

Online Population Size Adjusting Using noise and Sub-Structural Measurements

Tian-Li Yu, Kumara Sastry, David E. Goldberg

Illinois Genetic Algorithms Laboratory
Department of General Engineering
University of Illinois at Urbana-Champaign

<http://www-illigal.ge.uiuc.edu>

ksastry@uiuc.edu

Supported by AFOSR F49620-03-1-0129, NSF/DMR at MCC DMR-99-76550, NSF/ITR at CPSD DMR-0121695, DOE at FS-MRL DEFG02-91ER45439.

Motivation

- ❖ Facetwise population-sizing models
 - ◆ Adequate supply of sub-structures [Goldberg *et al*, 2001]
 - ◆ Good decisions between competing substructures [Goldberg *et al*, 1992, Harik *et al*, 1997]
 - ◆ Accurate sub-structure identification [Pelikan *et al*, 2003]
- ❖ Linkage (sub-structure) learning methods
 - ◆ Implicit (*e.g.*, LLGA, BOA)
 - ◆ Explicit (*e.g.*, eCGA, DSMGA)
- ❖ Utilize sub-structure information in estimating population size adaptively

Outline

- ❖ Background
- ❖ Population-sizing models
- ❖ Design structure matrix GA (DSMGA)
- ❖ Population-size estimation
- ❖ Population-size adjustment
- ❖ Summary & conclusions

Related Work

- ❖ Smith and Smuda (1993)
 - ◆ Target selection loss \hat{L}
 - ◆ Adjust the population size by the factor of $\frac{\hat{L}}{L_t}$
- ❖ Harik and Lobo (1999)–Parameterless GA
 - ◆ eCGA (Lobo, 2000)
 - ◆ hBOA (Pelikan and Lin, 2004)

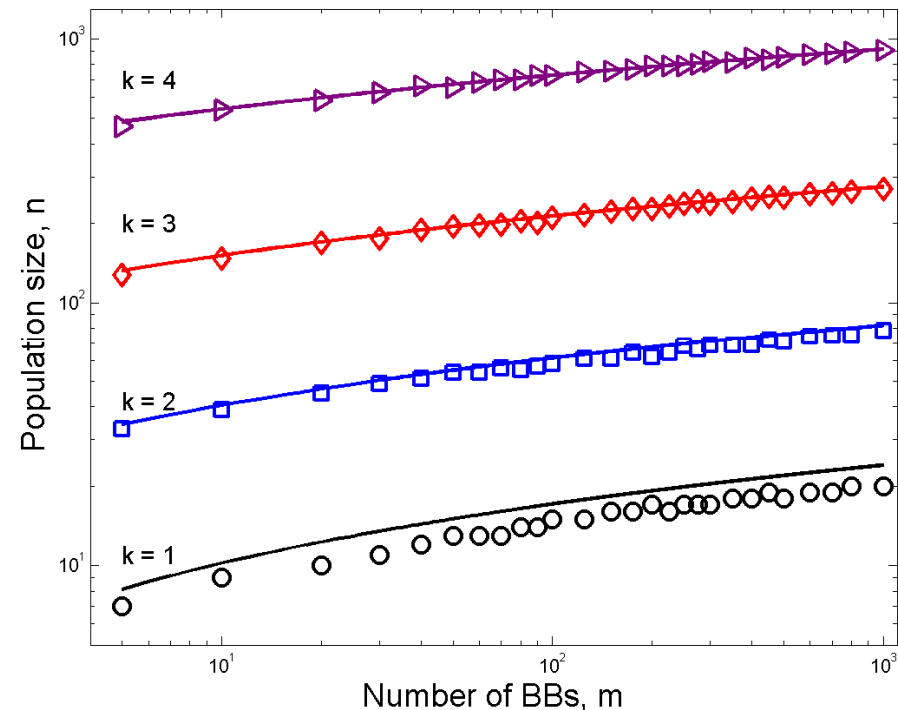
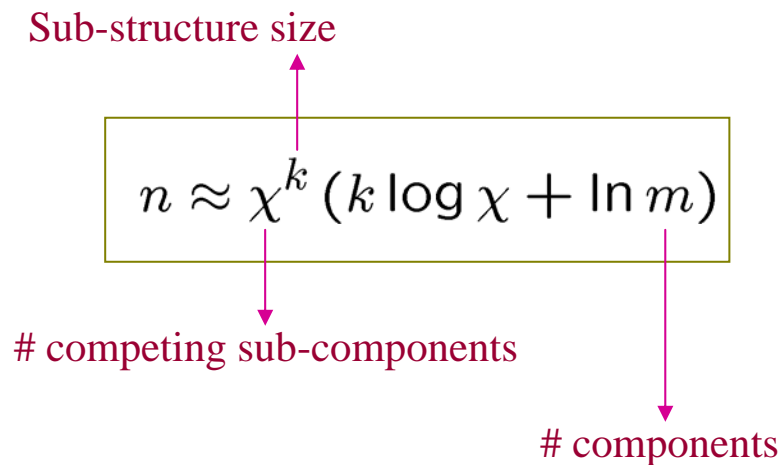
How Should I Size the Population Size?

1. Ensure an adequate supply of raw sub-solutions
 - ◆ Population size should be large enough to ensure at least one copy of all competing BBs in the population
2. Make decisions well among competing sub-solutions
 - ◆ Population size should be large enough to prefer the best BBs over worse ones with a high probability.
3. Identify and mix sub-solutions well
 - ◆ Population size should be large enough to ensure that the “innovation time” is less than “takeover or convergence time”.

