Funding Acknowledgements

University of Glasgow

A synergistic convergence

Next Generation Sequencing and Mathematical Modelling of *Mycobacterium bovis* transmission in British Cattle and Badgers

Rowland Kao

Boyd Orr Centre for Population and Ecosystem Health

From the questionnaire

- Mathematical Modelling
- Bayesian Statistics
- Whole Genome Sequencing
- Ecological Perspectives
- (Farmer attitudes/social factors)

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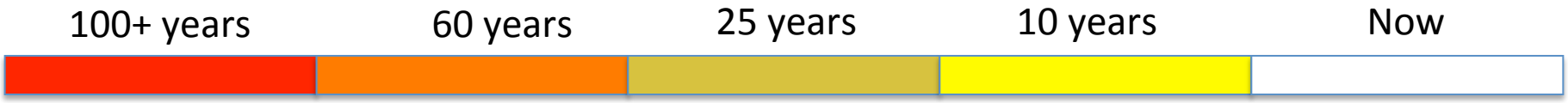


POPULATION MODELS WITH CONTACT HETEROGENEITY

Ross' Malaria Model (1911)

Hethcote and Anderson & May

Social Network Models

COMPUTING POWER

Babbage Engine (1822)

Transistor

Microcomputers

High Performance Computing Clusters

POPULATION DATA

Cholera Map 1854 (John Snow)

Measles dataset

Satellite data/GIS

Livestock movements

Electronic tagging

GENETIC DATA

Theory of Evolution (1859)

Discovery of DNA structure

PCR

Human Genome Project

Next Generation Sequencing

STATISTICAL INFERENCE

Bayes Theorem (1740s)

Growth in applied biostatistics (regression models)

