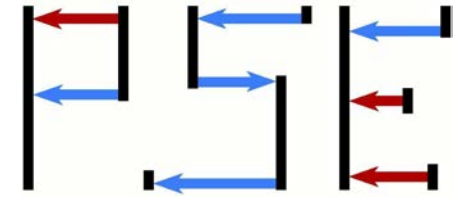


**SFB 680**  
**Molecular Basis of**  
**Evolutionary Innovations**



# **Fitness landscapes and adaptive evolution**

Joachim Krug

Institute for Theoretical Physics, University of Cologne, Germany

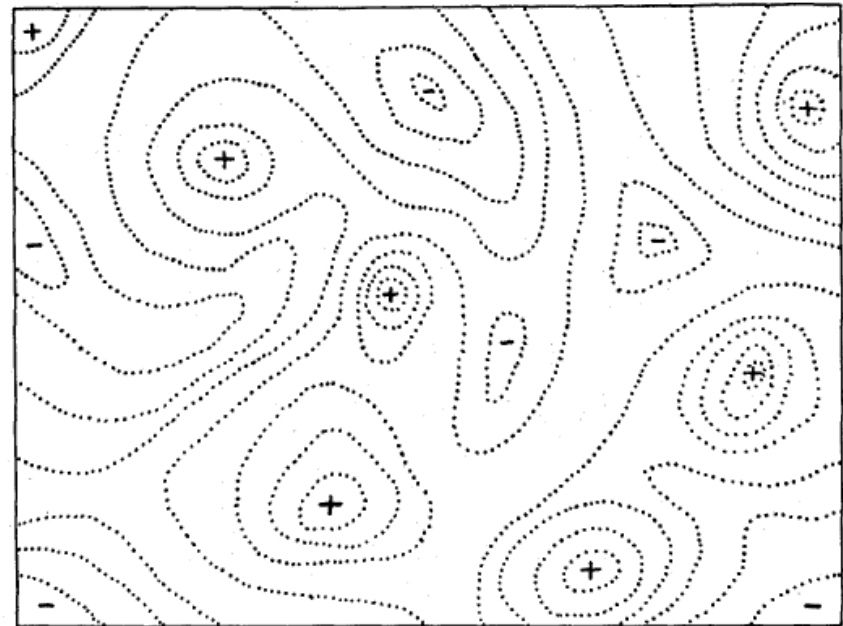
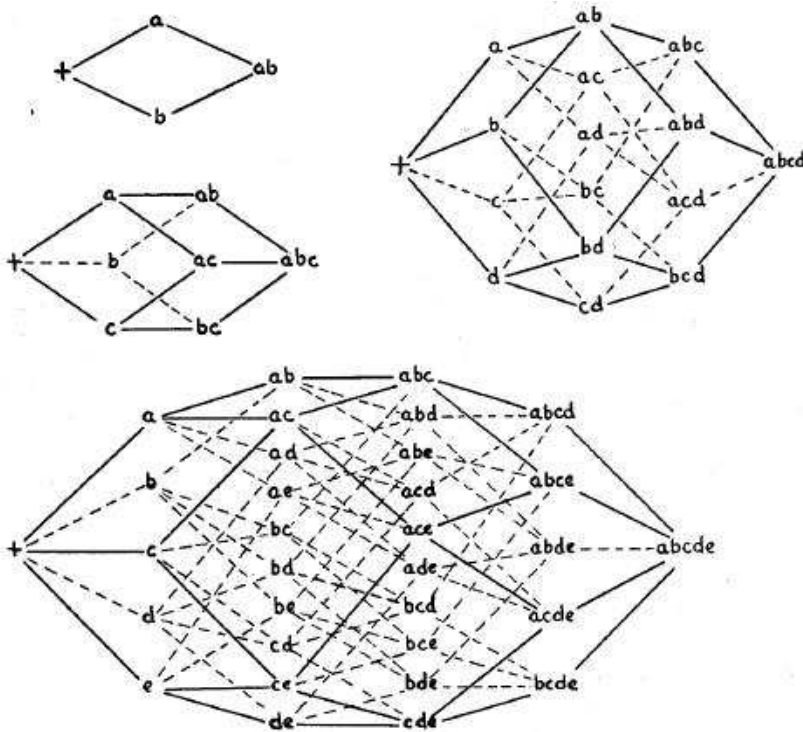
- Empirical fitness landscapes and measures of epistasis
- Accessible mutational pathways in random field models
- Adaptive walks

“Population Dynamics and Statistical Physics in Synergy”

EURANDOM, Eindhoven, August 27, 2014

# Fitness landscapes

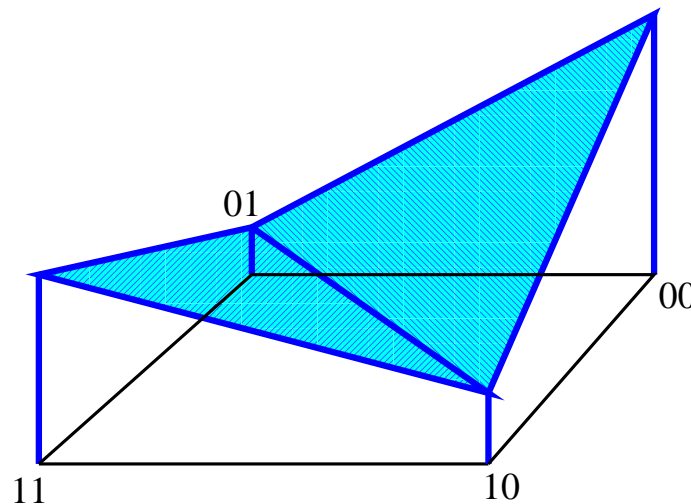
S. Wright, Proc. 6th Int. Congress of Genetics (1932)



“...selection will easily carry the species to the nearest peak, but there will be innumerable other **peaks** that will be higher but which are separated by ‘**valleys**’. The problem of evolution as I see it is that of a mechanism by which the species may continually find its way from lower to higher peaks...”

## Mathematical setting

- Genotypes are binary sequences  $\sigma = (\sigma_1, \sigma_2, \dots, \sigma_L)$  with  $\sigma_i \in \{0, 1\}$  or  $\sigma_i \in \{-1, 1\}$  (presence/absence of mutation).
- A **fitness landscape** is a function  $f(\sigma)$  on the space of  $2^L$  genotypes
- **Epistasis** implies interactions between the effects of different mutations
- **Sign epistasis**: Mutation at a given locus is beneficial or deleterious depending on the state of other loci Weinreich, Watson & Chao (2005)
- **Reciprocal** sign epistasis for  $L = 2$ :



# Measures of epistasis

## Local fitness optima

Haldane 1931, Wright 1932

- A genotype  $\sigma$  is a local optimum if  $f(\sigma) > f(\sigma')$  for all one-mutant neighbors  $\sigma'$
- In the absence of sign epistasis there is a single global optimum
- Reciprocal sign epistasis is a necessary but not sufficient condition for the existence of multiple fitness peaks Poelwijk et al. 2011, Crona et al. 2013

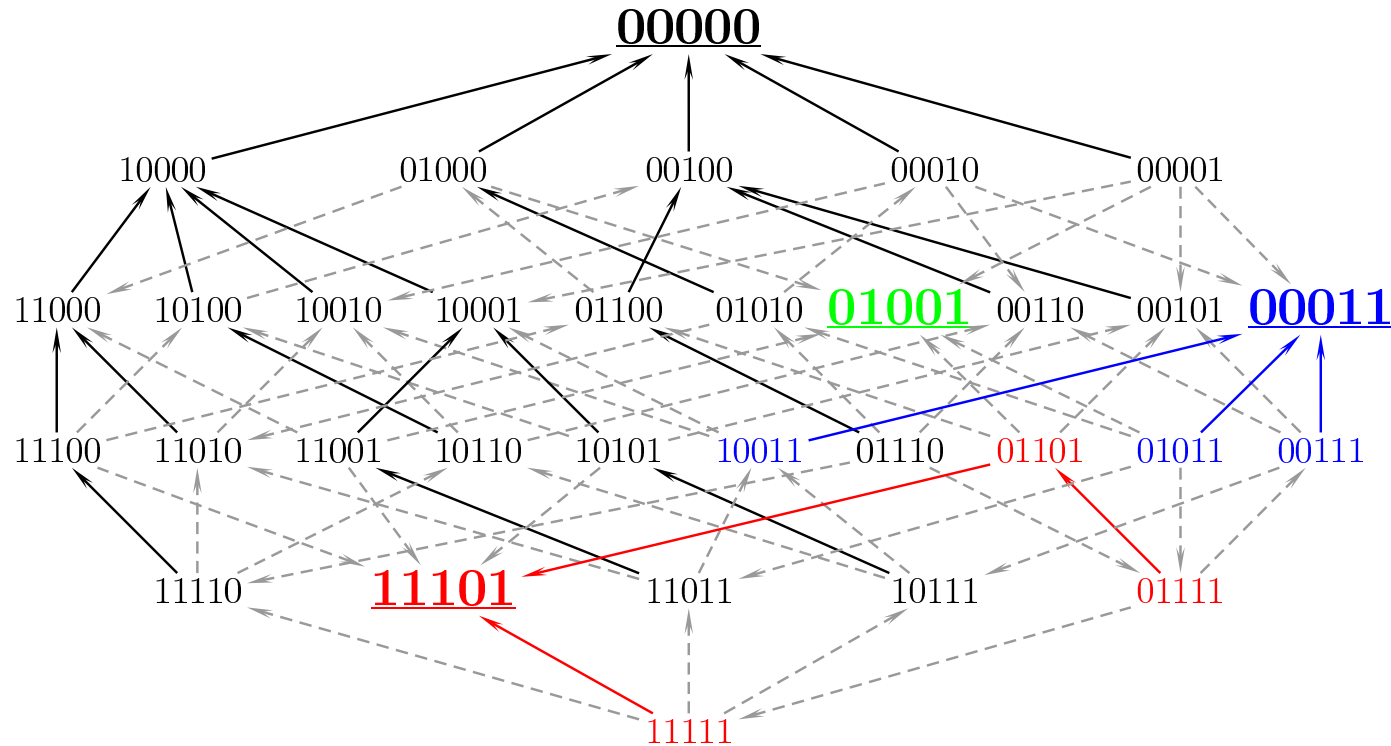
## Selectively accessible paths

Weinreich et al. 2005

- A path of single mutations connecting two genotypes  $\sigma \rightarrow \sigma'$  with  $f(\sigma) < f(\sigma')$  is **selectively accessible** if fitness increases monotonically along the path
- In the absence of sign epistasis all paths to the global optimum are accessible, and vice versa

## Empirical example: The *Aspergillus niger* fitness landscape

J.A.G.M. de Visser, S.C. Park, JK, *American Naturalist* **174**, S15 (2009)



