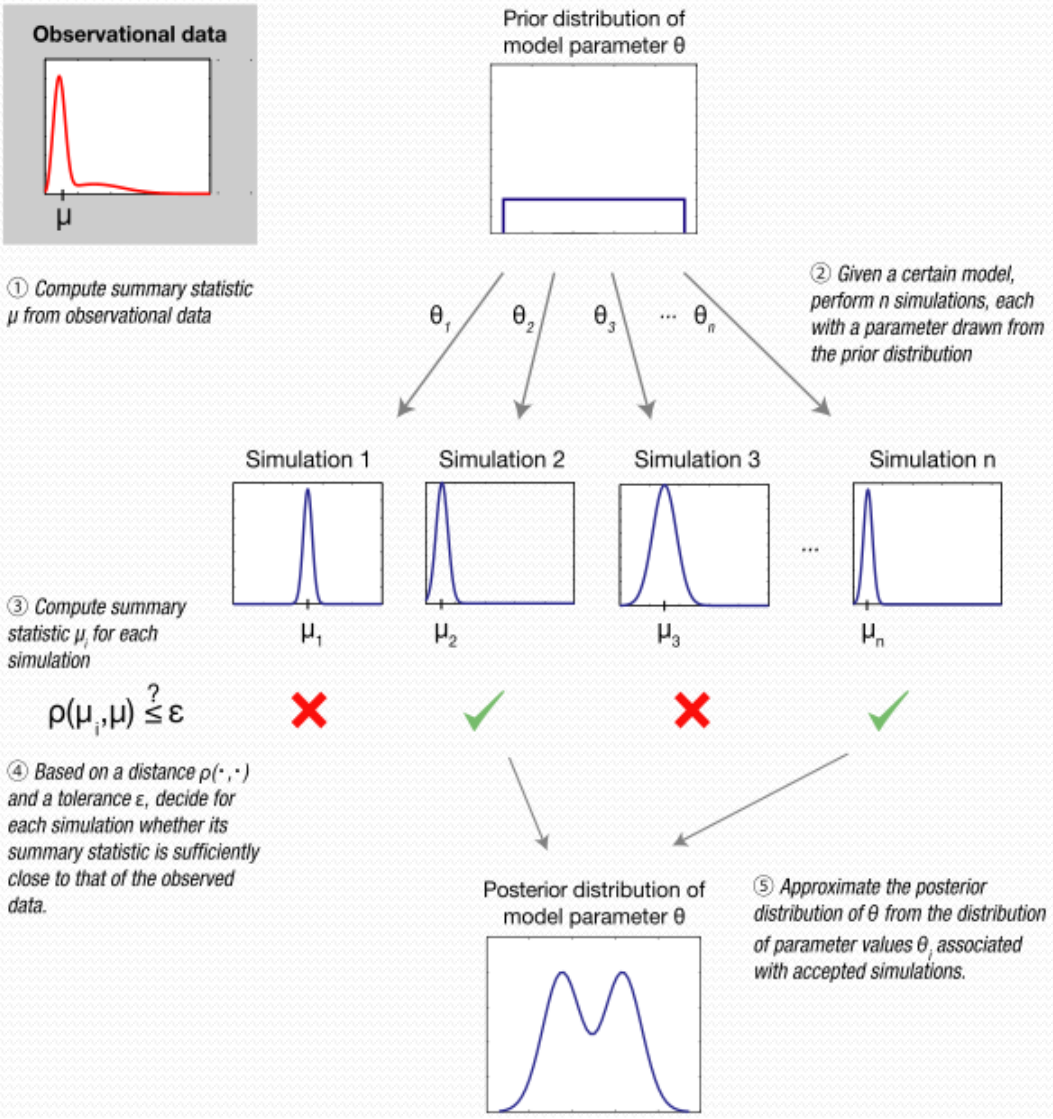
1	0.08	AABAAAABAAB AAABAAAAA	8	2	accepted
2	0.68	AABBABABAAAB BABABBAB	13	7	rejected
3	0.87	BBBABBABBBBA BABBBBBA	9	3	rejected
4	0.43	AABAAAAABBA BBBBBBBBA	6	0	accepted
5	0.53	ABBBBBAABBAB BABAABBB	9	3	rejected

