

Constraining population synthesis (and binary black hole inspiral rates) using binary neutron stars

Richard O'Shaughnessy

GWDAW-8

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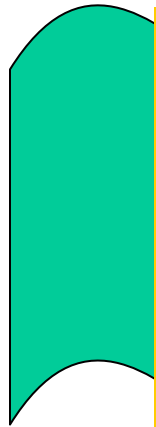
Outline

- Background and Motivation: Population synthesis
 - Fundamental approach to rates...but poor constraints (e.g. BBH merger rate)
 - New idea: Use neutron star rate as guide...
- It is possible !
- Constrain models for binary evolution
- Constrain BBH merger rate
 - Computational issues
- ~~Results~~ → Present status and future plans

Population Synthesis

Models

Probabilities, rates, ...



Many parameters...

but

- 1) many have **narrow** ranges
- 2) dependence is smooth
- 3) ...probably correlations too

H merger rate

S merger rate

ation rate

ra rate

s constraint
factor);

re predictions

n+1 dimens

Scale factor

number of star

Properties at forma

metallicity of ga

initial mass dist

...

Models for binary

supernova kick magnitude

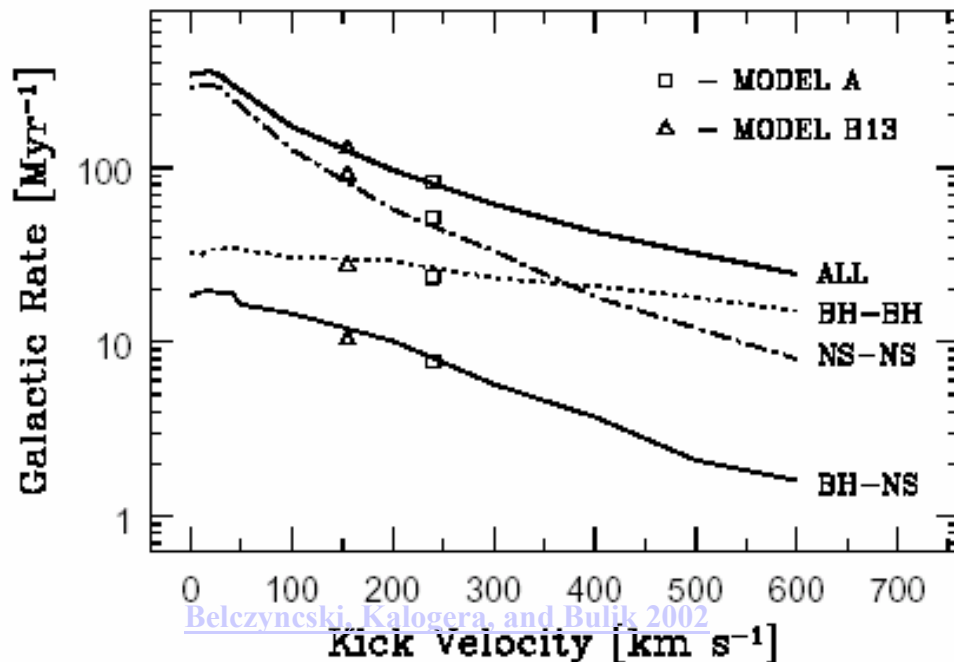
common envelope efficiency

...

Population Synthesis: Results

Despite best constraints on models

→ broad range of compact object merger rates:



Example:

Supernova kick
magnitude

Idea:

NS Rate \rightarrow constraints

Empirical distribution of binary NS merger rate \rightarrow

1. Constraints on population synthesis models
2. Distribution of BBH merger rates

(assuming equal prior probabilities of models)

Computational issues I:

Computation time

Computation time

- Number of models we can evaluate:
(1 model/20 minutes/node) * (1 year) * 10^3 nodes
~ **10^7 models**
- Intensive naïve approach:
 - 11 dimensional space
 - 10 points per dimension} 10^{11} models
→ **10^4 years (!)**

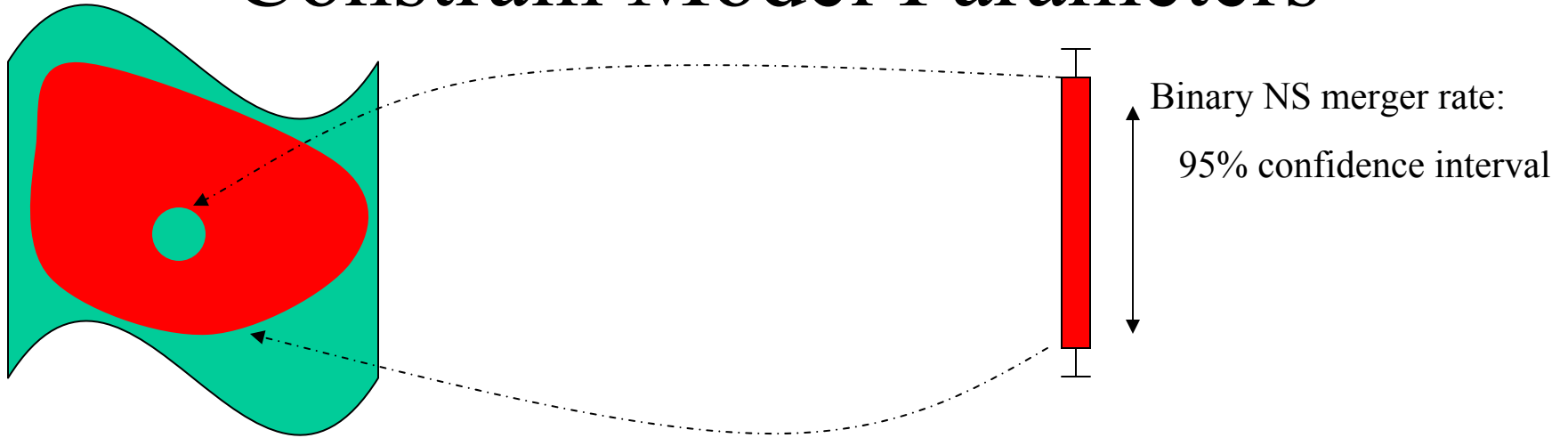
... **but** some parameters have narrow ranges