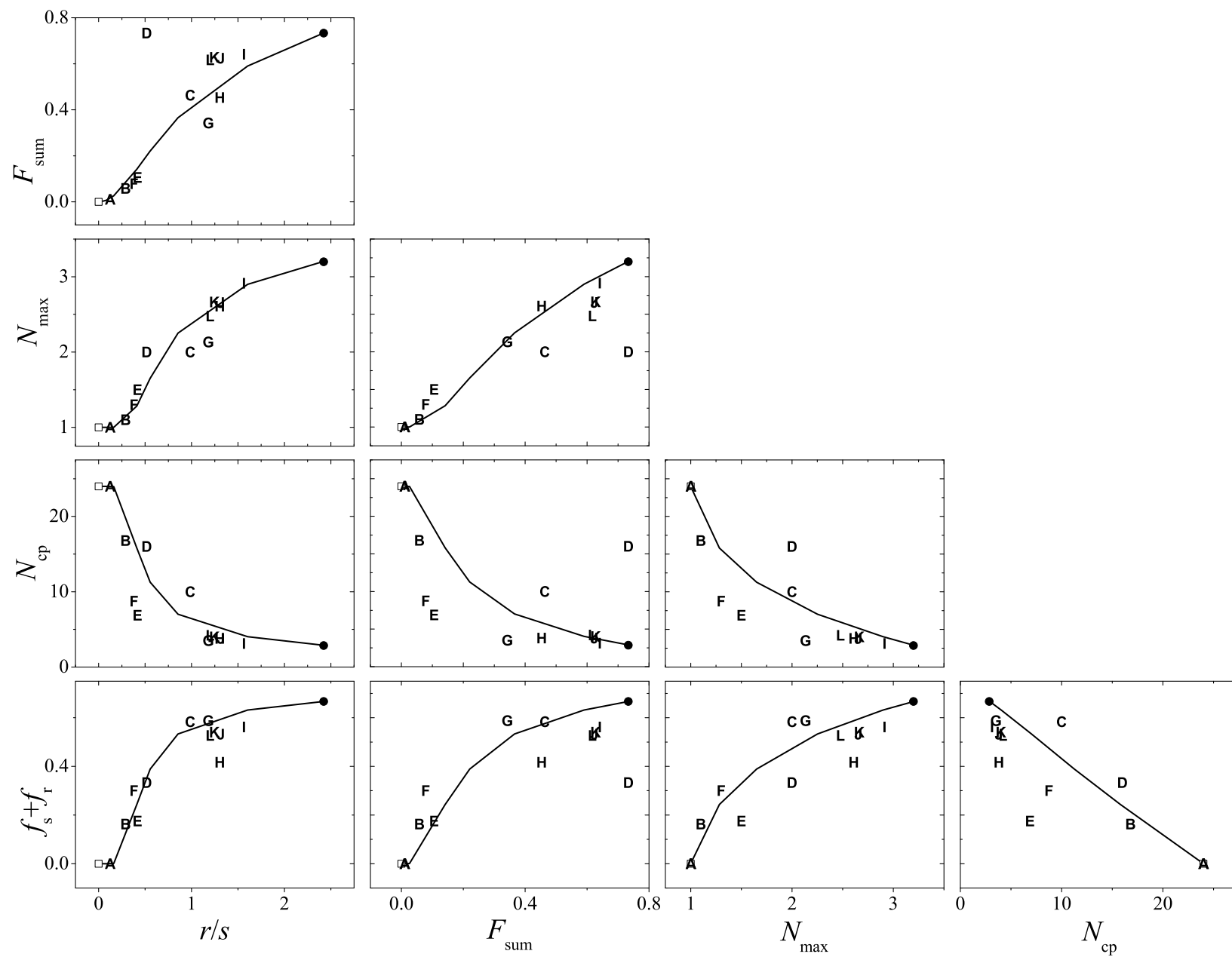
- Combinations of 8 individually deleterious marker mutations (one out of  $\binom{8}{5} = 56$  five-dimensional subsets shown)
- 3 local fitness optima, 25 out of 120 paths are accessible

# A metaanalysis of empirical data sets

Szendro et al., JSTAT 2013; de Visser & Krug, Nat. Rev. Genet. 2014

ID	System ( <i>organism/gene</i> )	$L$	Available combinations	Fitness (proxy)	Direction of mutations	Known effects
A	<i>Methylobacterium extorquens</i>	4	16/16	Growth rate	Beneficial	Combined
B	<i>Escherichia coli</i>	5	32/32	Fitness	Beneficial	Combined
C-D	Dihydrofolate reductase	4	16/16	Resistance/ Growth rate	Beneficial	Individual/ Combined
E	$\beta$ -lactamase	5	32/32	Resistance	Beneficial	Combined
F	$\beta$ -lactamase	5	32/32	Resistance	Beneficial	Combined
G	<i>Saccharomyces cerevisiae</i>	6	64/64	Growth rate	Deleterious	Individual
H	<i>Aspergillus niger</i>	8	186/256	Growth rate	Deleterious	Individual
I-J	Terpene synthase	9	418/512	Enzymatic specificity	—	—

# Comparison of epistasis measures



# **Random field models of fitness landscapes**



## Null model: House-of-cards

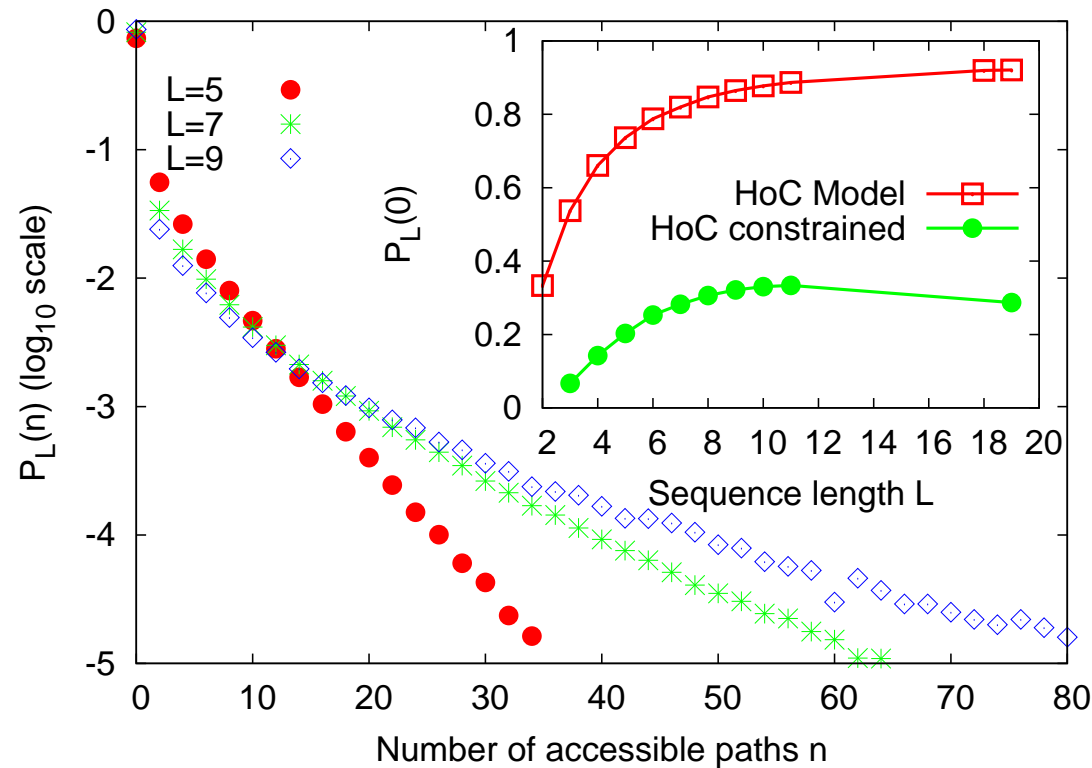
- In the **house-of-cards model** fitness is assigned randomly to genotypes  
Kingman 1978, Kauffman & Levin 1987
- What is the expected number of shortest, selectively accessible paths  $n_{\text{acc}}$  from an arbitrary genotype at distance  $d$  to the **global optimum**?
- The total number of paths is  $d!$ , and a given path consists of  $d$  independent, identically distributed fitness values  $f_0, \dots, f_{d-1}$ .
- A path is accessible iff  $f_0 < f_1 < \dots < f_{d-1}$
- Since all  $d!$  permutations of the  $d$  random variables are equally likely, the probability for this event is  $1/d!$

$$\Rightarrow \mathbb{E}(n_{\text{acc}}) = \frac{1}{d!} \times d! = 1$$

- This holds in particular for the  $L!$  paths from the **reversal genotype/antipode** of the global optimum.

# Distribution of number of accessible paths from reversal genotype

J. Franke et al., PLoS Comp. Biol. 7 (2011) e1002134



- "Condensation of probability" at  $n_{\text{acc}} = 0$
- Characterize the distribution  $P_L(n)$  by  $\mathbb{E}(n_{\text{acc}})$  and the probability  $P_L(0)$  that no path is accessible  $\Rightarrow$  define **accessibility** as  $\bar{P}_L \equiv 1 - P_L(0)$

## “Accessibility percolation” as a function of initial fitness

- When fitnesses are drawn from the uniform distribution and the fitness of the initial genotype is  $f_0$ , then [Hegarty & Martinsson, Ann. Appl. Prob. 2014](#)

$$\lim_{L \rightarrow \infty} \bar{P}_L = \begin{cases} 0 & \text{for } f_0 > \frac{\ln L}{L} \\ 1 & \text{for } f_0 < \frac{\ln L}{L}, \end{cases}$$

- This implies in particular that  $\lim_{L \rightarrow \infty} \bar{P}_L = 0$  for the HoC model with unconstrained initial fitness
- If arbitrary paths with backsteps are allowed, the accessibility threshold becomes independent of  $L$  [Berestycki, Brunet, Shi, arXiv:1401.6894](#)
- On a regular tree of height  $h$  and branching number  $b$  the accessibility threshold for  $h, b \rightarrow \infty$  occurs at  $h/b = e$  [Nowak & Krug, EPL 2013; Roberts & Zhao, ECP 2013](#)