Conceptual overview

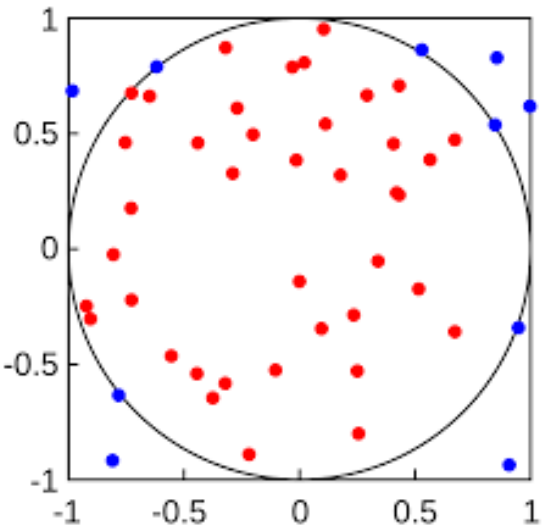


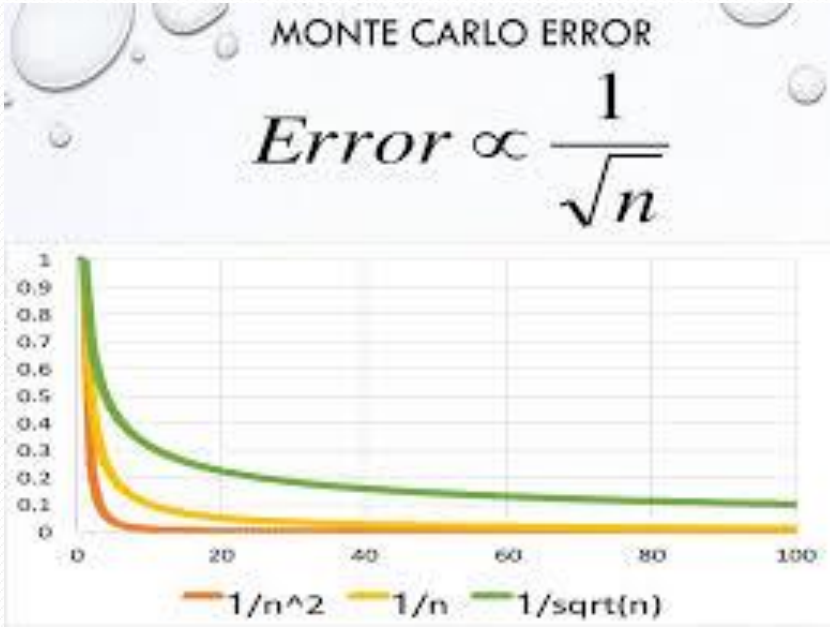
Choice of threshold level

- At the time of choice, we should make good balance between bias and Monte Carlo error.
- When value is 0, this is identical to algorithm.
- When this is 3, is better than previous one upto 100,000 simulations.
- But at the time of 5, bias dominates.

Monte Carlo integration & error

- In mathematics, **Monte Carlo integration** is a technique for numerical integration using random numbers.
- Points inside the circle is 40
- Points inside the square is 50
- Ratio: 40/50=0.8
- Circle area: 4 X 0.8= 3.2





Why we use ABC

- The availability of user-friendly software for running sophisticated models of evolution.

- The development of powerful models of data analysis.

Disadvantages

- Bayesian phylogenetic models are complex.
- Analyses are often conducted using default priors, which may not be appropriate and may lead to biased or incorrect results.
- The priors and model assumptions made in those programs are not always clear to the user.

Challenges

- First, data simulation, which is in the core of any ABC analysis, is specific to the model. Thus, many existing ABC software are specific to a particular class of models.

- Second, an ABC analysis often follows a trial–error approach, where users experiment with different models, ABC algorithms or summary statistics.

