#### The 'ABC' of Data Science on HPC Scale

Antonietta Mira joint work with Ritabrata Dutta

SOS21, Davos, March 21, 2017

#### BIG = E-NORMI = EX (out of) NORMA (norm) = EXTRA-ORDINARY LARGE

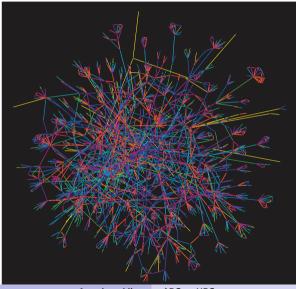
DATA = DATUS = GIVEN =Immediate, straightforward DATA SCIENTISTS mediate big data and extract information

- big data can be small or fat (small n, large p)
- but typically is complex: not i.i.d. not Gaussian not linear
- unstructured, distributed
- smart data
- value chain: information knowledge decisions actions

#### Terry Speed, 2014:

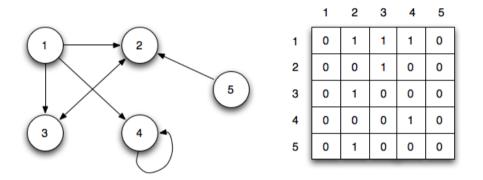
"... big data refers to things one can do at a large scale, that cannot be done at a smaller one, to extract new insights, or create new forms and value, in ways that change markets, organizations, the relationships between governments, citizens an more."

#### Communication network of 7 million nodes + 23 million ties



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#### $\mathsf{Relationships} \Longrightarrow \mathsf{Adjacency} \ \mathsf{matrix} \Longrightarrow \mathsf{Model}$



+ edge weights + covariates + time + spatial coordinates + . . . = complex relational/network data

- social network: friendships
- financial network: EU overnight interbank money transfer
- economy: EU countries import-export
- biology/ genetics networks: protein-protein interaction
- communication network: CDR
- information / knowledge network: patents
- citation / collaboration network: wikipedia

#### David Dunson, 2015:

"I would describe statistics as the science of variability, meaning that the main goal of statistics is to develop methods and algorithms for the mathematical exploration, elicitation and control of variability, and the uncertainty it generates. Inference and uncertainty quantification are at the core of statistics and they have generated correlated siblings like prediction, testing, controlling for dependence, confounding, randomization."

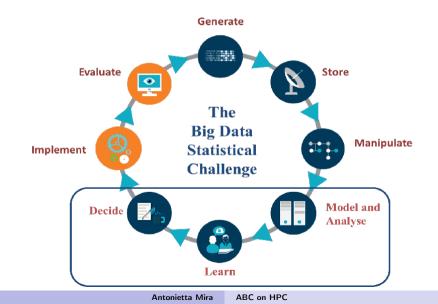




Data-driven approach

Data-driven model approach

### What is the role of statistics in the Big Data era?



- multi-resolution: separate signal from noise
- dive for perceived signals in what would have been discarded as noise a decade ago
- multi-phase: data arriving at my desk are almost never the original raw data
- too dirty, too confidential, too large
- pre-processing with different goals/assumptions
- a single model is too simple to handle heterogeneity
- multiplicity of models capture multiplicity of incompatible assumptions
- multi-source
- different sources and some not collected for inference purposes
- sampling bias of observational / self-reported data

- dimension reduction / summary / compression
- error rate control
- uncertainty quantification
- assure coherence among different scales of time/space
- support real-time decision making
- complex data complex models
- big data big errors
- big methodological and computational challenges

#### "A model-based revolution"

Sir Adrian Smith, DG Knowledge & Innovation, U. of London

Bayesian methods allow us to:

- Think differently about estimating and interpreting unknowns "what are possible values of this parameter?"
- Combine prior information with the data "what else do I know about this parameter and model?"
- Regularize the LHD and average the posterior
- Describe many sources of uncertainty in the model "how sure am I about the inputs and outputs of my model?"
- Analyze complex systems with hierarchical / multi-level models "Divide and conquer strategy"
- Perform model comparison and model averaging
- Bayesian non-parametric
- Bayesian computation (MCMC, Variational, INLA, ABC)

### Big picture of statistical inference

GIVEN:

- Data =  $y = (y_1, ..., y_n)$
- Statistical model which describes data,  $p_{y|\theta}(y|\theta)$ , indexed by Parameters =  $\theta = (\theta_1, \dots, \theta_d)$
- Observed data =  $y_{obs}$
- Prior probability density function for  $\theta$ ,  $p_{\theta}$

WANTED:

- Some probabilistic statement about  ${m heta}$ 
  - which value of heta has, most likely, generated  $y_{obs}$  ?
  - what is the mean value of  $\theta$  given  $y_{obs}$ ?
  - which interval contains  $\theta_1$  with probability 0.95 ?