# **Landscapes with tunable ruggedness**

## Kauffman's NK-model

Kauffman & Weinberger 1989

- Each locus interacts randomly with  $K \leq L - 1$  other loci:

$$f(\sigma) = \sum_{i=1}^L f_i(\sigma_i | \sigma_{i_1}, \dots, \sigma_{i_K})$$

$f_i$ : Uncorrelated RV's assigned to each of the  $2^{K+1}$  possible arguments

- $K = 0$ : Non-epistatic       $K = L - 1$ : House-of-cards

## Rough Mt. Fuji model

Aita et al. 2000; Neidhart et al., arXiv:1402.3065

- Non-epistatic ("Mt. Fuji") landscape perturbed by a random component:

$$f(\sigma) = -cd(\sigma, \sigma^{(0)}) + \eta(\sigma)$$

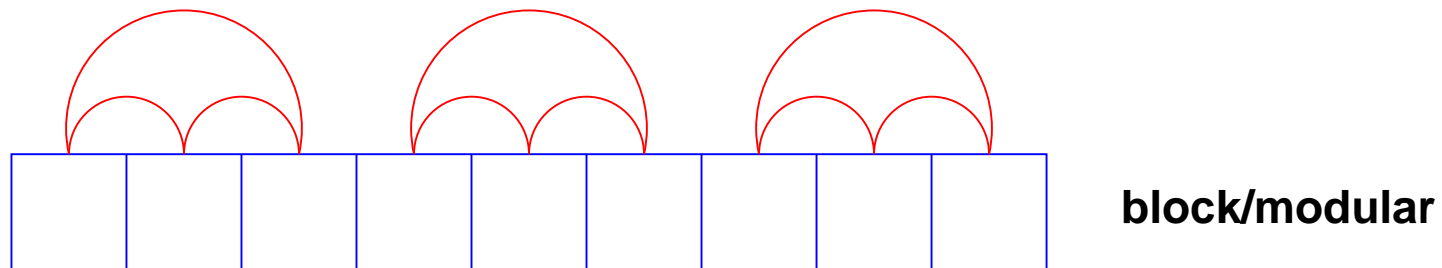
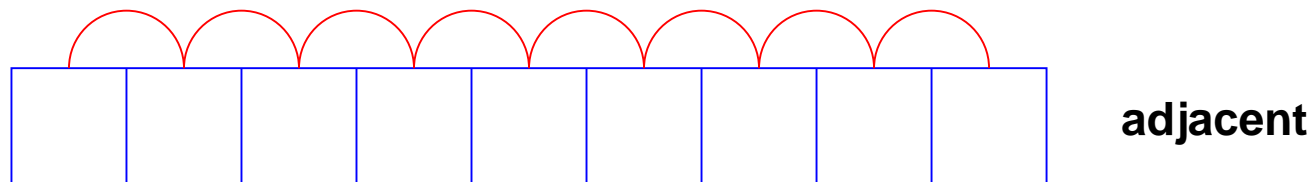
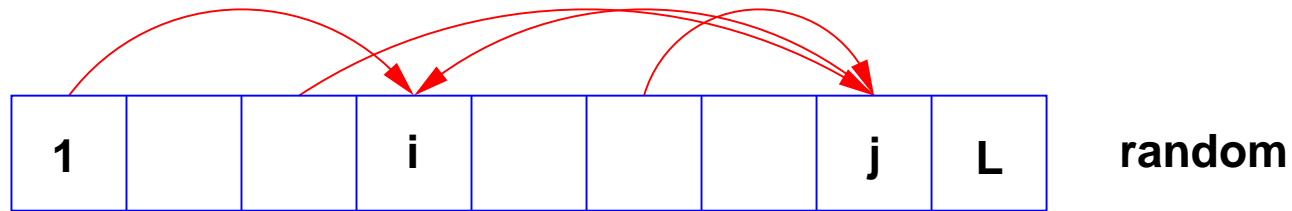
$c > 0$ : slope       $d(\sigma, \sigma')$ : Hamming distance       $\eta$ : i.i.d. RV's

- $\lim_{L \rightarrow \infty} \bar{P}_L = 1$  for any  $c > 0$

Hegarty & Martinsson 2014

# “Genetic architecture” in Kauffman’s NK-model

- Different schemes for choosing the interaction partners:



- Which properties of the fitness landscape are sensitive to this choice?

# “Genetic architecture” in Kauffman’s NK-model

- Fitness correlation function is manifestly independent of the neighborhood scheme

P.R.A. Campos, C. Adami, C.O. Wilke (2002)

J. Neidhart, I.G. Szendro, JK, JTB 2013

- In the block model, the mean number of local maxima is given exactly by

$$\mathbb{E}(n_{\max}^{\text{block}}) = \frac{2^L}{(K+2)^{L/(K+1)}} \quad \text{A.S. Perelson, C.A. Macken (1995)}$$

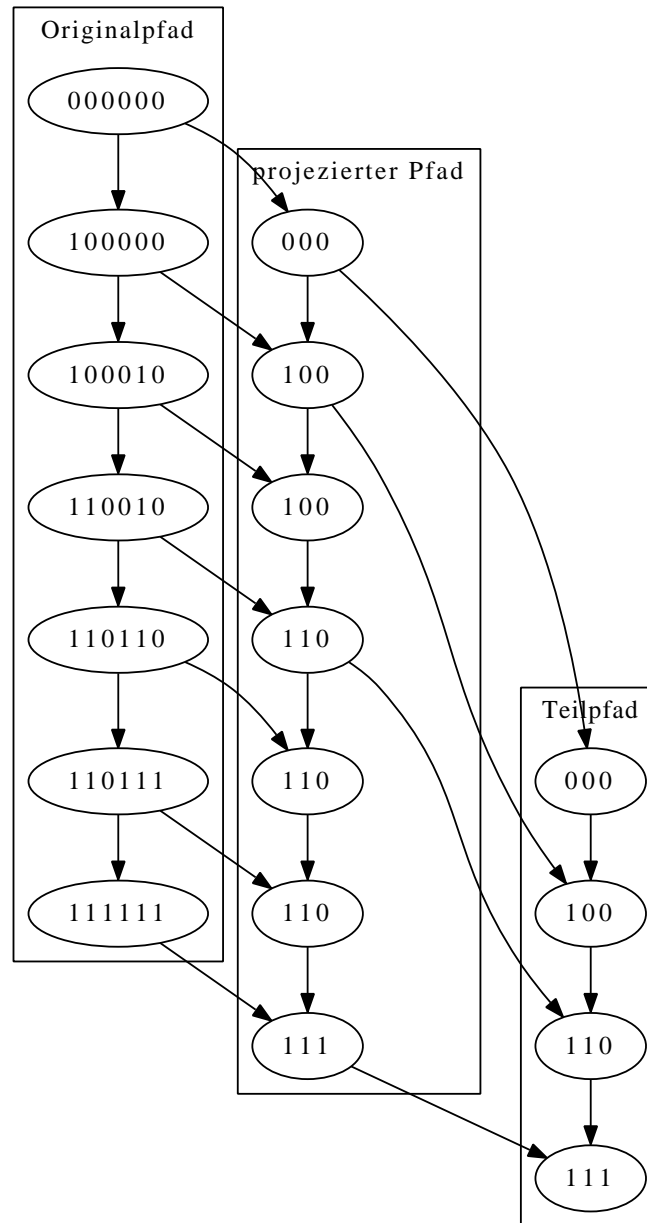
which is very close (but not identical) to rigorous results for the adjacent model

Durrett & Limic (2003), Limic & Pemantle (2004)

- Mean number of accessible paths in the block model:

$$\mathbb{E}(n_{\text{acc}}^{\text{block}}) = \frac{L!}{[(K+1)!]^{L/(K+1)}} \quad \text{B. Schmiegel, JK 2013}$$

# Path decomposition for the block model





# Evolutionary accessibility in the block model

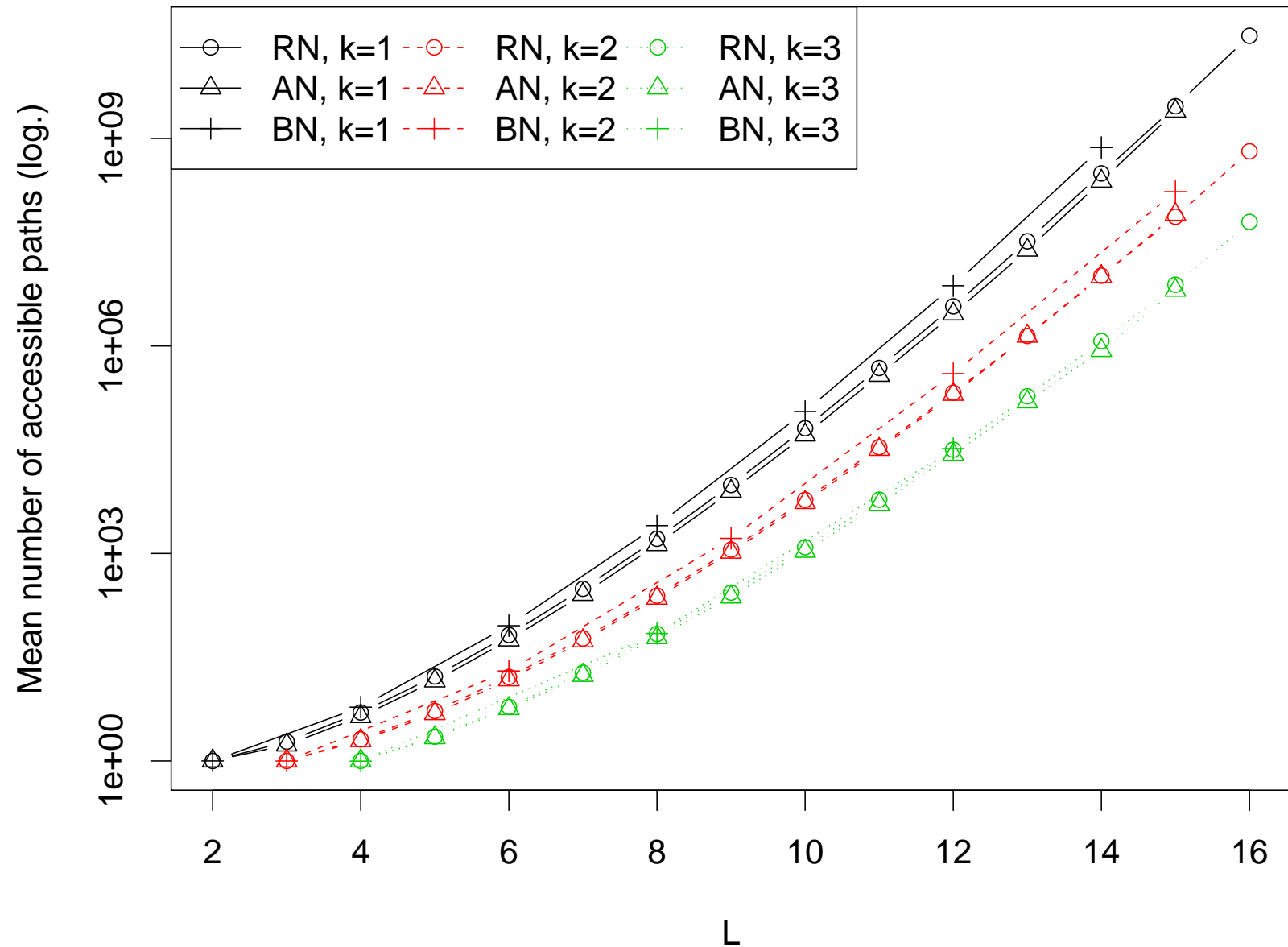
B. Schmiegelt, JK, J. Stat. Phys. **154**, 334 (2014)

- A given pathway spanning the whole landscape is accessible iff all subpaths within the  $B = L/(K+1)$  blocks are accessible
- Each combination of accessible subpaths can be combined into  $\frac{L!}{[(K+1)!]^B}$  global paths