[Goldberg (2002). Design of Innovation]

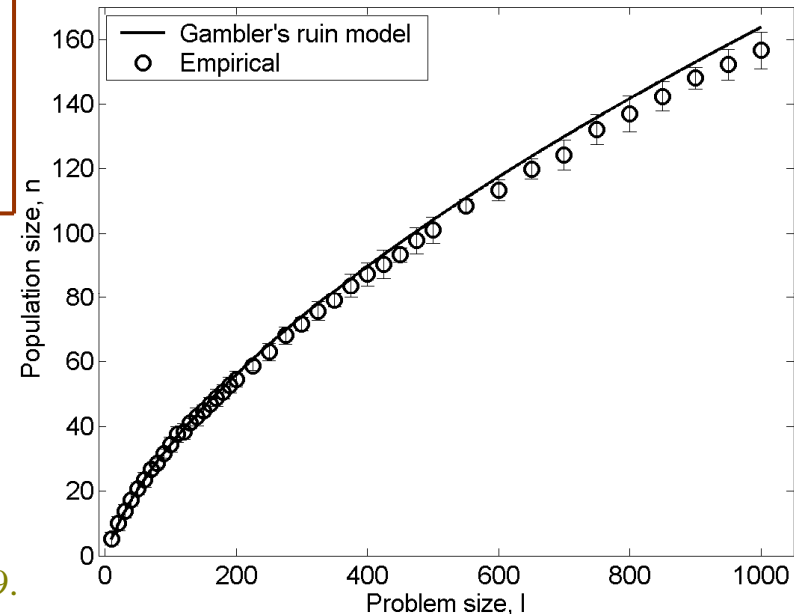
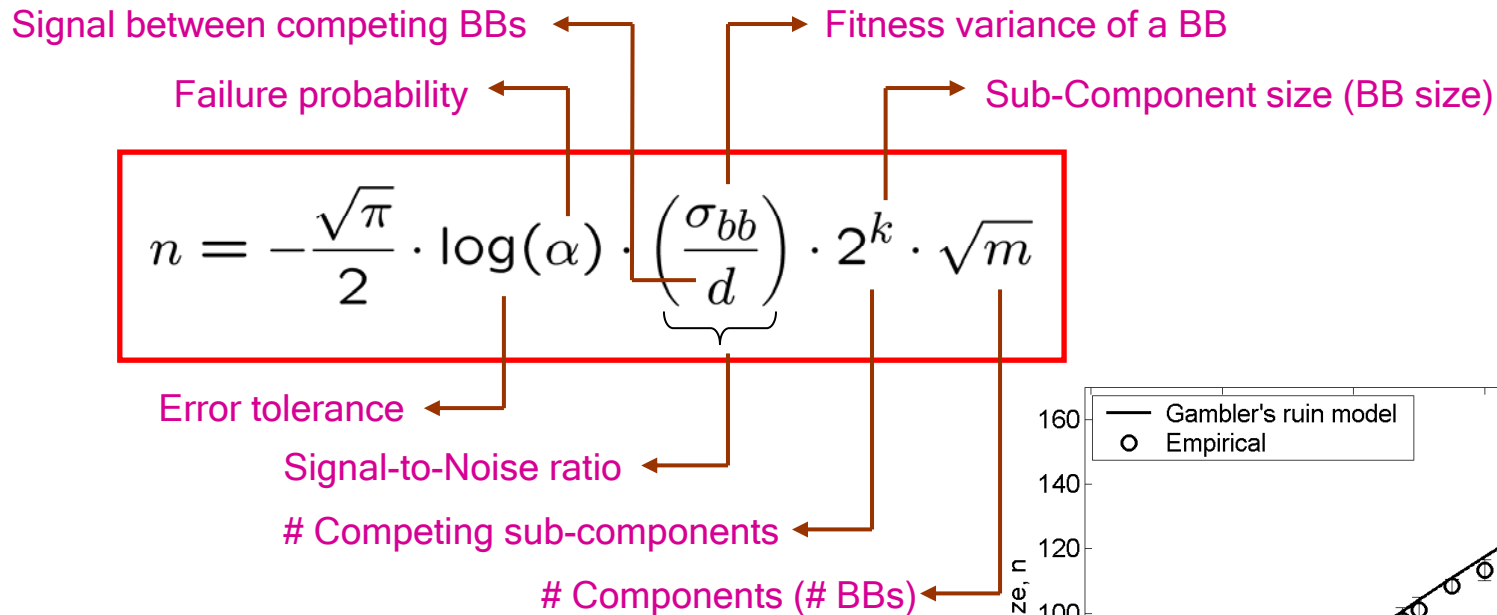
Building-Block Supply

- ❖ Ensure the presence of competing schema
 - ◆ Temporally through genetic operators
 - ◆ Spatially (Initial population) [Holland, 1975; Goldberg, 1989; Reeves, 1993; Goldberg, Sastry, & Latoza, 2001; [Sastry, O'Reilly, Goldberg, & Hill, 2003](#)]



Gambler's Ruin Population Sizing Model

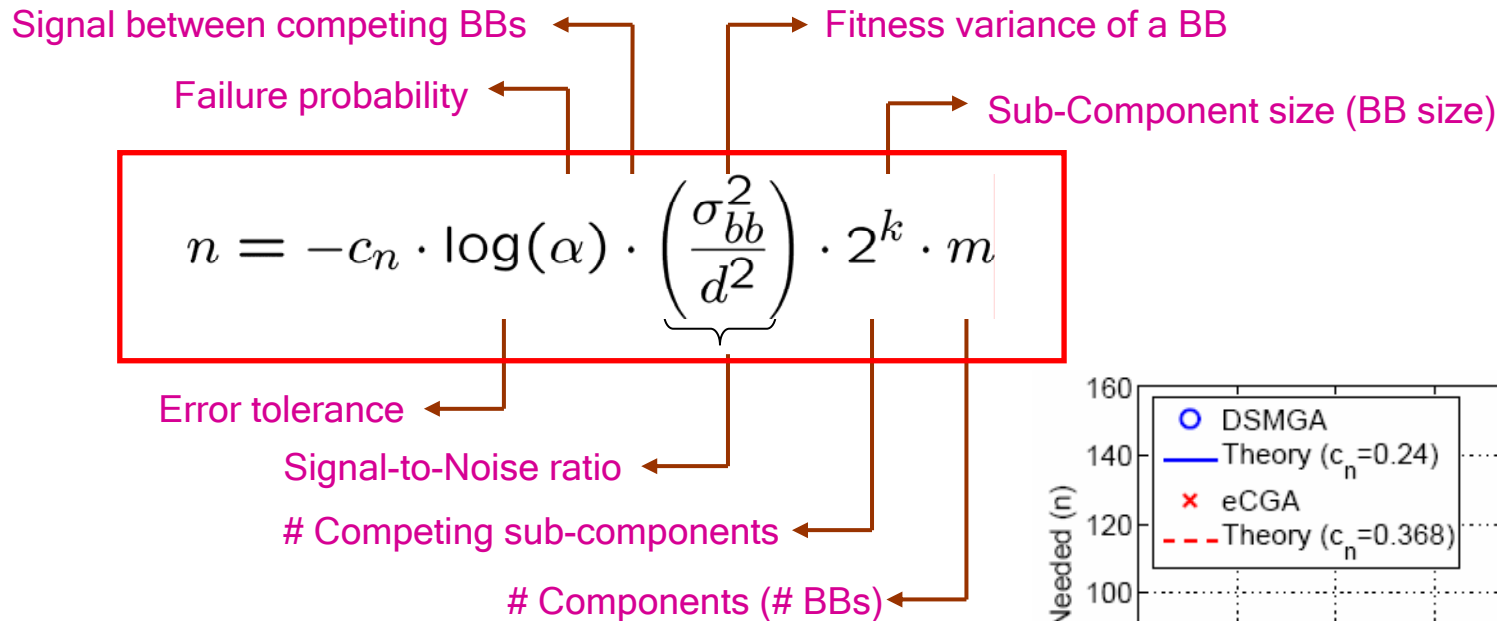
- ❖ Combines decision-making and supply models [Harik, Cantú-Paz, Goldberg, and Miller, 1997]