• ...

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## Different types of statistical models

**•** Statistical model as family of pdfs, e.g.

$$p_{y|\theta}(y|\theta) = \prod_{i=1}^{n} \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{1}{2\sigma^2}(y_i - \mu)^2\right), \quad \theta = (\mu, \sigma)$$

Onnormalized statistical model

(the partition function, of  $p_{y|\theta}$  is not known)

$$p_{y| heta}^{0}(y|oldsymbol{ heta}) \propto \prod_{i=1}^{n} \exp\left(-rac{1}{2\sigma^{2}}(y_{i}-\mu)^{2}
ight)$$

Simulator-based (generative/mechanistic) model

(shape and scale of  $p_{y|\theta}$  are not known but sampling is possible if parameters are given)

$$y \sim p_{y| heta}(y|oldsymbol{ heta}), \qquad y_i = \mu + \sigma z_i \quad z_i \sim \mathcal{N}(0,1)$$

### Big picture of statistical inference

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  - ...

• Likelihood function: pdf of the observed data  $y_{obs}$  as a function of the model parameters

$$L( heta) \propto p_{y| heta}(y_{obs}| heta)$$

- Plays a central role in statistical inference
  - Maximum likelihood estimation:

$$\hat{\boldsymbol{ heta}}_{ ext{MLE}} = \operatorname{argmax}_{\boldsymbol{ heta}} \boldsymbol{L}(\boldsymbol{ heta})$$

• Bayesian inference:

$$p_{ heta \mid y}( heta \mid y_{obs}) \propto L( heta) p_{ heta}( heta)$$

• Not available for unnormalized and simulator-based models

- Allow to use knowledge domain on how the data were generated without having to make excessive compromises in the modeling
- Neat interface with physical, social, medical, biological . . . models of data
- Scale well with big data
- No limits on the number of unobserved/latent variables
- Easier to study the effect of interventions on simulator-based (mechanistic) models rather than statistical models

### Examples

#### • Astrophysics:

Simulating the formation of galaxies, stars, or planets

• Evolutionary biology:

Simulating species evolution

• Ecology:

Simulating species migration over time

• Neuroscience:

Simulating neural circuits

• Health science:

Simulating the spread of an infectious disease

• Meteorology :

Simulating weather prediction

# Approximate Bayesian Computation (ABC) references

- ABC in population genetics, Beaumont, Zhang, Balding Genetics, 2002
- Comparative evaluation of a new effective population size estimator based on approximate Bayesian computation Tallmon, Luikart, Beaumont Genetics, 2004
- Inferring population history with DIY ABC: a user-friendly approach to ABC, Cornuet, Santos, Beaumont, Robert, Marin, . . . Bioinformatics, 2008
- COMPUTER PROGRAMS: onesamp: a program to estimate effective population size using ABC, Tallmon, Koyuk, Luikart, Beaumont Molecular Ecology Resources, 2008
- Adaptive ABC, Beaumont, Cornuet, Marin, Robert Biometrika, 2009
- Approximate Bayesian computation without summary statistics: the case of admixture, Sousa, Fritz, Beaumont, Chikhi Genetics, 2009
- Review: Marin, Statistics and Computing, 2012

- Replace LHD,  $p_y(y|\theta)$ , by SUMMARY LHD  $p_S(S(y)|\theta)$ where S(y) = summary statistics
- But  $p_S(S(y)|\theta)$  is also unknown
- Use an APPROXIMATE SUMMARY LHD:  $\tilde{\rho}_{S}(S(y)|\theta)$ , based on pseudo data  $y^{*}$  generated from the model
- The POSTERIOR is also approximate and summarized:  $\tilde{p}_{S}(\theta|S(y)) \propto p(\theta)\tilde{p}_{S}(S(y)|\theta)$