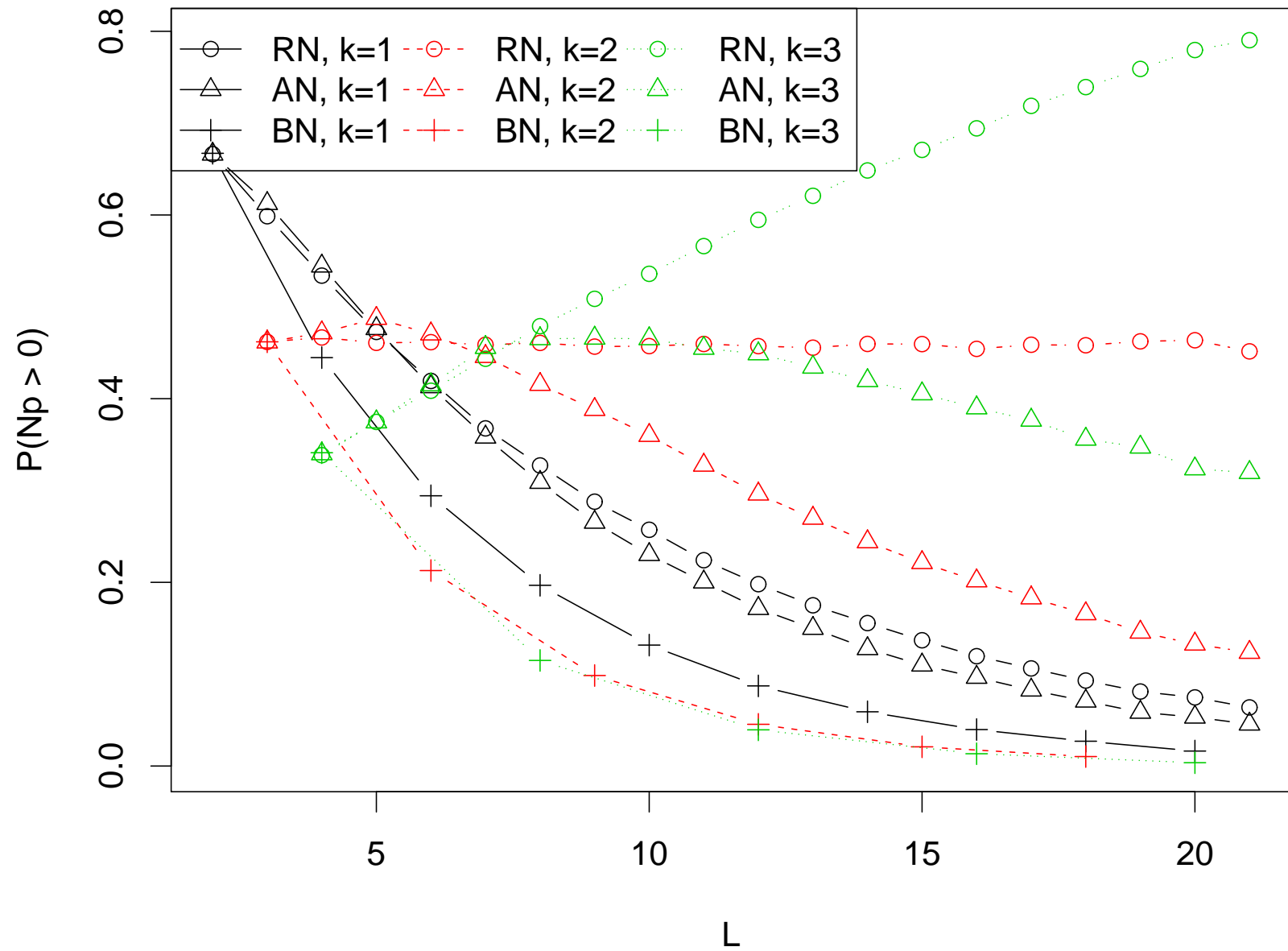
$$\Rightarrow n_{\text{acc}}^{\text{block}} = \frac{L!}{[(K+1)!]^B} \prod_{i=1}^B n_{\text{acc}}^{(i)}$$

- Since the blocks are HoC-landscapes of size  $K+1$ , the expected number of accessible paths is  $\mathbb{E}(n_{\text{acc}}^{\text{block}}) = \frac{L!}{[(K+1)!]^B}$  and the accessibility is  $\bar{P}_L^{\text{block}} = [\bar{P}_{K+1}^{\text{HoC}}]^{\frac{L}{K+1}}$  which approaches zero **exponentially fast** in  $L$  for any  $K$
- Full distribution of  $n_{\text{acc}}^{\text{block}}$  can be computed in terms of the HoC distributions, explicit results for  $K=1$  and  $K=2$ .

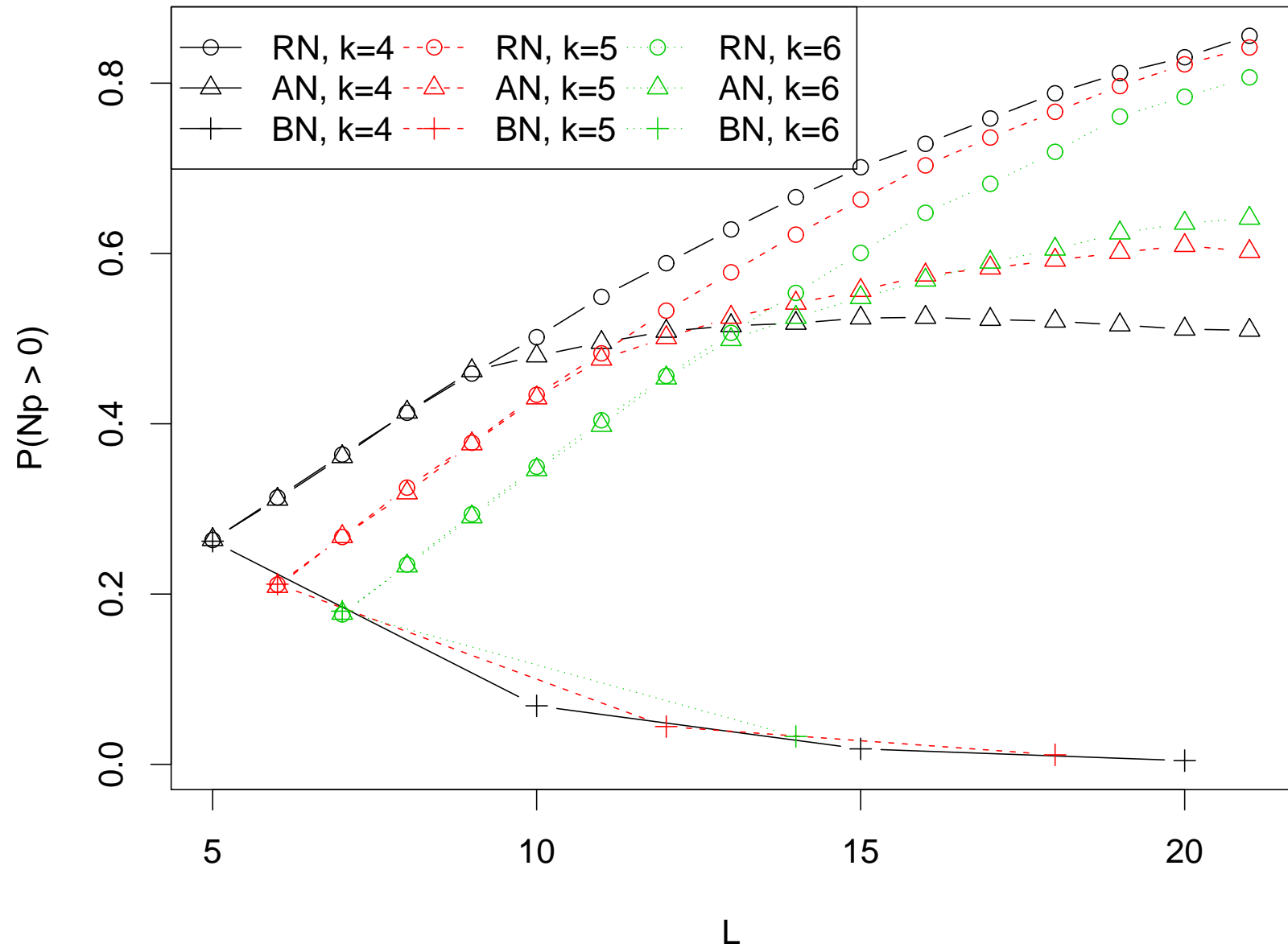
# Mean number of paths is insensitive to genetic architecture



...but accessibility is very sensitive....

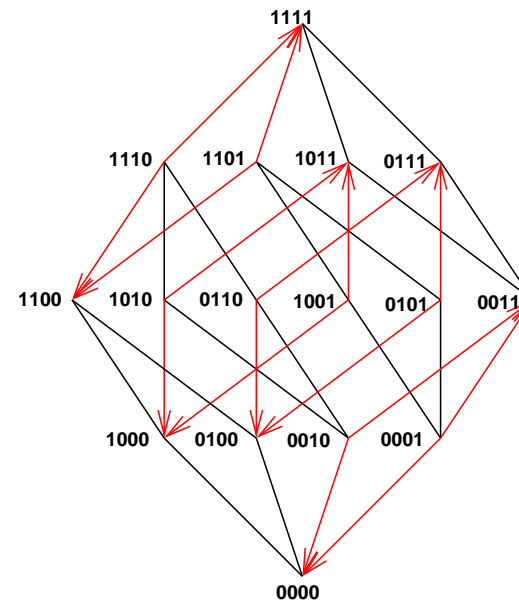
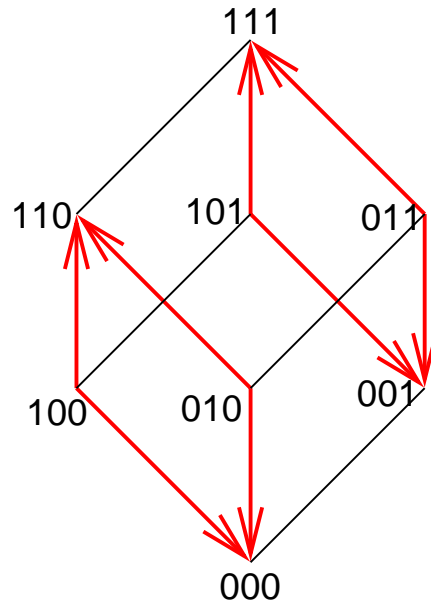


...at least for system sizes that can be simulated!