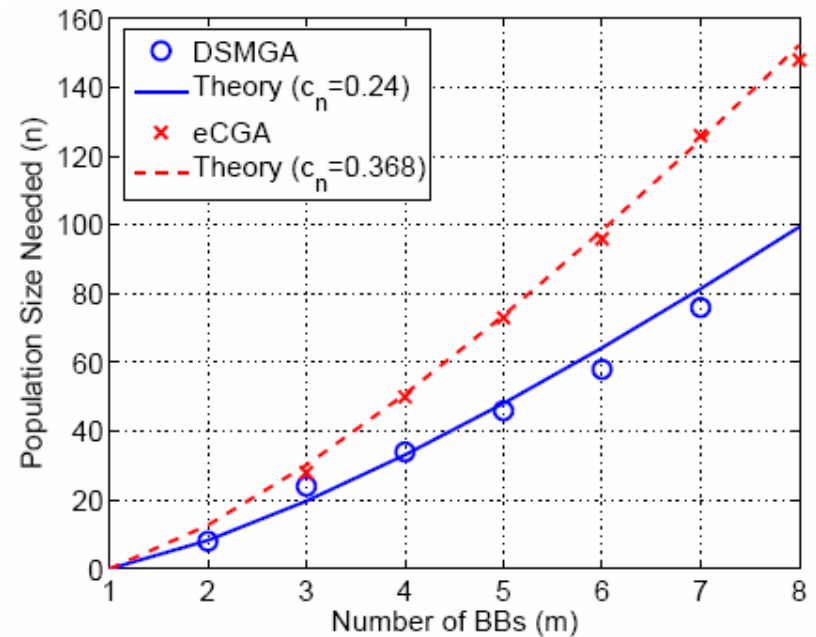
Harik, Cantú-Paz, Goldberg, & Miller, *ECJ* 7(3) 1999.

Population Sizing For Sub-Structure Identification

- ❖ Estimation of distribution algorithms [Pelikan, Goldberg, and Cantú-Paz, 2001; Sastry & Goldberg, 2001; Pelikan, Sastry, and Goldberg, 2002]



Bounds DSMGA/EDA population sizing



Purpose: Online Population-Sizing Framework

- ❖ Develop an online population-sizing framework using sub-structural information
- ❖ Sub-structure identification
 - ◆ What are the components?
- ❖ Sub-structure quality estimation
 - ◆ What are the relative quality of sub-components?
- ❖ Sub-structure-based population sizing estimate
 - ◆ Ensure adequate supply of good sub-structures?
 - ◆ Ensure growth of good sub-structures?

Sub-Structure Identification: Use Linkage-Learning Techniques

- ❖ **Sub-structure identification**
 - ◆ What are the components?
- ❖ Use linkage-learning techniques
 - ◆ Demonstrate using DSMGA [Yu *et al*, 2003]
 - ◆ Can also use extended compact GA [Harik, 1999]
- ❖ Brief description of DSMGA next...

Design structure matrix (DSM)

❖ GM powertrain development teams [McCord & Eppinger, 1993]

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U	V	
Engine Block	A	3	3	3	1	3	1	3	3	3	1	1	1						3	3	2		
Cylinder Heads	3	B	3	2		1		3	1	3	3								2		1	3	
Camshaft/Valve Train	3	3	C	1		1			2	1	1								1		1	2	
Pistons	3	3	2	D	2	2	1		2	2	1				2				1			3	
Connecting Rods	2	1		3	E	3			2	1												2	
Crankshaft	3	1	1	3	3	F	3	2	3	1									2	1		2	
Flywheel	1					3	G		1													2	2
Accessory Drive	3	3	1			2		H	1	3	3	2	2	2	3	3	3	1	1	1	1	2	
Lubrication	3	1	2	2	1	2	1	1	I	1		1								1		2	3
Water Pump/Cooling	3	3	2	2				3	2	J		2	1	1		1	1					1	2
Intake Manifold	2	3	1					3	1	3	K									2	2		3
Exhaust	1							1	1	1		L	3	1	3	2				2	2	1	2
E.G.R.	1							1		1		3	M		1	1	1		1	3	1	2	
Air Cleaner								3				1		N	2	1	3						
A.I.R.	1							3	1		3	1	2		O		1				2	1	2
Fuel System								2	1			1	1	1		P	1	1				2	2
Throttle Body								2	2			2	3	1	2		Q	3	1	3		2	
EVAP																2	3		R		2	1	
Ignition	3	3	3	1		3	3	2	1	1	2	3	1			3	1			S	3	3	3
E.C.M.	1	1	1			2	1	1	1	3	2	1	2		2	3	2	3	3		T	3	2
Electrical System	3	1	2	1		1	2	1	2	1	1	3	1		1	2		1	3	3		U	3
Engine Assembly	3	3	2	3	2	3	2	2	3	2	3	2	2		2	3	2	1	3	2	3		V