Bayesian Statistical Inference

Increase in computing power

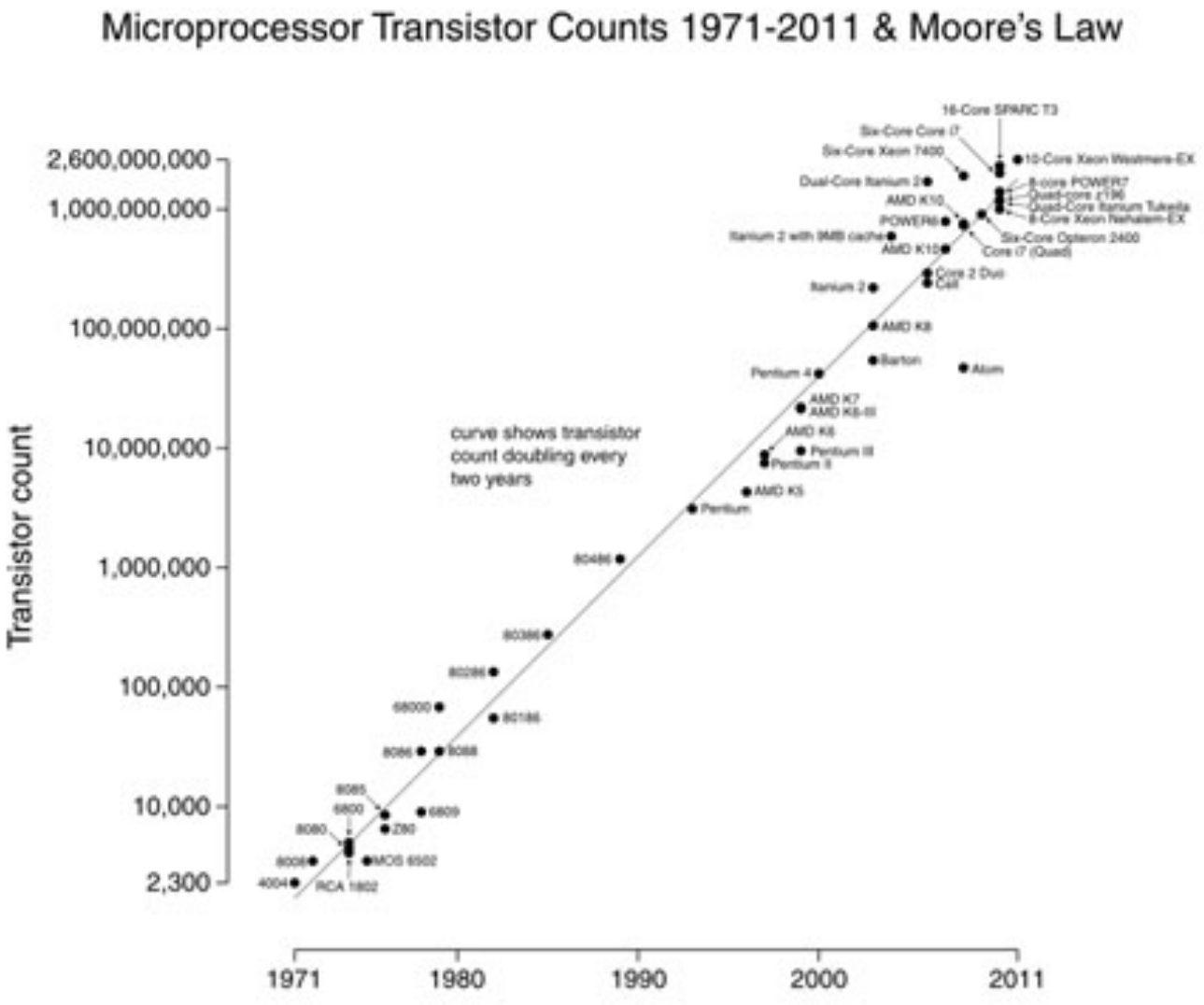
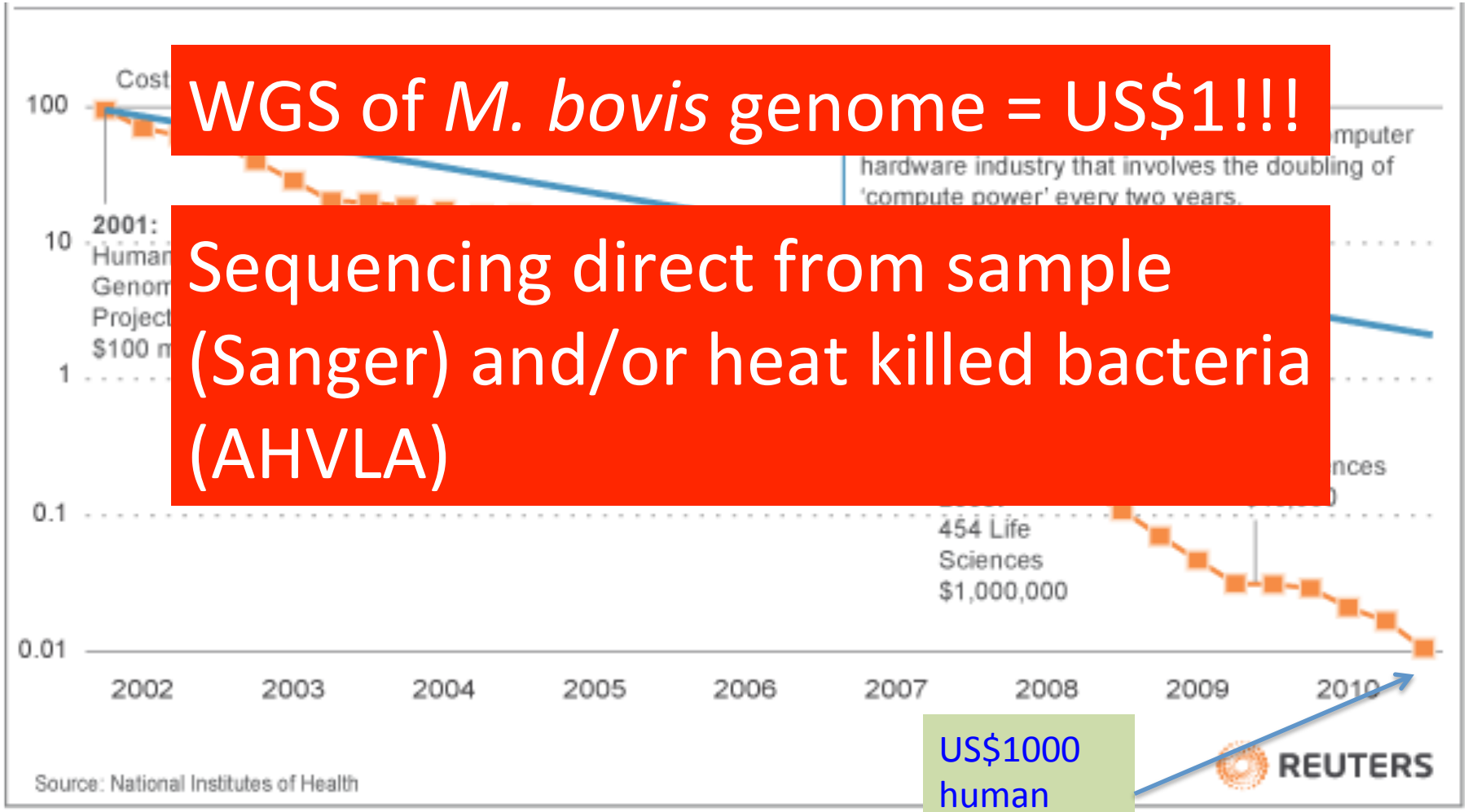