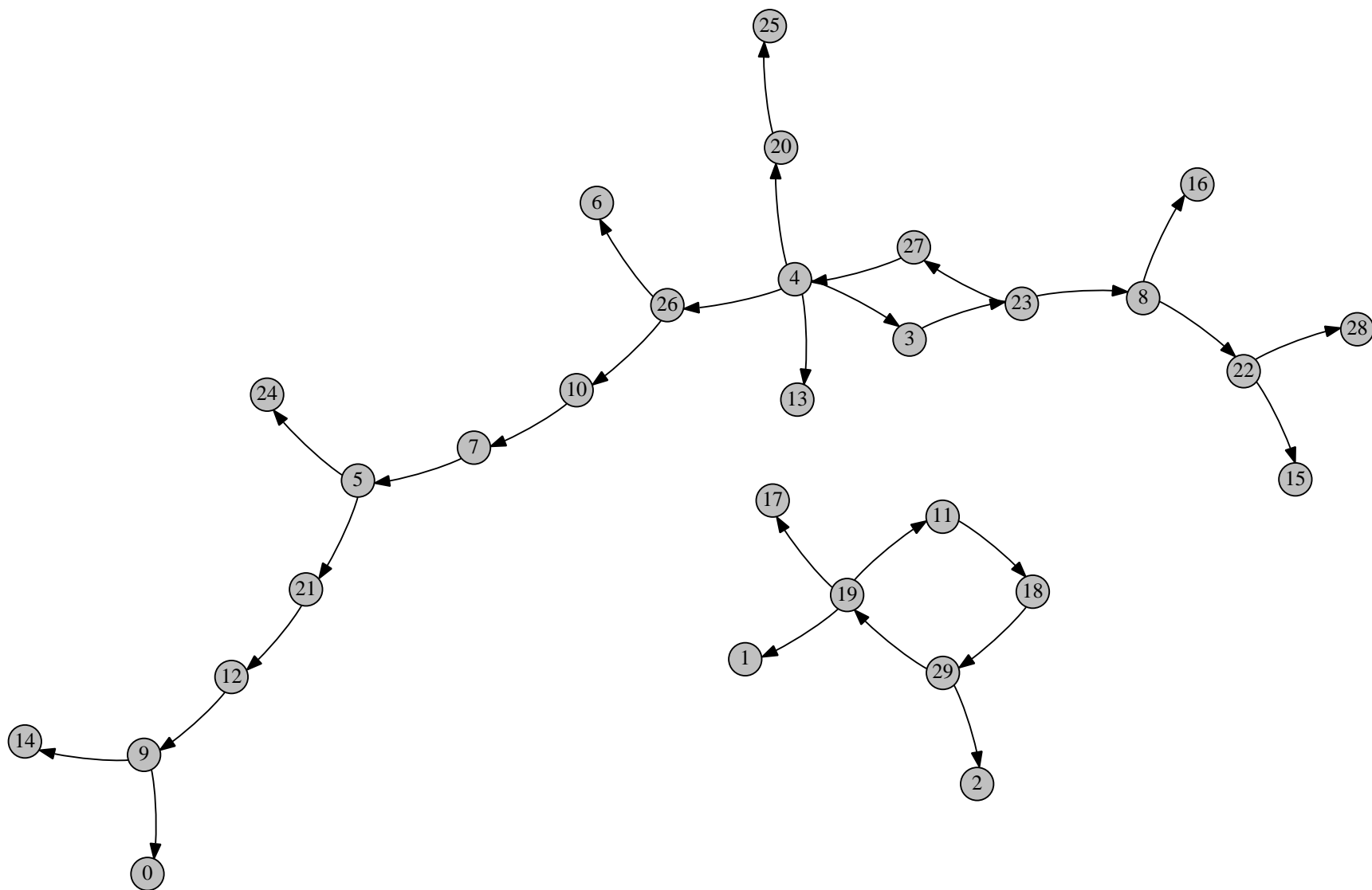
# Global reciprocal sign epistasis

- A fitness landscape displays global reciprocal sign epistasis if there is a pair of loci that has reciprocal sign epistasis in all possible backgrounds:

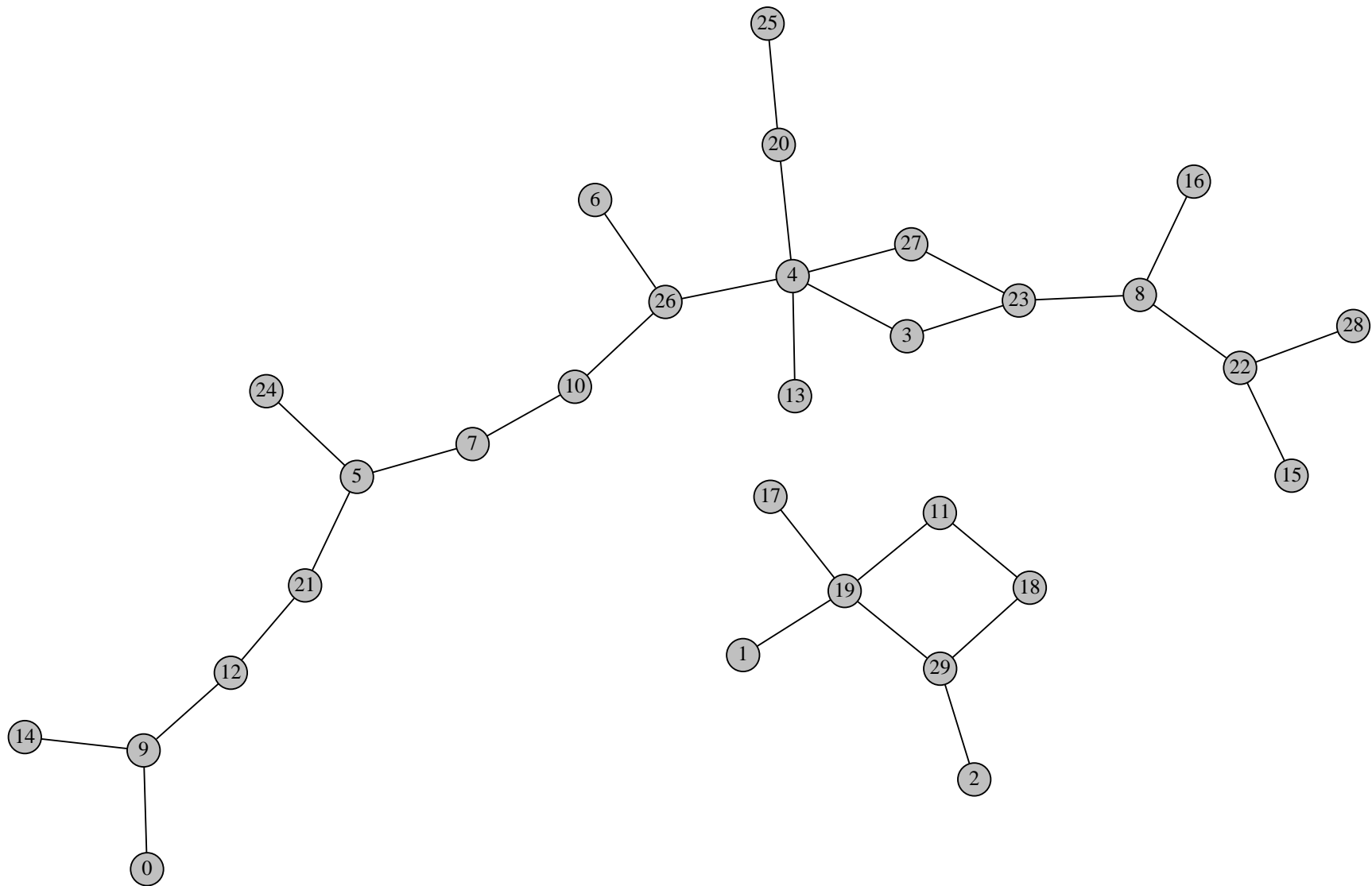


- In the presence of global reciprocal sign epistasis there are no accessible paths across the hypercube
- **Proposition:** (B. Schmiegel)  
Global reciprocal sign epistasis exists with probability tending to unity for  $L \rightarrow \infty$ ,  $K$  fixed, for any neighborhood choice of the NK-model

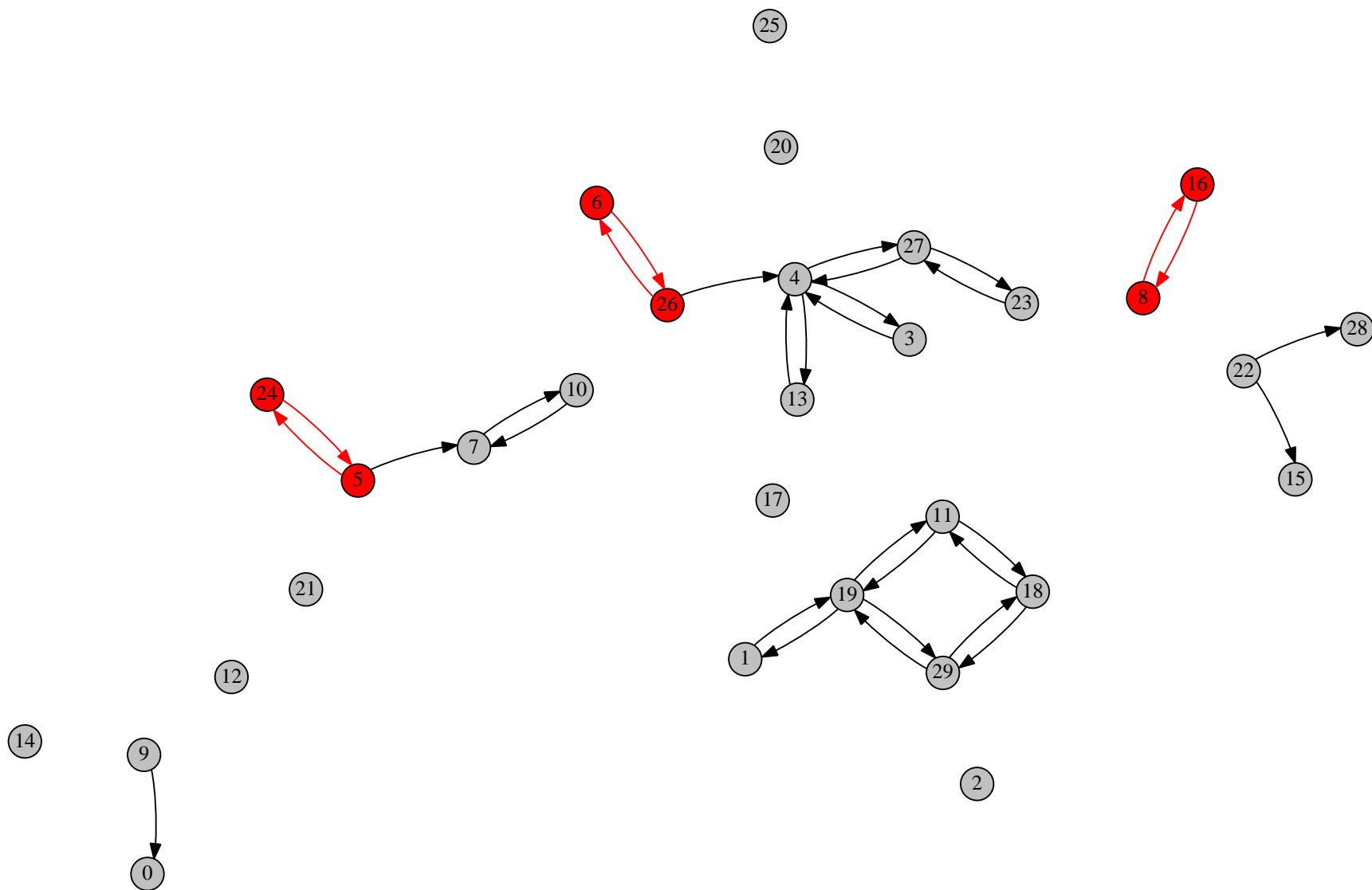
## Random NK-model with $L = 30, K = 1$ : Neighborhood graph