0: No interaction

1: low interaction

2: med interaction

3: high interaction

DSM clustering

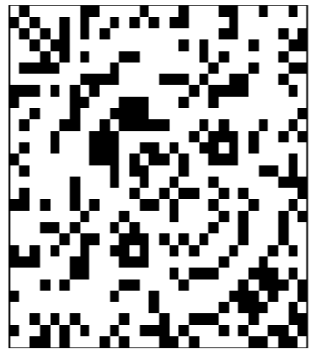
	P	N	Q	R	B	C	J	K	A	D	I	F	G	E	O	L	M	H	S	T	U	V	
Fuel System	P	1	1	1			1							1	1			2			2	2	
Air Cleaner	1	N	3											2	1			3					
Throttle Body	2	3	Q	3			2							1	2			2	1	3		2	
EVAP	2		3	R																	2	1	
Cylinder Heads					B	3	3	3	3	2	1	1							3	2		1	3
Camshaft/Valve Train					3	C	1	1	3	1	2	1								1		1	2
Water Pump/Cooling	1	1	1		3	2	J	2	3	2	2					1		3			1	2	
Intake Manifold					3	1	3	K	2		1								3	2	2		3
Engine Block					3	3	3	1	A	3	3	3	1	1		1	1	3	3		3	2	
Pistons	2				3	2	2	1	3	D	2	2	1	2						1		3	
Lubrication					1	2	1		3	2	I	2	1	1		1		1	1		2	3	
Crankshaft					1	1	1		3	3	3	F	3	3				2	2	1		2	
Flywheel									1		1	3	G								2	2	
Connecting Rods					1		1		2	3	2	3		E								2	
A.I.R.		2	1				1	1							O	3	1	3		2	1	2	
Exhaust	2	1					1	1	1						3	L	3	1	2	2	1	2	
E.G.R.	1		1				1	1							1	3	M	1	1	3	1	2	
Accessory Drive	3	2	3	1	3	1	3	3	3		1	2			3	2	2	H	1	1	1	2	
Ignition	3		1		3	3	1	2	3	1	1	3	3			3	1	2	S	3	3	3	
E.C.M.	3		2	3	1	1	3	2	1		1	2	1	2	2	1	2	1	3	T	3	2	
Electrical System	2			1	1	2	1	1	3	1	2	1	2		1	3	1	1	3	3	U	3	
Engine Assembly	3		2	1	3	2	2	3	3	3	3	3	2	2	2	2	2	2	2	3	2	3	V

Reordered

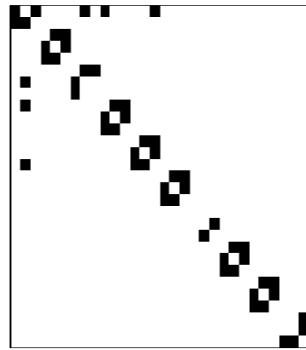
Clusters

Bus modular

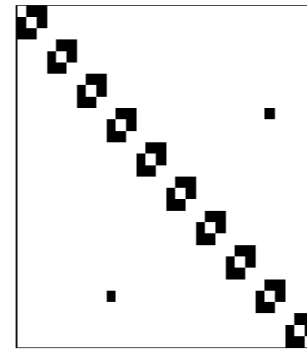
DSMGA



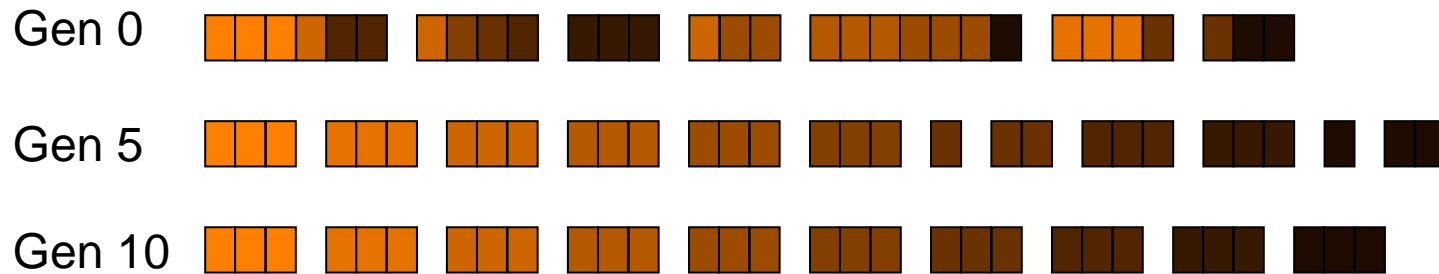
Generation 0



Generation 5



Generation 10



10 3-bit Trap Function

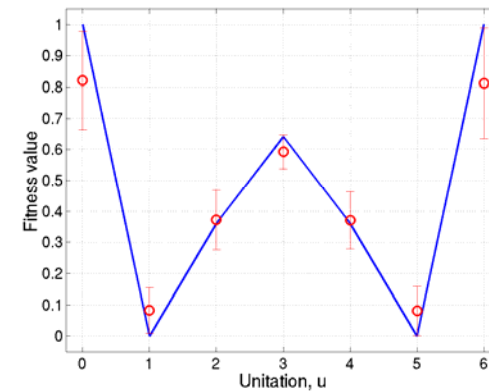
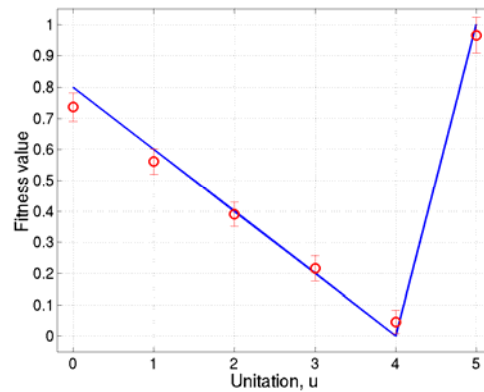
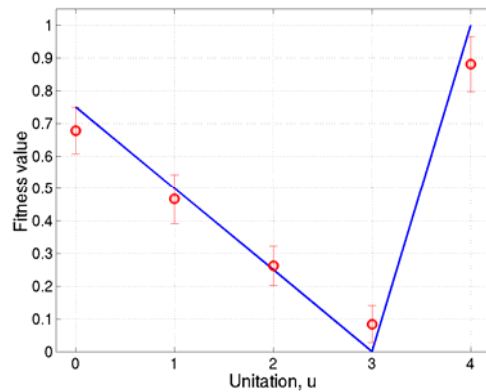
Online Adjustment of Population Size