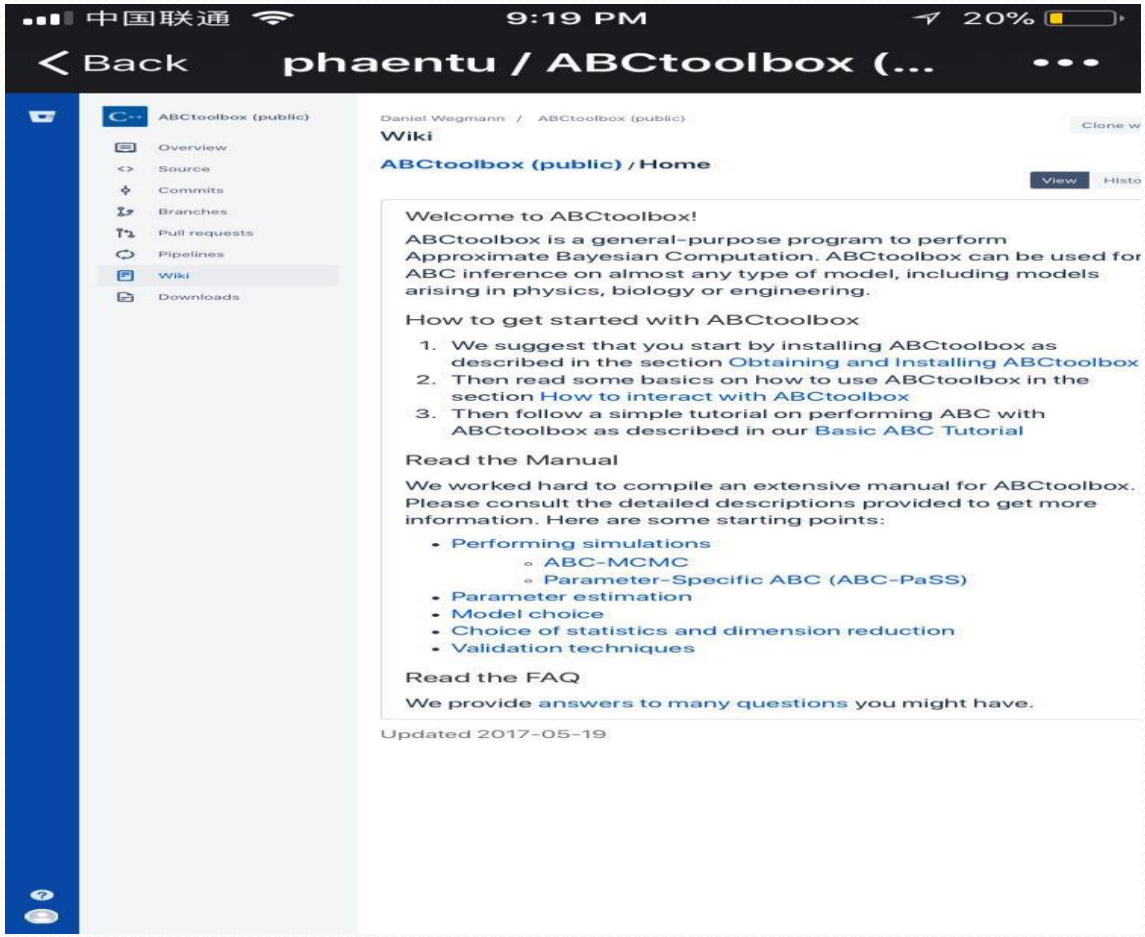
- Third, ABC is subject to intensive research, and many new algorithms have been published in the past few years .