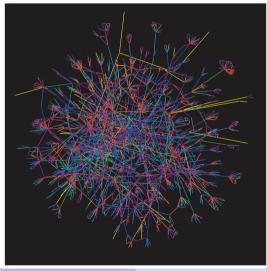
• ABC algorithms are iterative

The basic steps at each iteration are:

- (1) proposing a parameter  $\theta^*$ ,
- 2 simulating pseudo data y\*
- **(3)** accepting or rejecting the proposed  $\theta^*$  based on a comparison
  - of  $y^*$  with the real observed data  $y_{obs}$
- How to actually measure the discrepancy between the observed and the simulated pseudo data is a major difficulty in these methods

## Motivating example

Technology generates new types of data and new modeling challenges



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- Systems of scientific and societal interest have large numbers of interacting components
- Representation as networks:

node = component, edge = interaction

- E.G.: Friendship/Advisory network, Citation network, Webpage link network, Protein-Protein interactions
- Distinction between models of two things:
  - Models of network structure (e.g, Erdös-Rényi)
  - Models of dynamical processes on networks (e.g., SI model)
- Why care about network structure?
  - Interplay between network structure and the behavior of dynamical processes on networks (e.g., hubs in epidemics)

Distinction between two types of models of network structure:

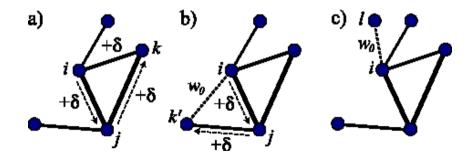
- Statistical models (e.g. ERGM,Goyal-Blitzstein-DeGruttola) DATA DRIVEN
  - Pros: inference on model parameters; hypothesis testing; model selection
  - Cons: scalability; hard to incorporate domain knowledge
- Mechanistic models (e.g. Price model) KNOWLEDGE DRIVEN

assume that microscopic mechanisms that govern network formation and evolution are known, ask what happens if we apply these mechanisms repeatedly

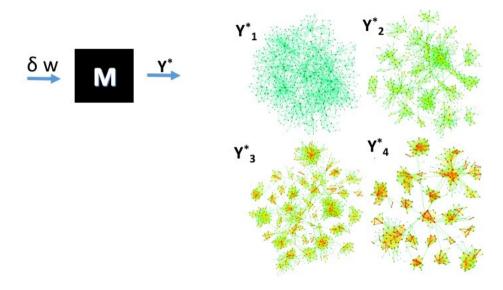
- Pros: easy to incorporate domain knowledge, scalability
- Cons: no inferential tools; no model comparison

## Mechanistic Model of Social and Contact Networks

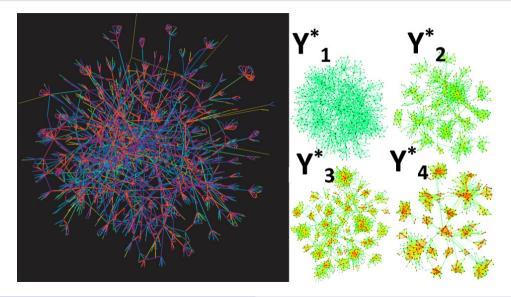
- From the perspective of time expenditure of subject *i*:
  - spend time with existing friends (a)
  - become friend of a friend (b)
  - make totally new friends (c)



### Mechanistic Model of Social and Contact Networks



### Mechanistic Model of Social and Contact Networks



# Approximate Bayesian Computation (ABC)

• ABC rejection sampler is the simplest form of ABC

#### ABC rejection sampler

- Sample parameter  $\theta^*$  from the prior  $p(\theta)$
- Simulate dataset  $y^*$  under the given model specified by  $\theta^*$ :  $y^* \sim p(\cdot | \theta^*)$
- Accept  $\theta^*$  if  $\rho(y^*, y) \leq \epsilon$
- Distance measure  $\rho(y^*, y)$  determines the level of discrepancy between the simulated data  $y^*$  and the observed data y
- The accepted  $\theta^*$  are approximately distributed according to the desired posterior and, crucially, obtained without the need of explicitly evaluating the LHD