- ❖ Sub-structure identification
 - ◆ Use linkage-learning techniques
 - ★ E.g., DSMGA, eCGA, BOA
- ❖ Sub-structure quality estimation
 - ◆ What are the relative quality of sub-components?
- ❖ Use fitness-estimation technique used in developing probabilistic endogenous fitness model
 - ◆ Pelikan *et al*/2004, Sastry *et al*/2004

Sub-Structure Quality Estimation

- ❖ Identify key sub-structures of the search problem
- ❖ Estimate the fitness of sub-structure instances

$$\text{Fitness of substructure instance} = \text{Average fitness of all evaluated individuals with the schema instance} - \text{Average fitness of all evaluated individuals in the population}$$

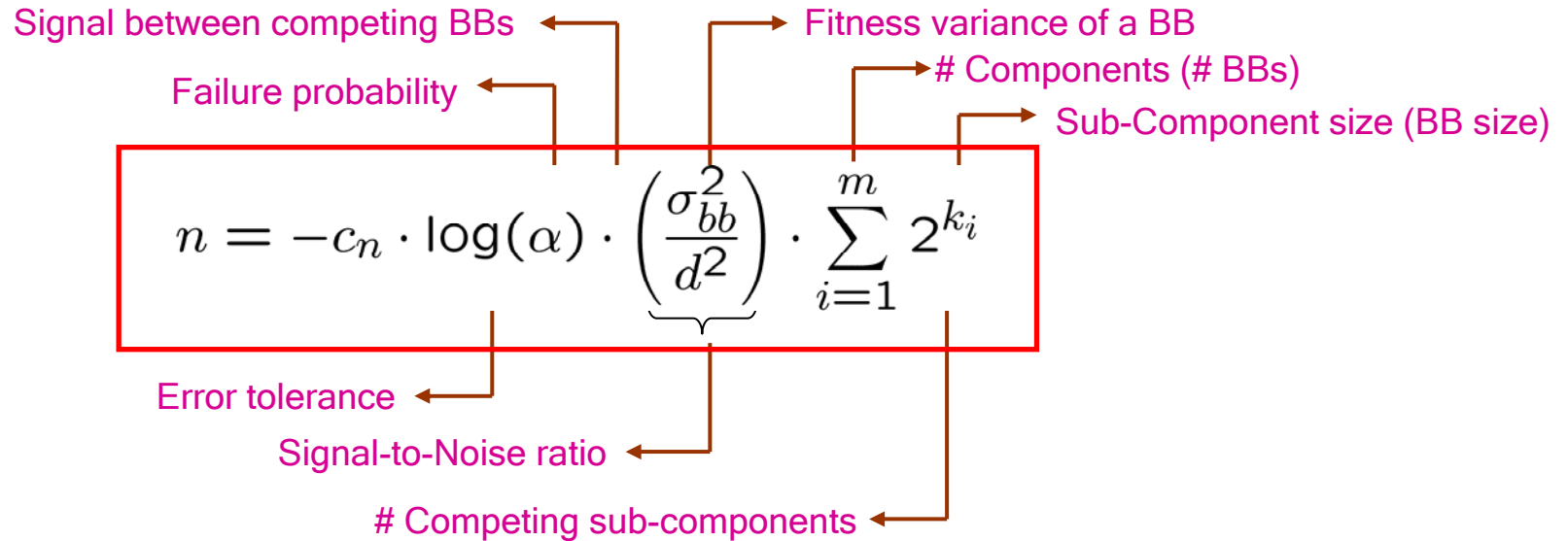


- ❖ Used to estimate fitness of individuals [[Sastry, Pelikan, & Goldberg, 2004](#). [Pelikan, Sastry & Goldberg, 2004](#)]

Online Adjustment of Population Size

- ❖ Sub-structure identification
 - ◆ Use linkage-learning techniques
- ❖ Sub-structure quality estimation
 - ◆ Schema fitness estimation
- ❖ Population-size estimation based on sub-structure info
 - ◆ Bounded by sub-structure identification
 - ◆ Estimate all parameters on-line using sub-structural measurements

Online Population Size Estimation



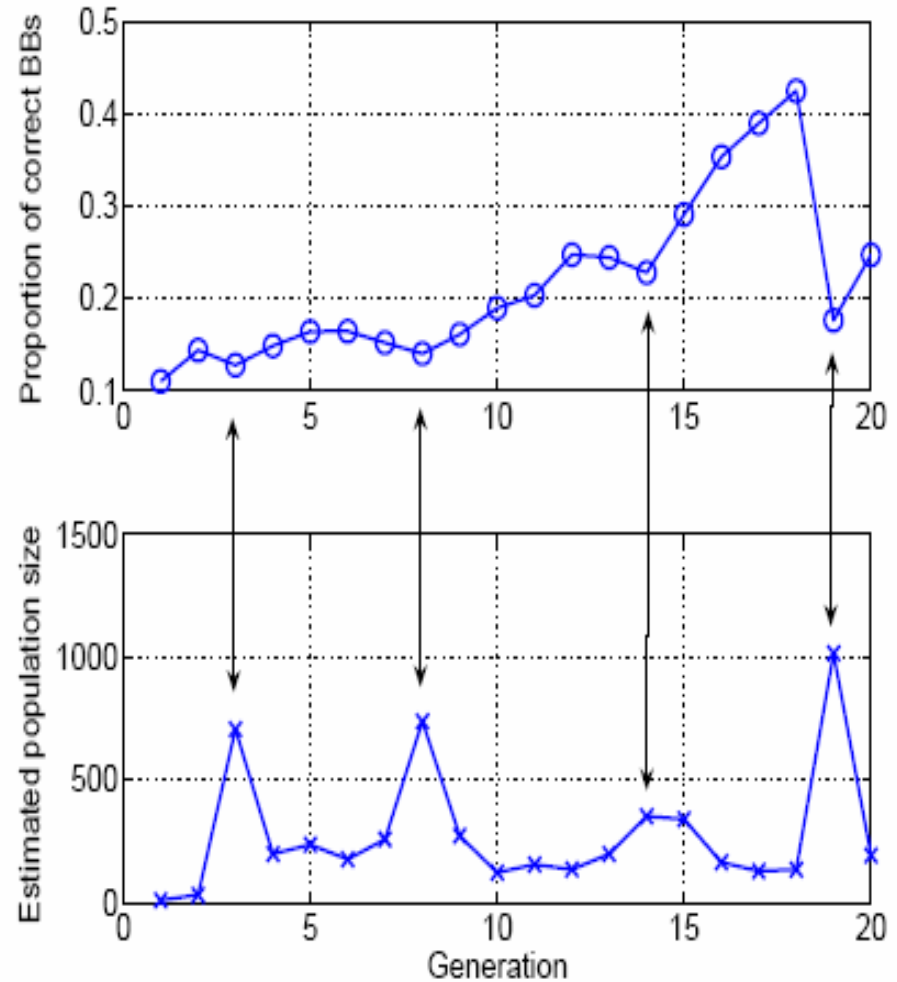
- ❖ Sub-structure models gives m and k_i
- ❖ H_{BB_i} : Schema of the i^{th} sub-structure