Image from http://www.motherjones.com/kevin-drum/

Decline in sequencing costs



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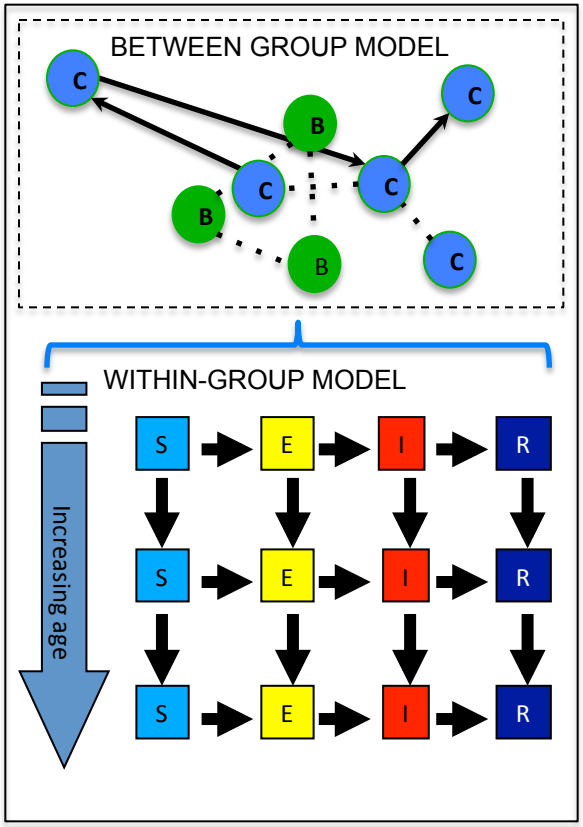
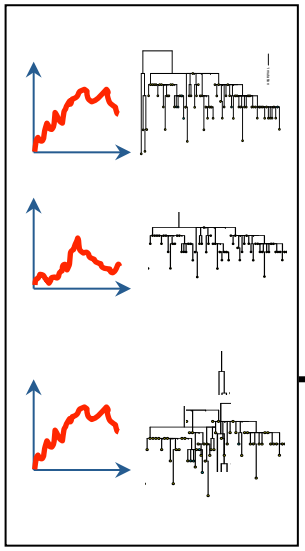
Phylodynamic approaches