# Approximate Bayesian Computation (ABC)

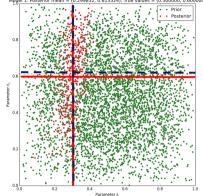
- It may be unfeasible to compute the distance  $\rho(y^*, y)$  for high-dimensional data
- Lower dimensional summary statistic S(y) to capture the relevant information in y
- Comparison is done between  $S(y^*)$  and S(y): accept  $\theta^*$  if  $\rho(S(y^*), S(y)) \leq \epsilon$
- If S is sufficient wrt  $\theta$ , then it contains all information in y about  $\theta$  (by definition), and using S(y) in place of the full dataset does not introduce any error
- For most models it may be impossible to find sufficient statistics *S*, in which case application relevant summary statistics need to be used
- Use of non-sufficient summary statistics introduces a further level of approximation

• ABC + mechanistic network models = generic + sound inferential framework

#### ABC rejection sampler for mechanistic network models

- Observe an empirical graph G
- Set up mechanistic network model M
- Sample parameter  $\theta^*$  from the prior  $p(\theta)$
- Simulate graph  $G^*$  from the mechanistic network model M using parameter  $\theta^*$
- Accept  $\theta^*$  if  $\rho(S(G^*), S(G)) \leq \epsilon$  using application relevant summaries S
- Some simple network summaries: degree sequence, *k*-stars, subgraph counts, centrality measures (betweenness, eigenvector, random walk, etc.), etc.
- Can use KNN to identify points in the space of summary statistics close to S(G)
- From Rejection-ABC to SMC-ABC by Drovandi + Pettitt (2015)

# Inference on $\delta$ and w



ABC + generative network model Prior and posterior draws True parameter values:  $\delta = 0.3$  and w = 0.6 (solid lines) Posterior means:  $\delta = 0.299$  and w = 0.613 (dashed lines) Antonietta Mira ABC on HPC

 $H_0: \delta > \delta^*$  VS  $H_1: \delta \le \delta^*$  for some arbitrary  $\delta^* = 0.35$ 

Bayesians compute  $P(H_0|y) = \int_{\theta^*}^{\infty} p(\theta|y) d\theta$ The integral can be estimated by summing over a finite set of samples  $\theta_t$  from the posterior resulting in the estimator  $\hat{P}(H_0|y) = \frac{1}{T} \sum_{t=1}^{T} \mathbf{1}_{\delta_t > \delta^*}$ The posterior odds are defined as

$$\frac{P(H_0|y)}{P(H_1|y)} = \frac{P(H_0|G)}{P(H_1|G)} = \frac{P(H_0|G)}{1 - P(H_0|G)} \approx \frac{0.032}{0.968} \approx 0.033,$$

suggesting that  $H_1$  is 1/0.033 = 30.25 i.e. over 30 times more likely than  $H_0$ We can confidently reject the null HP

#### ABC for model comparison (Part I)

- Observe an empirical graph G
- Identify alternative possible mechanistic network models  $M_1$  and  $M_2$
- Draw model index from the model prior:  $\tau_1 = P(\mathcal{M} = 1) = P(\mathcal{M} = 2) = \tau_2$
- Draw parameter  $\theta^*$  from the prior  $p(\theta|\mathcal{M})$
- Simulate graph  $G^*$  from the given mechanistic network model using parameter  $\theta^*$
- Accept  $\theta^*$  if  $\rho(S(G^*), S(G)) \le \epsilon$  using any summaries S

#### ABC for model comparison (Part II)

- Draw from the ABC approximation of the joint posterior  $p(\theta, \mathcal{M}|y)$
- Generate *n* independent pseudo-data sets for each such draw (ABC approximation of the posterior predictive distribution)
- Compute posterior error rate using the random forest classifier i.e., how frequently it returns the true model index

ABCpy: efficient library to automatically parallelize ABC algorithms with a modular structure that allows

- no-HPC experts and no-ABC experts from different domains to run ABC in parallel USER-FRIENDLY
- ABC experts to develop parallel versions of different algorithms **MODULAR**
- HPC experts to develop different parallelization frameworks for ABCpy **EXTENSIBLE**
- researchers to compare efficiency parallelized ABC algorithms **BENCHMARK**