$$\sigma_{BB_i}^2 = \text{Var}_i[f(H_{BB_i})]$$

$$d_i = \max_i[f(H_{BB_i})] - \text{second_max}_i[f(H_{BB_i})]$$

How To Inject New Individuals?

- ❖ **Aim:** Increase the success rate of small initial population size
- ❖ **Inject new individuals to ensure**
 - ◆ BB supply
 - ◆ Diversity
- ❖ **Issues to be addressed**
 - ◆ Average fitness decreases
 - ◆ Convergence difficulty



Injection scheme: Initialize Early and Recombine Later

❖ Observations

- ◆ Injection of new individuals → BB supply → early stage of GA run
- ◆ Recombination → BB mixing → later stage of GA run

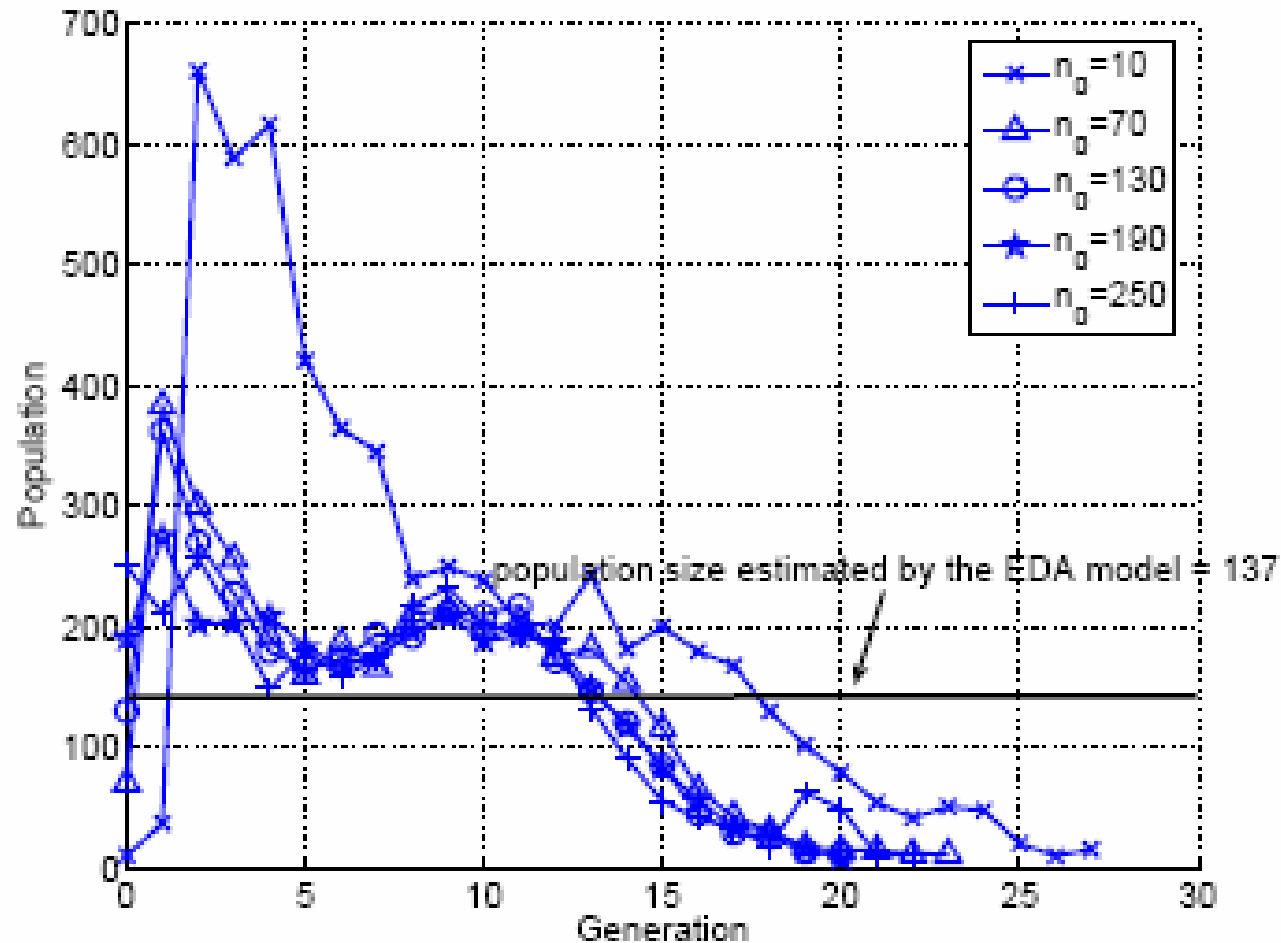
❖ Injection scheme, when $n_{t+1} > n_t$

- ◆ Early stage: Generate n_t children by recombination, and inject $(n_{t+1} - n_t)$ new individuals.
- ◆ Later stage: Simply generate n_{t+1} children.

❖ When to switch?

- ◆ The population-size estimation indicates large population is not needed.