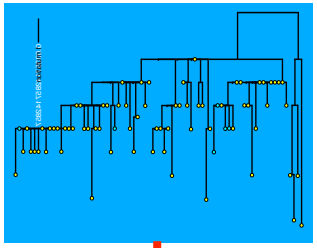


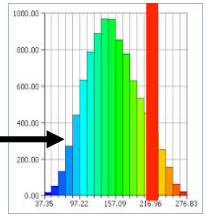
Mathematical Models

Simulated 'data'



inferred phylogeny



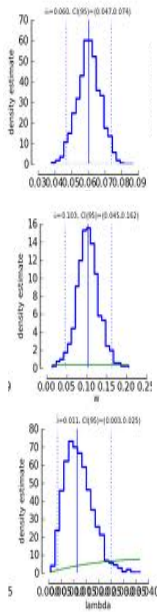


Compare summary measure(s) to aggregated simulations

Accepted proposals

Whole Genome Sequences

Output:



posterior distns of parameters

Bayesian Likelihood Inference

Update proposals

Proposed parameter values

Prior epidemiological and genetic paramter estimates

Integrated Datasets

Whole Genome Sequencing + Mathematical Modelling

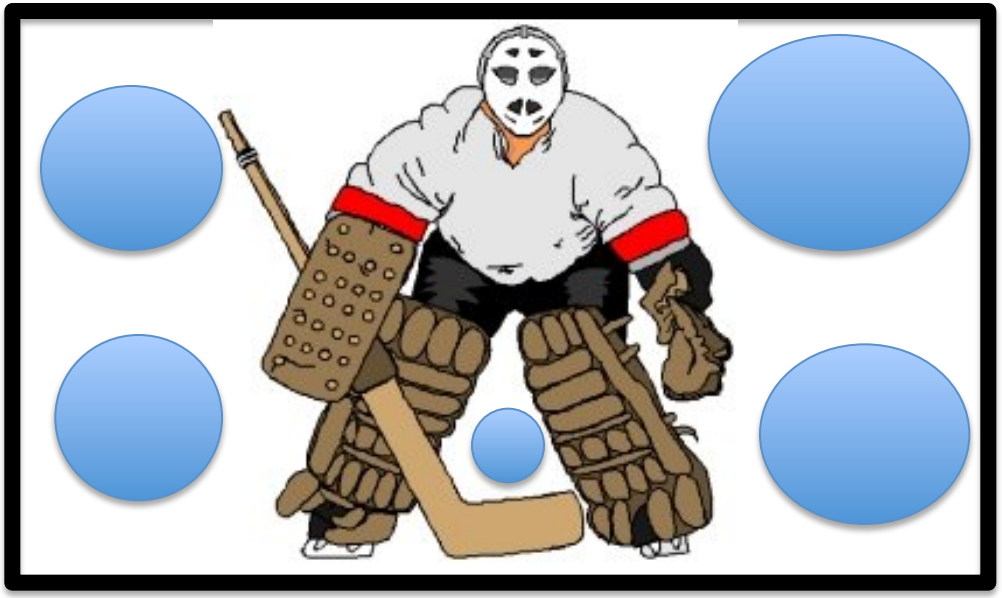
- Expanding datasets detailing contact structure
- Computational power expanding rapidly
- Epidemiological (mathematical & statistical) modelling identifies how the PATTERN in the population structure influences the PROCESS of how, when and where disease transmission occurs
- Tracing mutations of pathogens (WGS) from individual-to-individual reveals the transmission PROCESS

Whole Genome Sequencing of *M. bovis*

- Entirely new technological approach
- Increasingly inexpensive
- Obvious uses retain challenges of interpretation
- Are there any 'un-obvious' uses?
- It isn't the solution but it unifies disparate datasets

Most of us see this

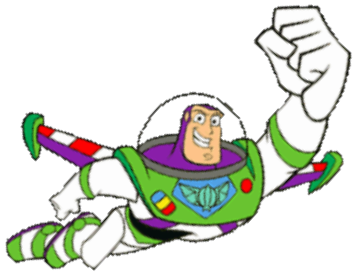
But we should (sometimes) look for this



Things to think about

- What are the scientific questions that WGS can be used to address in different ways?
  - And what are the limitations?
- What can it do to change our understanding of the epidemiology
- What can it do to change our disease control paradigms?

For Today …



To infinity and beyond!