# ABCpy: Modular architecture - class diagram

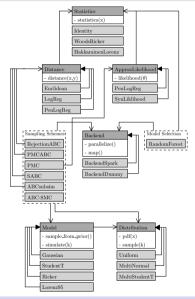
Abstract classes dark grey

Derived classes light grey

Filled arrows inheritance

No filled arrows association

map-reduce framework with master/worker architecture



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ABC on HPC

### Ricker Model: Stochastic population growth

• The unobservable population size N(t) is

$$N(t) = rN(t-1)\exp\left(rac{\sigma e(t)}{N(t-1)}
ight)$$

• The observable population size y(t) over discrete time t = 0, ..., T is

 $y(t) \sim Poisson(\phi N(t))$ 

- r is the growth rate,  $\sigma$  is the deviation of the innovation rate, and  $\phi$  is a scaling parameter
- Goal: estimate the parameters  $r, \sigma, \phi$  given the observed data

- Modification of weather prediction model of Lorenz (1995) when fast weather variables are unobserved (Wilks, 2005)
- $(Y_1^t, \ldots, Y_{40}^t)$ : slow weather variables observed at time t
- Known: Initial value  $(Y_1^0, \ldots, Y_{40}^0)$
- Goal: Simulate weather variables in future for numerical weather prediction with  $t \in [0, 4]$  corresponding to 20 days

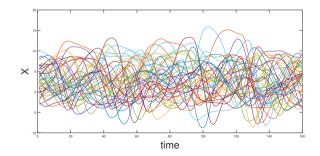
- The weather variables follow the coupled Stochastic DE:  $\frac{dy_k^{(t)}}{dt} = -y_{k-1}^{(t)}(y_{k-2}^{(t)} - y_{k+1}^{(t)}) - y_k^{(t)} + 10 - g(y_k^{(t)}, \theta) + \eta_k^{(t)}$
- $g(y_k^{(t)}, \theta) =$  deterministic parametrization of the net effect of the unobserved (fast) variables on the observable ones

$$g(y_k^{(t)}, \theta) = \sum_{i=1}^2 \theta_i \left(y_k^{(t)}\right)^{i-1}$$

- $\eta_k^{(t)} = \text{stochastic}$  forcing term representing the uncertainty due to forcing the fast variables, updated for an interval  $\Delta t$  $\eta_k^{(t+\Delta t)} = \phi \eta_k^{(t)} + (1-\phi^2)^{\frac{1}{2}} e^{(t)}, t \in \{0, \Delta t, \dots, T\Delta t\} \ \eta^{(0)} = (1-\phi^2)^{\frac{1}{2}} e^{(0)}$  and  $e^{(t)}$  are indep. standard normal r.v.
- we discretize the 20 days time interval in 5760 steps and use an **SDE 4th order** solver

### Inference: Unknown coupling Parameters

- Unknown parameters:  $(\theta_1, \theta_2)$
- Observed weather variables for t ∈ [0, 4] in T = 160 equal intervals simulated using (θ<sub>1</sub>, θ<sub>2</sub>) = (2.1, 0.1)



#### We consider:

- The speedup S<sub>A</sub>(n) of a parallel algorithm A on n cores with respect to a baseline (number of cores) m, m ≤ n, is the ratio of the algorithms running time t(m) on m cores and the running time t(n) on n cores:
   S<sub>A</sub>(n) = t(m)/t(n)
- The efficiency  $\mathcal{E}_{\mathcal{A}}(n)$  of an algorithm  $\mathcal{A}$  on n cores is the speedup normalized by the numbers of cores:  $\mathcal{E}_{\mathcal{A}}(n) = \mathcal{S}_{\mathcal{A}}(n)/n$

# PMCABC: Linear scaling up

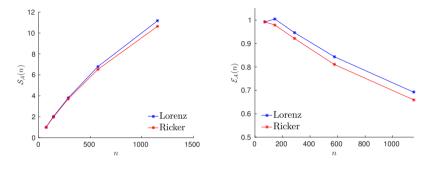
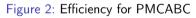


Figure 1: Speedup for PMCABC



Data simulation from Ricker model: milliseconds Data simulation from Lorenz model: seconds CSCS Piz Daint with Apache Spark: 1 master, 2 to 32 workers, 72 to 1152 cores 10 min at most (32 workers)

# PMC: Linear scaling up

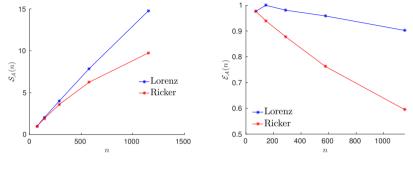


Figure 3: Speedup for PMC

Figure 4: Efficiency for PMC

Amdahl's law Data simulation from Ricker model: milliseconds Data simulation from Lorenz model: seconds