- Revised naïve approach:
 - 10 points needed in each of 3 dimensions
 - 3 points needed in others} 10^7 models

This is search by exhaustion

→ can do even better...

Application I: Constrain Model Parameters



Generally: For any merger rate, $n-1$ dimensional manifold of model parameters consistent with rate

Application: Find confidence-interval **boundaries** in model space

Computational issues II:

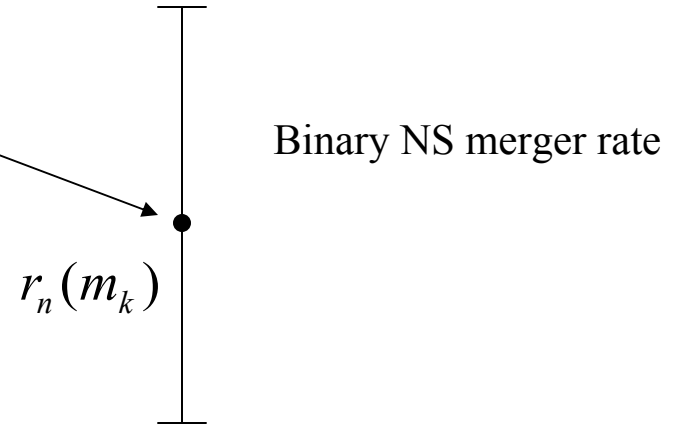
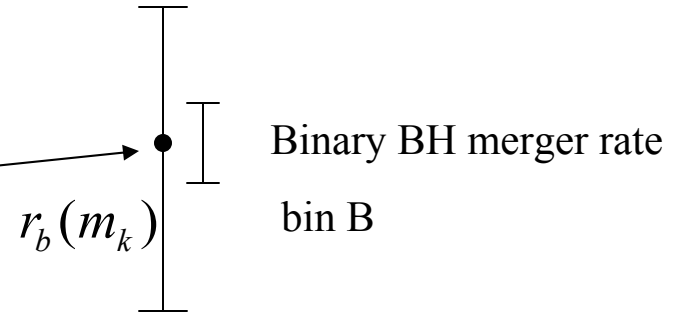
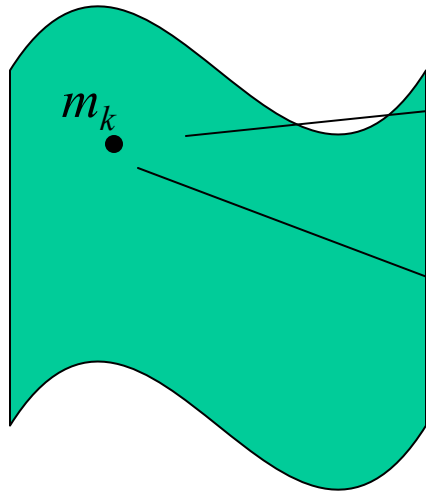
Root finding via genetic algorithms

- Need: Robust way to **find** $n-1$ dimensional manifold of **all** solutions

- Solution: Genetic algorithms
 - (still under development)
 - Example*: Finding a single root
 - Robust: noisy functions, multiple maxima, high dimensions
 - Efficient: Exponential convergence

Application II: BBH merger rate distribution

Monte carlo:



1. Select many random models m_k
(=equal prior probability)
2. Count number of models with BH merger rates in a bin B, **weighted** by binary NS rate:

$$count(B) = \sum_k \Theta(r_b(m_k) \in B) \frac{p_n(r_n(m_k))}{const}$$

→ **histogram**

Probability distribution formulae

- Explicit formula:

$$A_n(m) = \int d\bar{m} \delta(r_n(\bar{m}) - r_n(m))$$

$$p_m(m) = \frac{p_n(r_n(m))}{A_n(m)}$$

$$p_b(R_b) = \int d\bar{m} p_m(\bar{m}) \delta(R_b - r_b(\bar{m}))$$

Key

$r_n(m)$ rate of binary NS merger for model m

$r_b(m)$

$p_n(r)dr$ probability for binary NS rate to be in
[$r, r+dr$]

Status

- Present status:
 - Constrain population synthesis
 - Algorithm development
 - Determine BH merger rate distribution
 - Monte Carlo accumulating...
 - Also...looking for simplifications (correlations, etc)
- Future plans:
 - Improvements
 - Include for prior probability distributions for parameters (e.g. supernova kick distribution)
 - Include more constraints (e.g. statistics of x-ray binaries; etc.)
 - Additions
 - Account for other known uncertainties in analysis (e.g. statistical fluctuations in rate calculations)
 - Long-term improvements (exploring):
 - Nonrandom (bayesian) searches [=maximize information obtained at each step]