## Random NK-model with $L = 30, K = 1$ : Epistasis graph

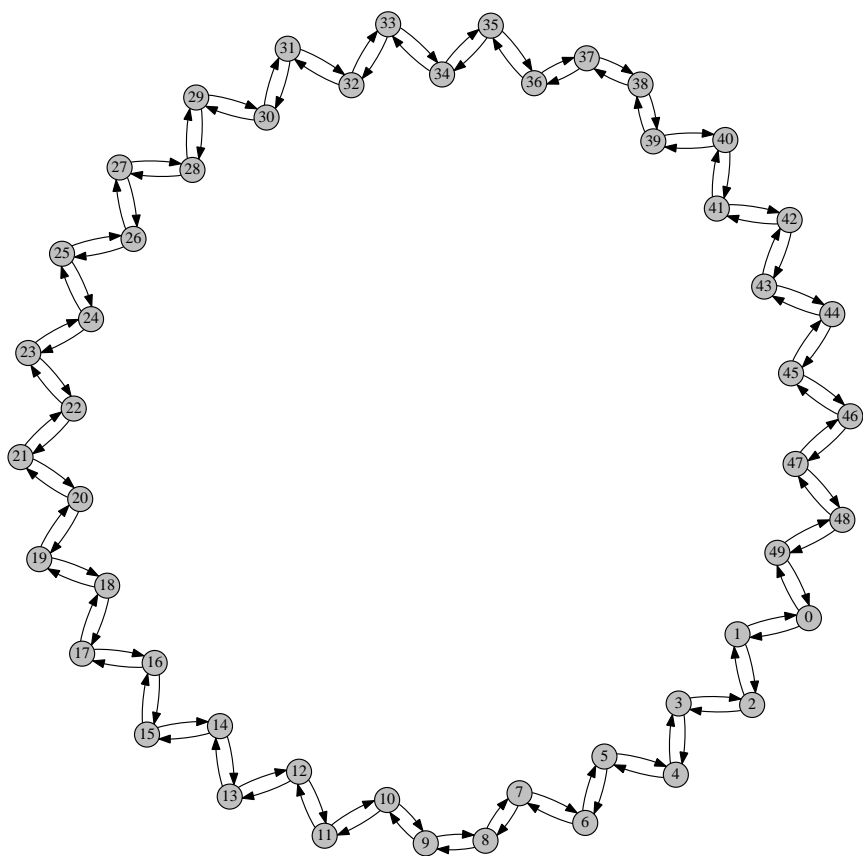


# Random NK-model with $L = 30, K = 1$ : Sign epistasis graph

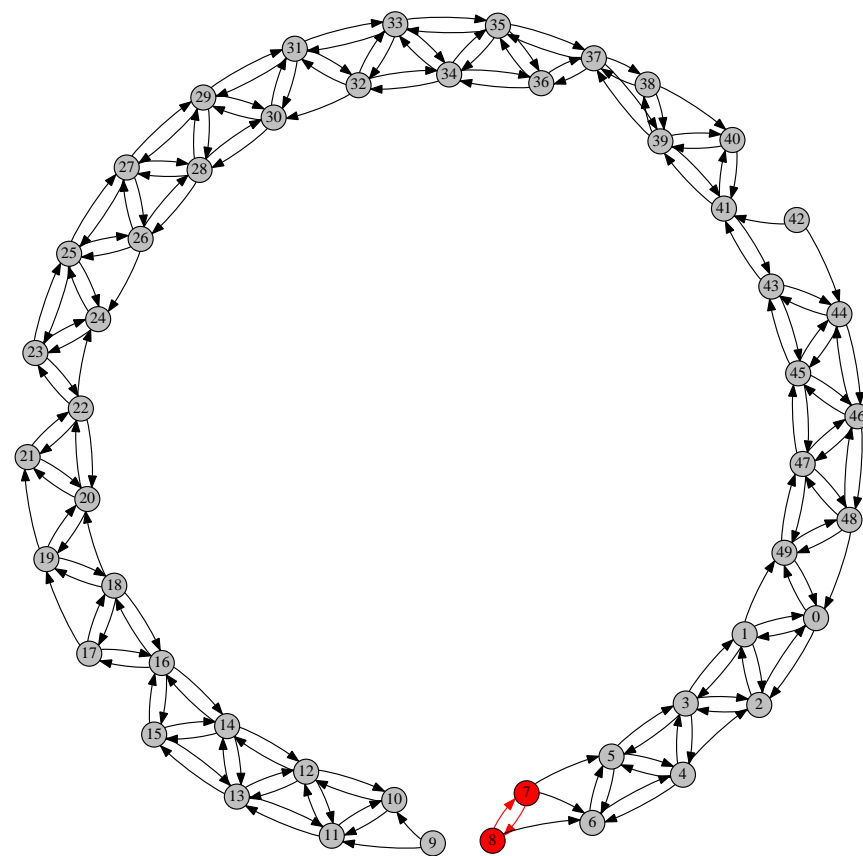




## Adjacent NK-model with $L = 50, K = 2$



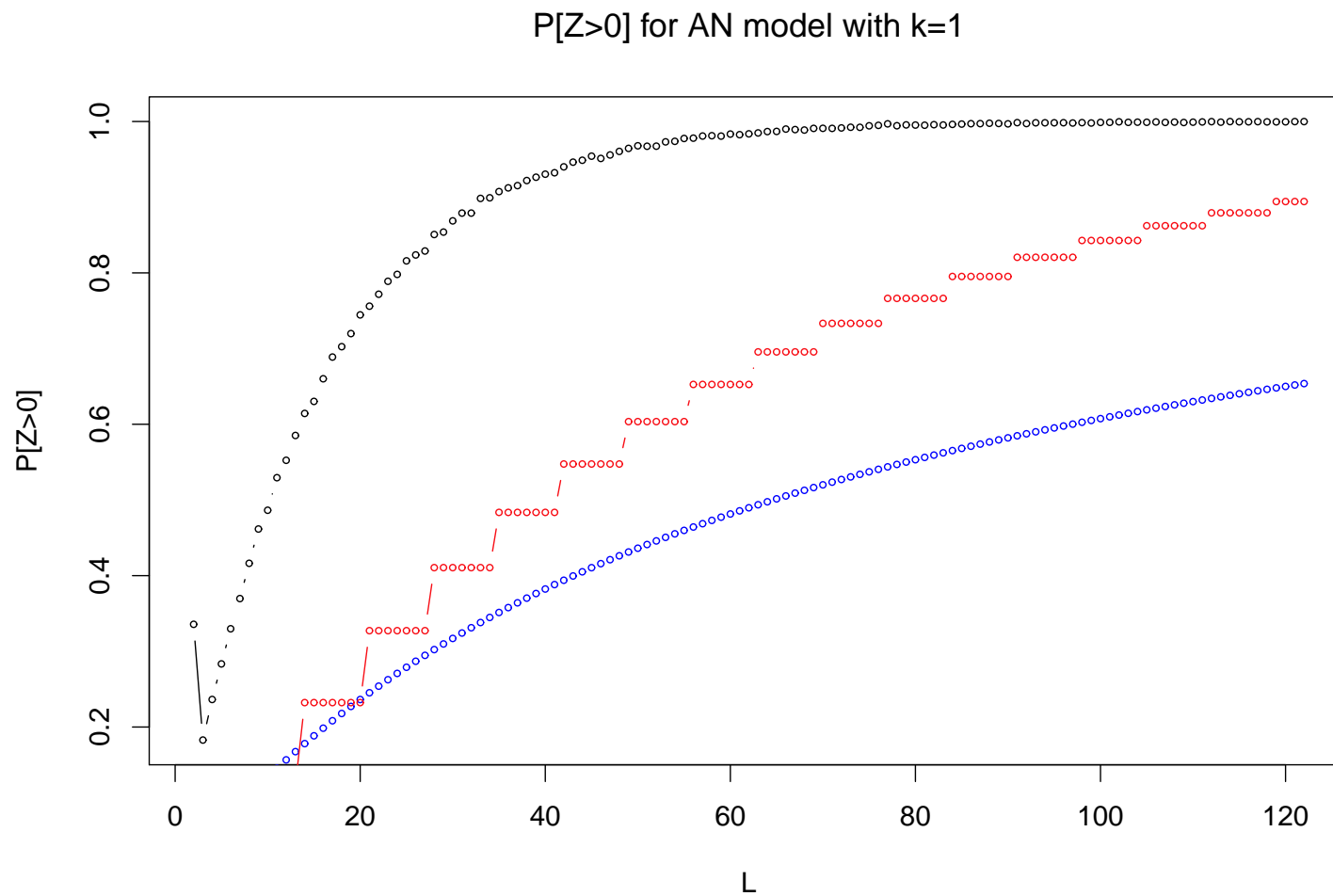
● interaction graph



● sign epistasis graph

# Global reciprocal sign epistasis in the adjacent NK-model: $K = 1$

B. Schmiegelt (unpublished)

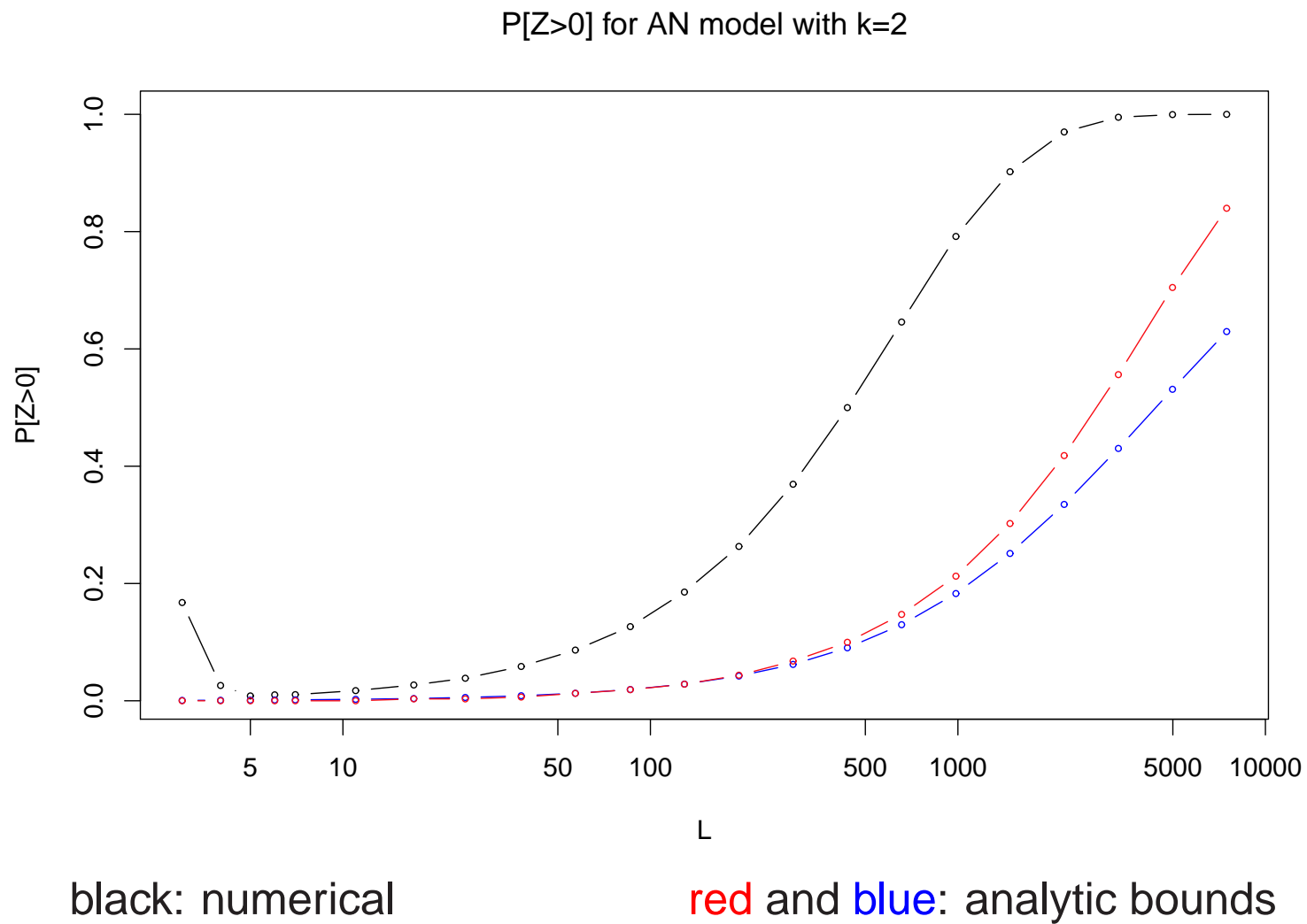


black: numerical

red and blue: analytic bounds

# Global reciprocal sign epistasis in the adjacent NK-model: $K = 2$

B. Schmiegel (unpublished)



# **Adaptive walks**

# Adaptive walks

- An adaptive walk is a Markov chain on sequence space that is constrained to move to genotypes of larger fitness and terminates at local fitness maxima
- Three flavors of adaptive walks differing in their transition probabilities:

## Random Adaptive Walk (RAW)

Macken & Perelson 1989

All fitter genotypes are chosen with equal probability

## Greedy Adaptive Walks (GAW)

Orr 2003

The most fit genotype is chosen deterministically

## True Adaptive Walk (TAW)

Transition rate is proportional to the fitness difference between the resident and mutant genotype

Gillespie 1983, Orr 2002

- Quantities of interest: Average **length**  $\ell$  and achieved fitness (**height**)  $f^*$

## Walk length in the HoC landscape

- RAW's and GAW's are fully determined by the **rank ordering** of the fitness landscape. Their properties are independent of the fitness distribution and only depend on the **number of uphill directions**  $L$  in the initial state.