Population-size adjustment on-the-fly

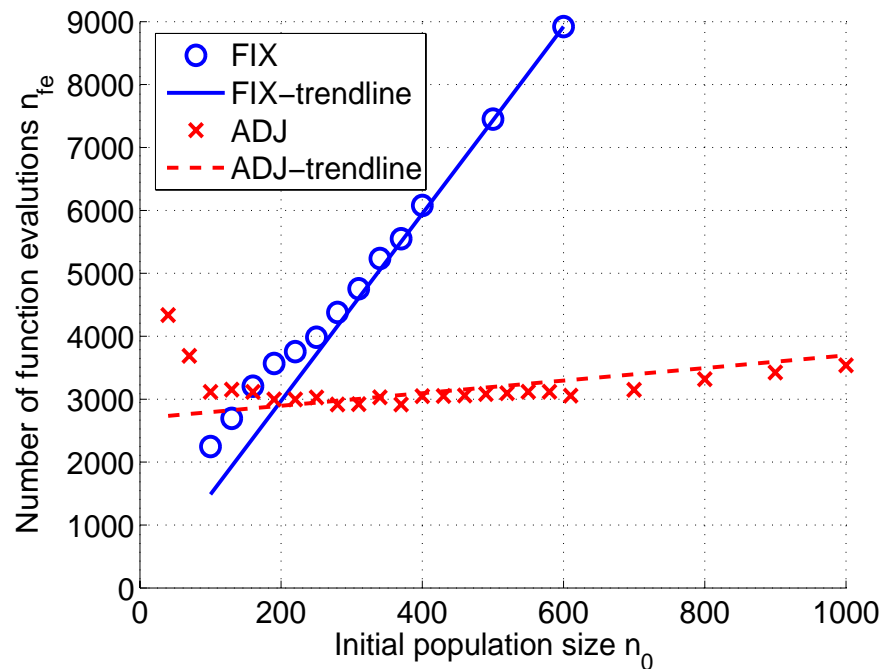


Similar behavior for different initial population sizes (except at extremely small initial population size).

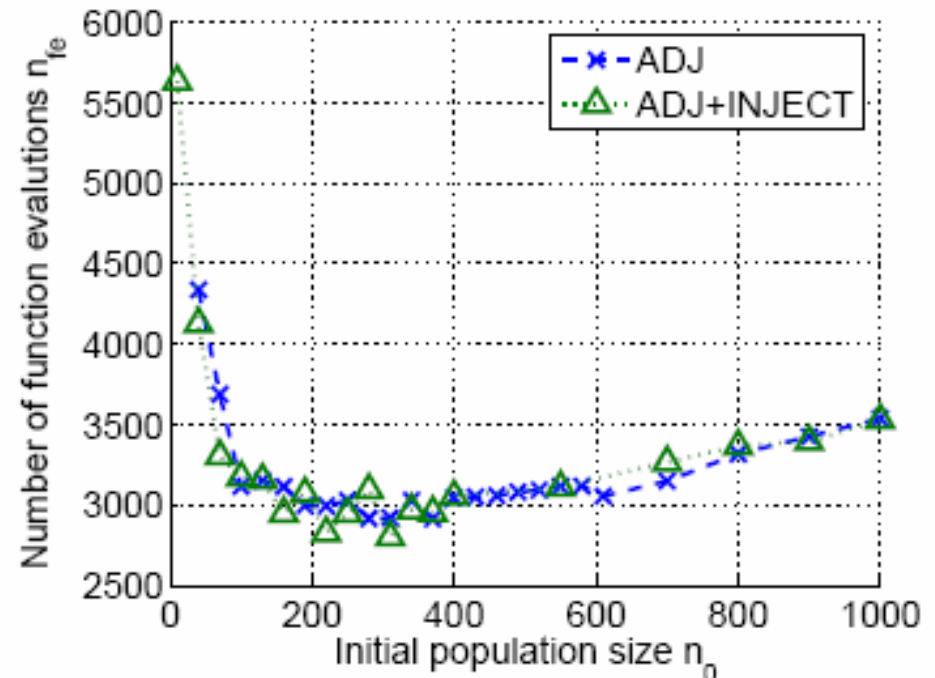
Efficiency: Adaptation Doesn't Require Significantly Extra Evaluations

❖ Large n_0 does not cost too much.

Generate new individuals by recombination



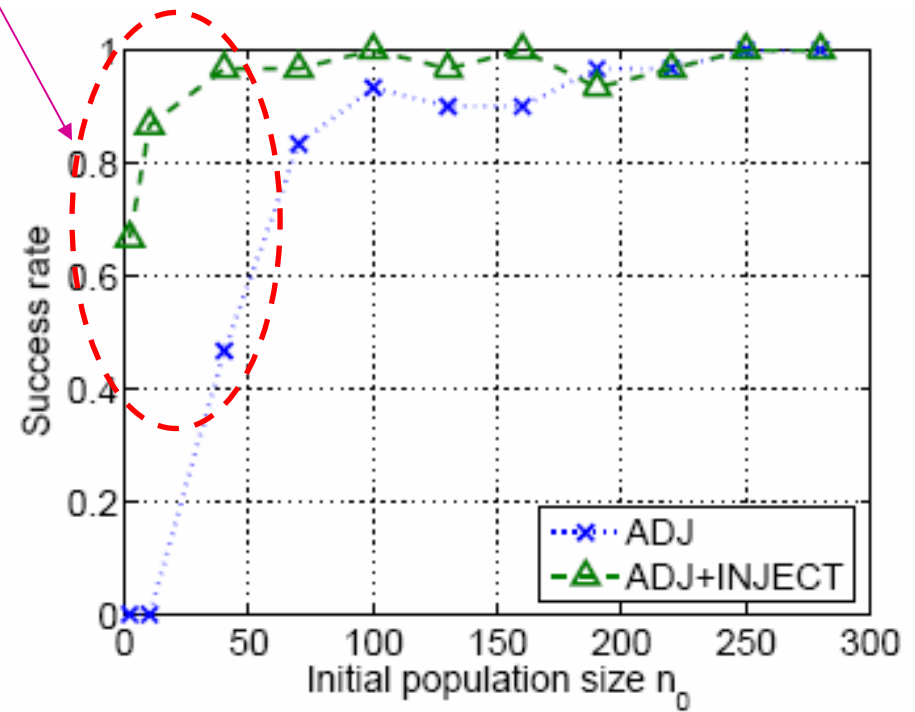
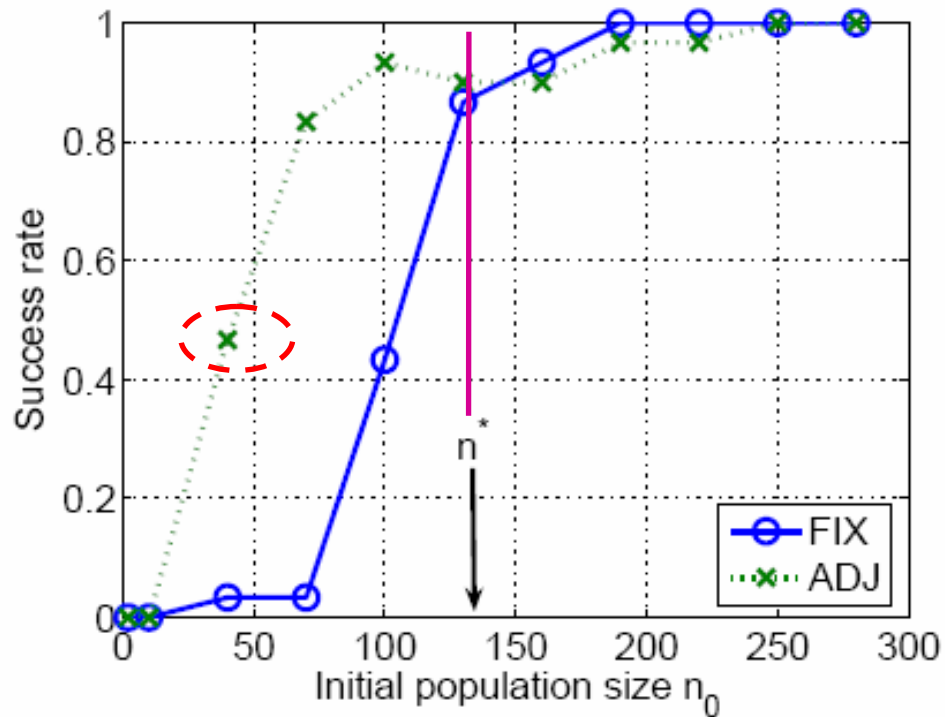
Initialize early recombine later