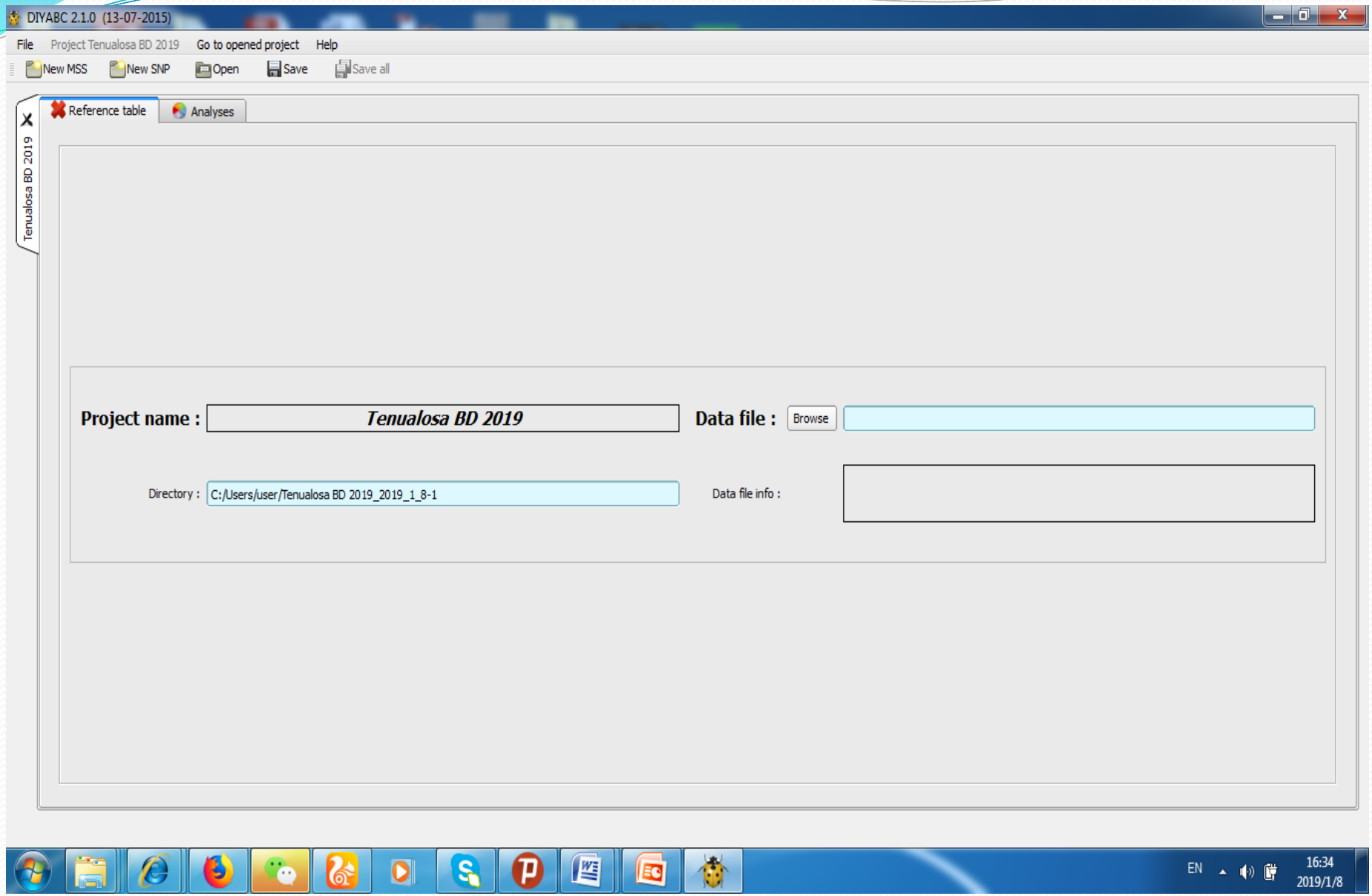
ABC-softwares

- DIY-ABC
- abc R package
- Easy ABC R package
- ABC-SysBio
- ABCtoolbox
- msBayes
- PopABC
- ONeSAMP
- ABC4F
- 2BAD
- ELFI

Web-address of ABCtoolbox

https://bitbucket.org/phaentu/abctoolbox-public/wiki/Home




DIYABC 2.1.0 (13-07-2015)
File
Project Tenualosa BD 2019
Go to opened project
Help
New MSS
New SNP
Open
Save
Save all
Tenualosa BD 2019
Reference table
Analyses
Project name :
Tenualosa BD 2019
Data file :
Browse
Directory :
C:/Users/user/Tenualosa BD 2019_2019_1_8-1
Data file info :
EN
16:34
2019/1/8

Thanks to all