- RAW:  $\ell \approx \ln(L) + 1.1$  for large  $L$  Flyvbjerg & Lautrup 1992
- GAW:  $\ell \rightarrow e - 1 \approx 1.71828...$  Orr 2003
- TAW length asymptotics depends on the **extreme value index**  $\kappa$  of the fitness distribution according to Neidhart & Krug 2011, Jain 2011

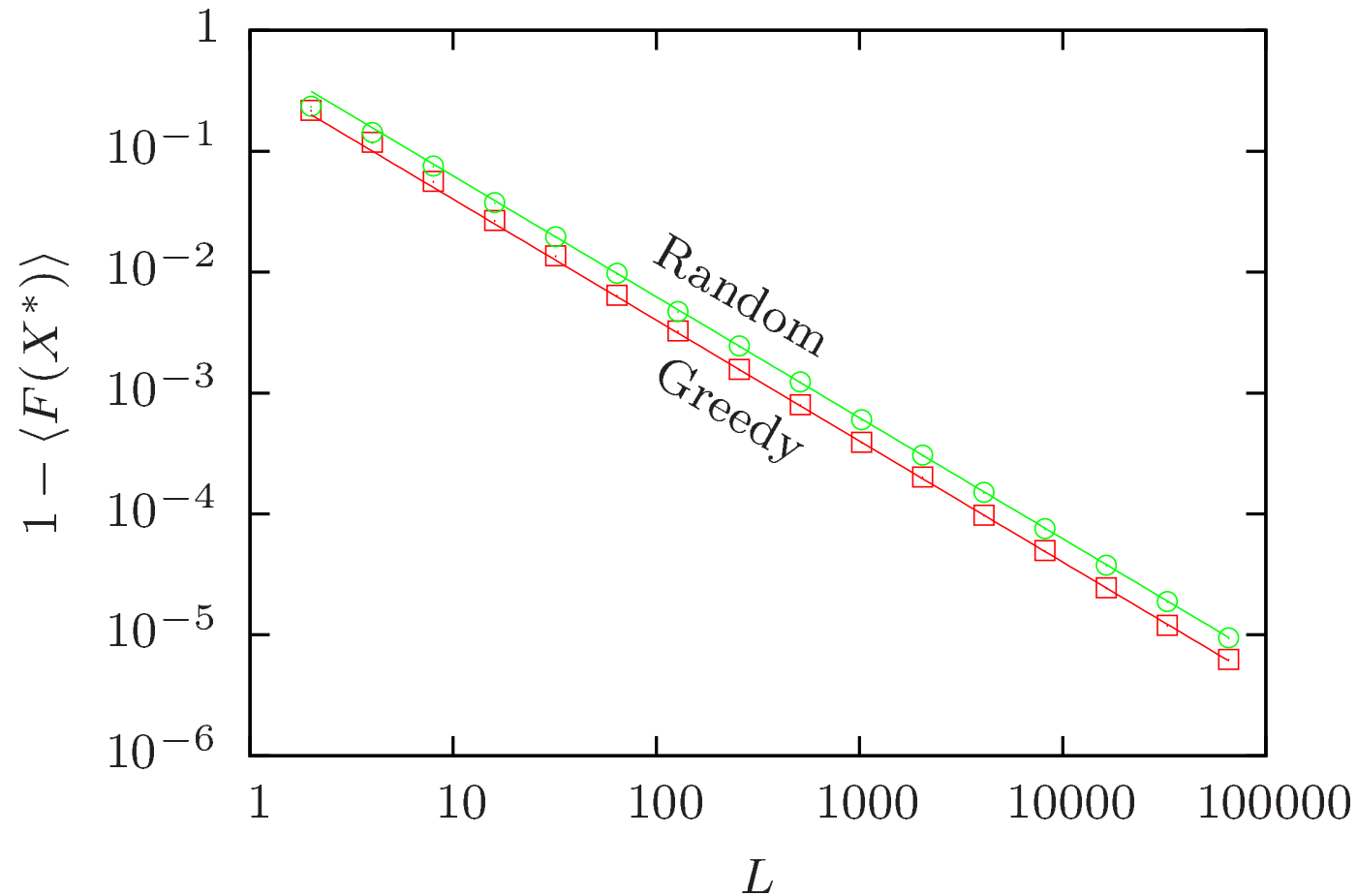
$$\ell \approx \frac{1 - \kappa}{2 - \kappa} \ln(L) + c_\kappa \quad \text{for } \kappa < 1$$

where  $\kappa > 0$ ,  $\kappa = 0$  and  $\kappa < 0$  correspond to the Fréchet, Gumbel and Weibull classes, respectively.

- The TAW becomes effectively random (greedy) for  $\kappa \rightarrow -\infty$  ( $\kappa \rightarrow 1$ )

# Walk height in the HoC landscape

S. Nowak (unpublished)



- For uniform fitness distribution the expected final fitness is of the form  $1 - \mathbb{E}(f^*) \approx \frac{\beta}{L}$  with  $\beta_{\text{RAW}} \approx 0.6243..$  and  $\beta_{\text{GAW}} \approx 0.4003...$

# Random adaptive walks in the RMF landscape

S.-C. Park, I.G. Szendro, J. Neidhart, JK, arXiv:1408:4856

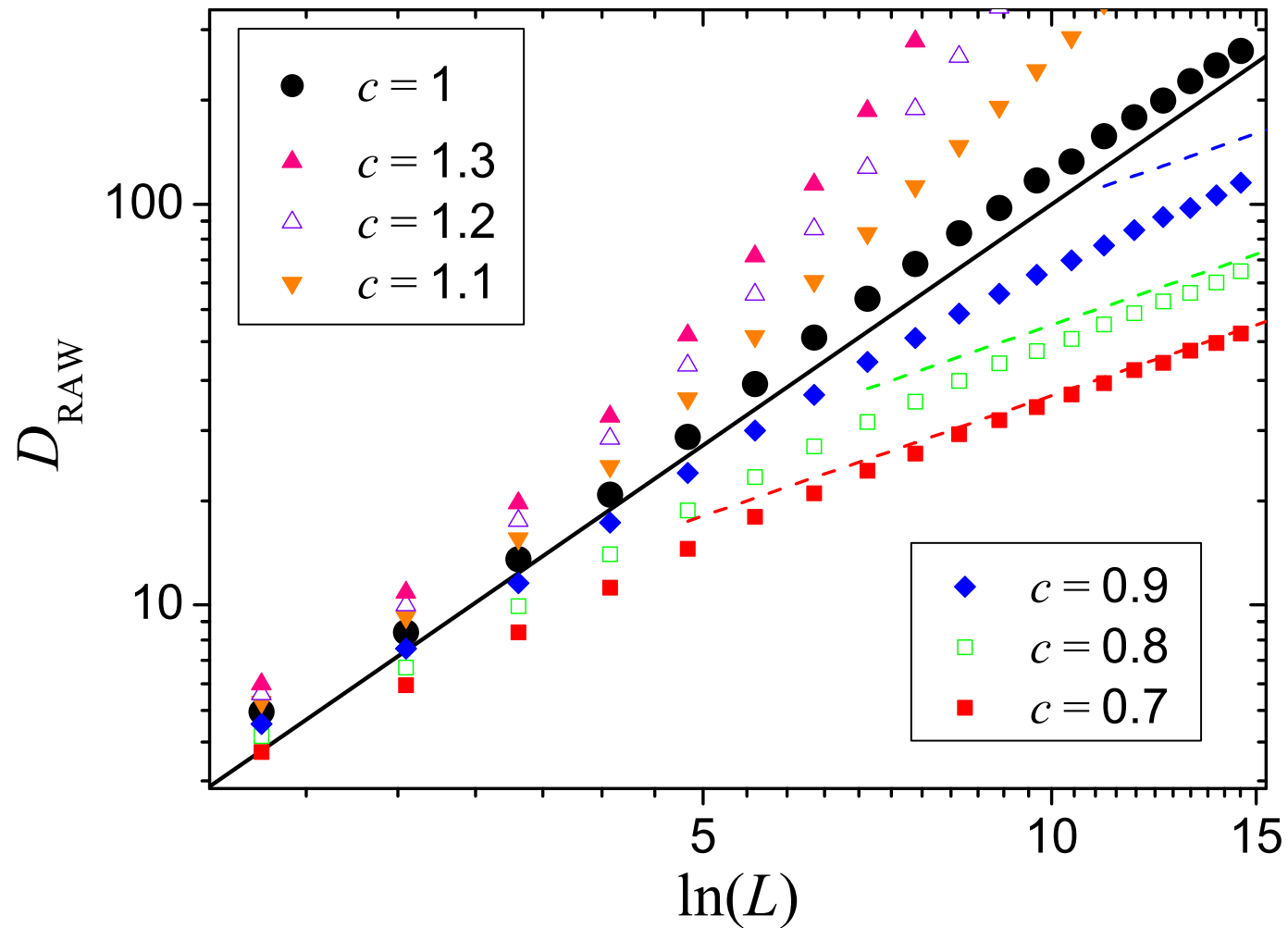
- RAW's starting at antipode (maximal distance  $L$  from reference sequence)
- Assume RAW takes only 'uphill' steps that decrease  $d(\sigma, \sigma^{(0)})$ , and draw random fitness component from exponential distribution with mean 1
- Then the mean walk length can be computed analytically and displays a **phase transition** at  $c = 1$ :

$$\ell \propto \begin{cases} \ln L / (1 - c), & c < 1 \\ (\ln L)^2, & c = 1, \\ O(L), & c > 1. \end{cases}$$