Robustness: Small Initial Population Sizes Yield Success

- ❖ Small n_0 does not easily cause GA failure.

Recovered from small initial population sizes.



What's next?

- ❖ Other linkage learning GEAs

- ❖ Update rule

- ◆ $n_{t+1} = \alpha n_t + (1 - \alpha) \hat{n}_{t+1}$

- ◆ Pros: The change of the estimated population size are smoother. A more noise-robust scheme.

- ◆ Cons: Another parameter to tune.

- ❖ Optimal switch time

- ◆ When do we have high enough confidence to switch from the individual injection scheme to the regular recombination?

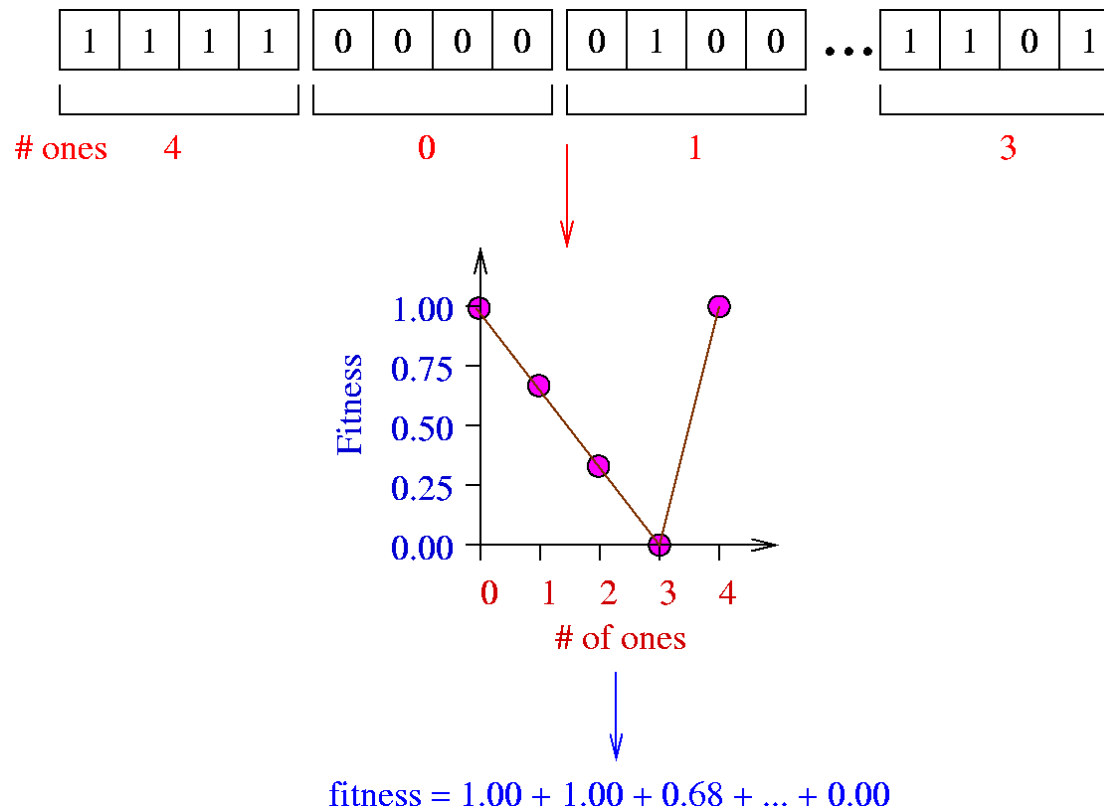
- ❖ Real-world problems

Initial guess

- ❖ Not seriously sensitive
- ❖ Prior knowledge ($k=4\sim 8$, an antenna problem)
- ❖ Doubling scheme
 - ◆ Start from small initial population
 - ◆ Keep doubling it until the parameter (m, k, \dots) does not vary much
 - ◆ Use the final result as the initial guess of population size
 - ◆ Worst case: 4 times of what is needed, but only for the first generation.

Test Problem: Modified m-k Trap Functions

- ❖ Linkage learning is **critical** to GA success
- ❖ **Massively multimodal**: 2^m distinct optima



[Ackley, 1987; Goldberg, 1987; Deb & Goldberg, 1993]