- For tails thinner (fatter) than exponential,  $\ell \sim L$  ( $\ell \sim \ln L$ ) for all  $c > 0$
- Equivalent to zero temperature Metropolis dynamics of a random energy spin glass in an external field



## Random adaptive walks in the RMF landscape



- Numerical verification of phase transition in simulations with backsteps

# Greedy adaptive walks in the RMF landscape

S.-C. Park, J. Neidhart, JK, in preparation

- For Gumbel-distributed random fitness components, the length of GAW's starting from the antipode of the reference sequence satisfies

$$\mathbb{P}(\text{length} \geq l) = \prod_{k=1}^l \frac{1 - e^{-c}}{1 - e^{-kc}} = \frac{1}{[l]_{e^{-c}}!}$$

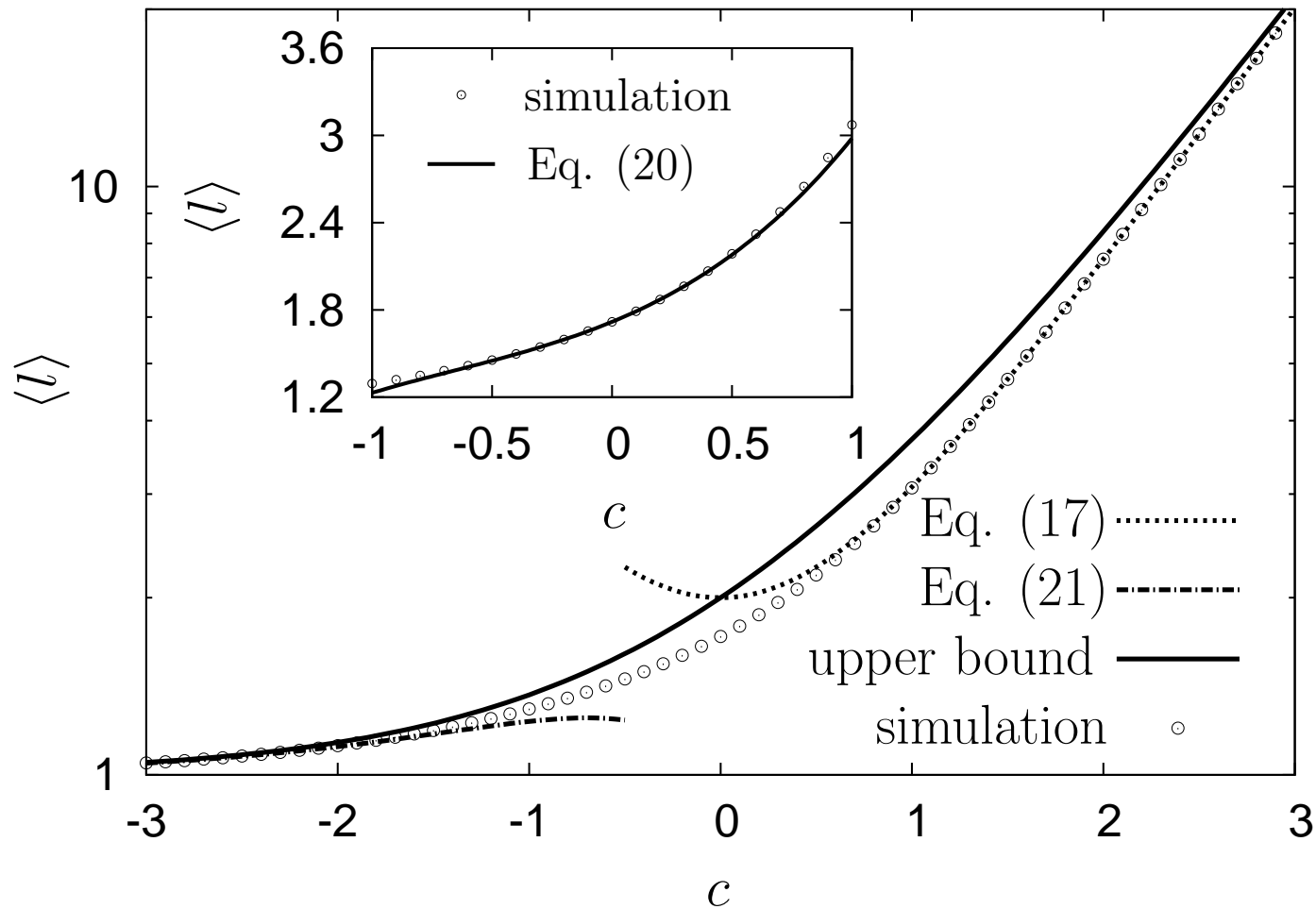
where  $[n]_q = \frac{1-q^n}{1-q}$  is the  $q$ -number.

- Correspondingly the mean walk length is given by the  $q$ -exponential

$$\ell = \exp_{e^{-c}}(1) - 1 \rightarrow e - 1 \quad \text{for } c \rightarrow 0$$

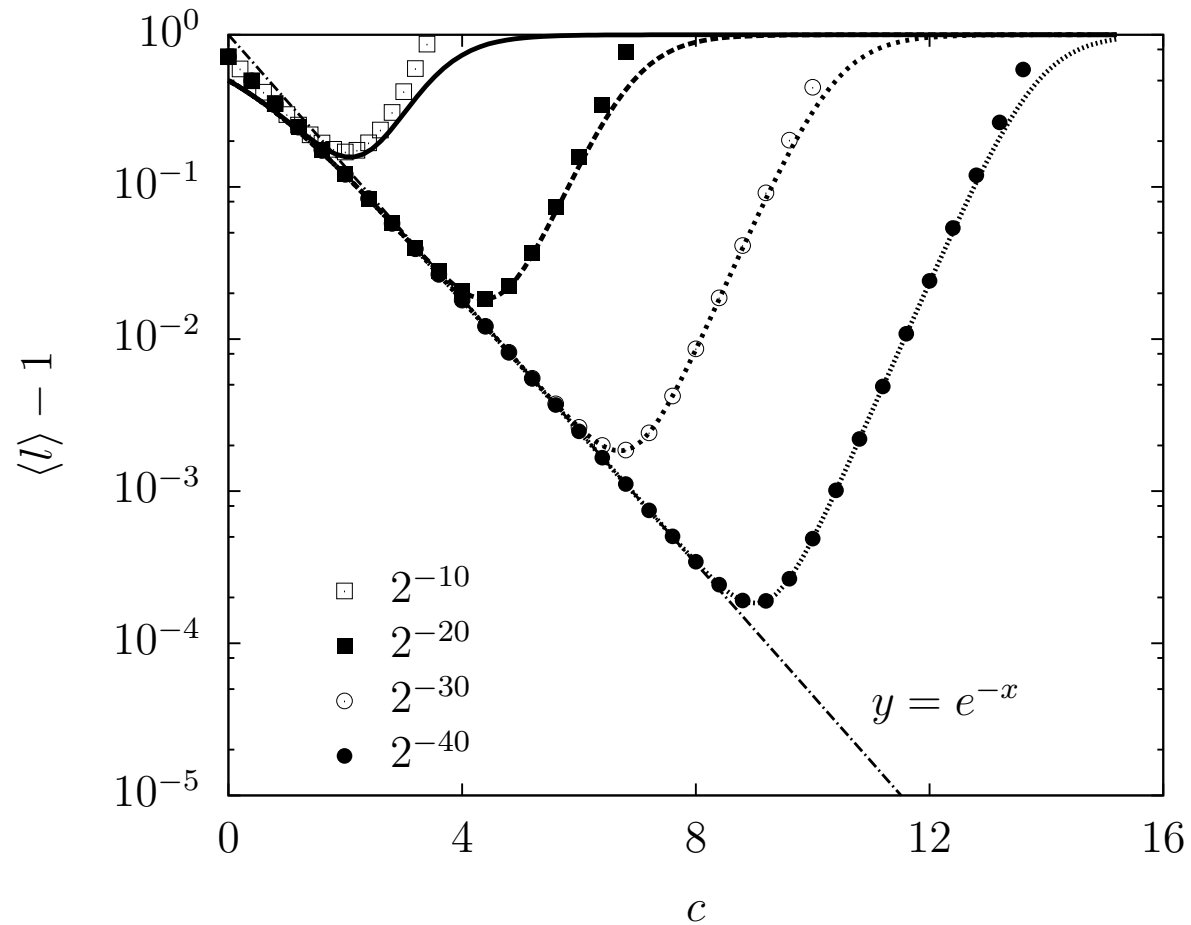
- If the walk starts at distance  $d = \alpha L$  from the reference sequence with  $\alpha < \frac{1}{2}$ , the walk length is nonmonotonic in  $c$  and reaches  $\ell \rightarrow 1$  for  $\alpha \rightarrow 0$

# Mean length of GAW's with Gumbel-distributed randomness



• upper bound:  $\ell = 1 + e^c$

# Minimum in GAW length with Gumbel-distributed randomness



- $\alpha = 2^{-10} \dots 2^{-40}$ , location of minimum varies as  $c_{\min} \sim \frac{1}{3} \ln(\alpha)$

# Summary

- Increasing number of empirical fitness landscapes provide insights into patterns of epistasis
- Existence of accessible pathways is not simply correlated to overall 'ruggedness' of the landscape:
  - In the **RMF model** pathways exist with unity probability for any  $c > 0$
  - In the **NK-model** accessibility vanishes asymptotically for  $L \rightarrow \infty$ , possibly at hyperastronomically large values of  $L$
- **Static** view focused on landscape structure is complemented by **dynamic** view of accessibility in term of adaptive walks

# Summary

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Arjan de Visser (Wageningen), Su-Chan Park (Seoul)