

Evocell 2012 meeting

workshop

nels elde & Harmit malik



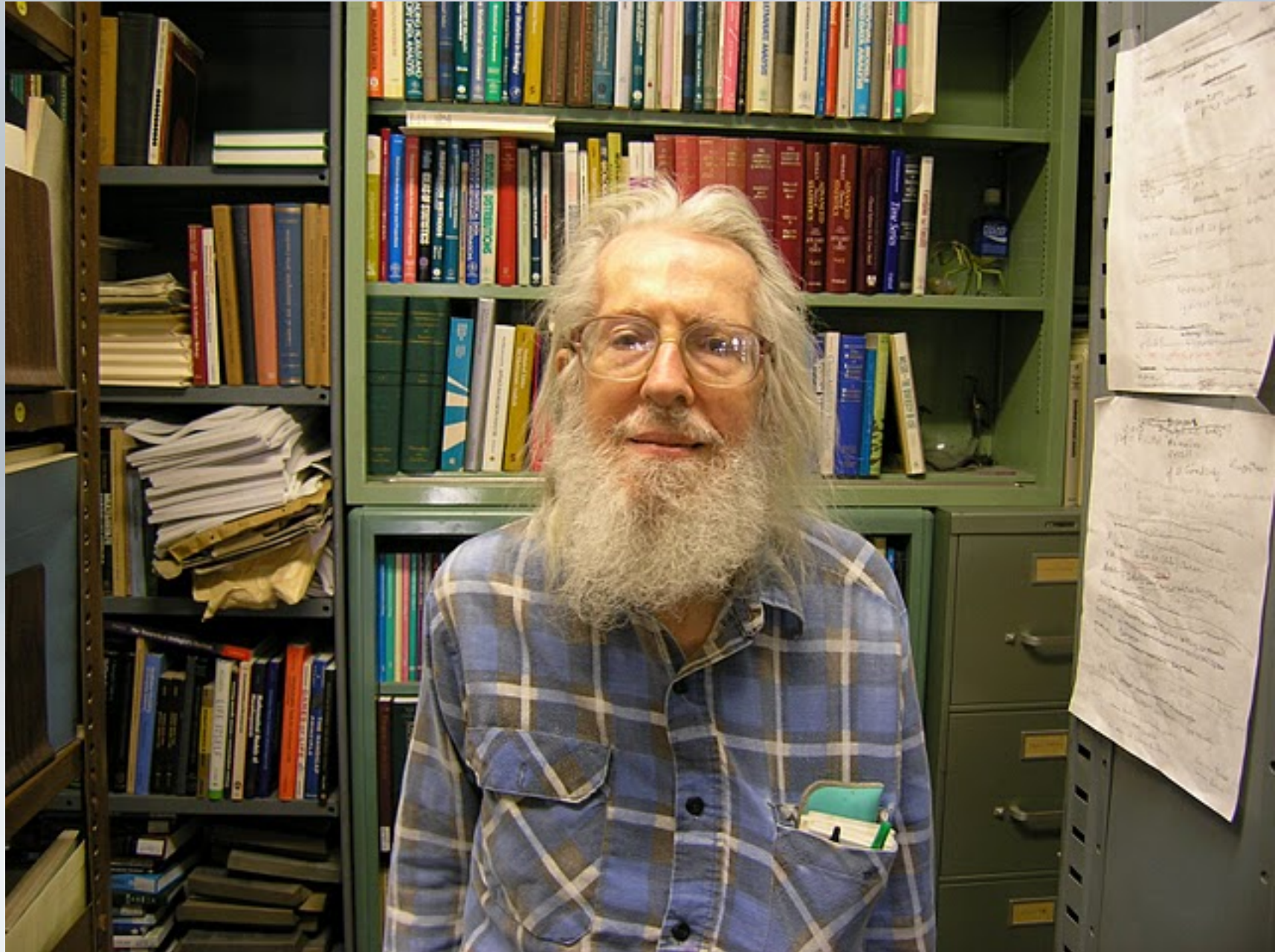
model



mimic



# leigh van valen



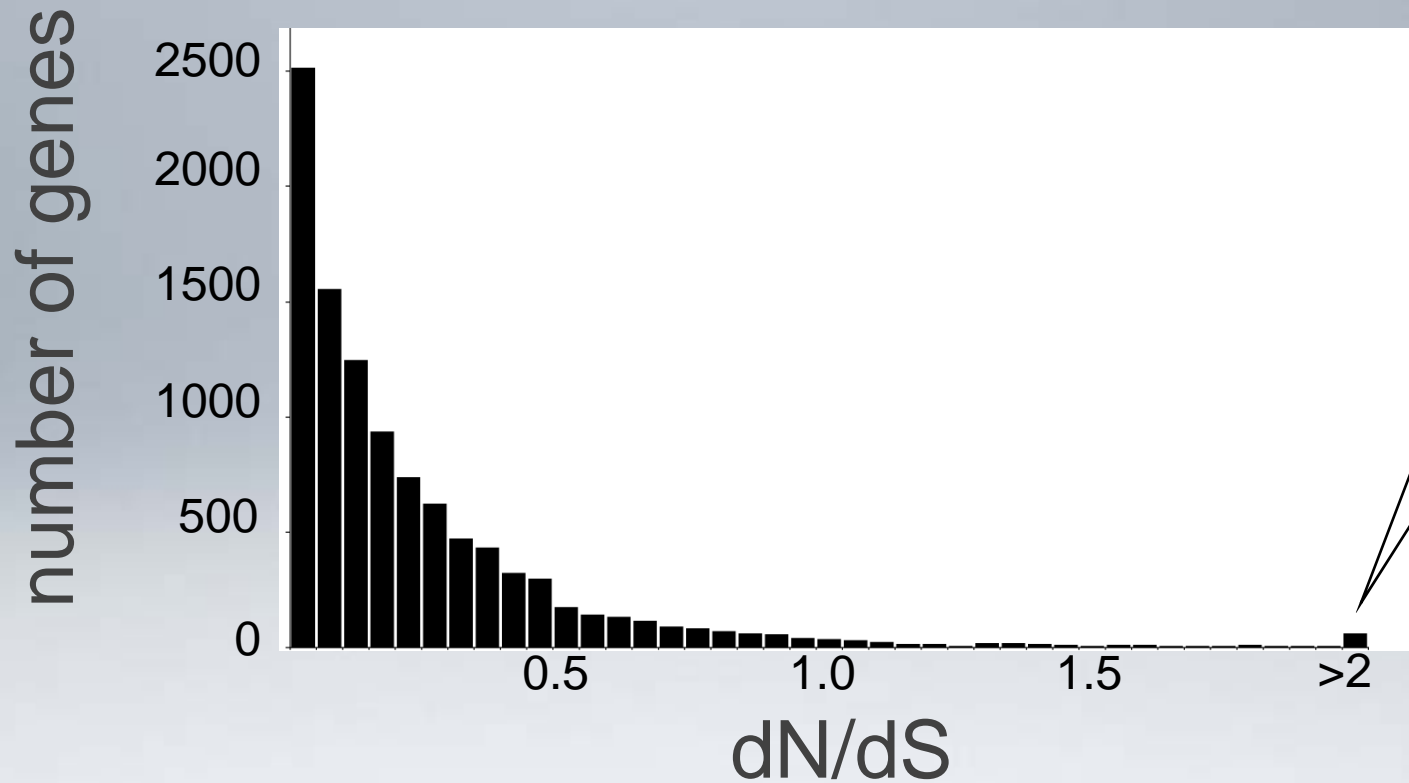
We can think of the Red Queen's Hypothesis in terms of an unorthodox game theory. To a good approximation, each species is part of a zero-sum game against other species. Which adversary is most important for a species may vary from time to time and for some or even most species no one adversary may ever be paramount. Furthermore, no species can ever win, and new adversaries grinningly replace the losers.

From this overlook we see dynamic equilibria on an immense scale, determining much of the course of evolution by their self-perpetuating fluctuations. This is a novel way of looking at the world, one with which I am not yet comfortable. But I have not yet found evidence against it, and it does make visible new paths and it may even approach reality.

does this apply to genes?



# genome-wide view of selection



purifying

— neutral — positive selection

genes in conflict

intergenomic conflicts

host v. pathogen

male v. female

mitochondria v. nucleus

intragenomic conflicts

retrotransposon v. genome

centromere v. chromosome







# PKR

Us11 (herpes virus)

NS1A (influenza)

E3L (poxvirus)

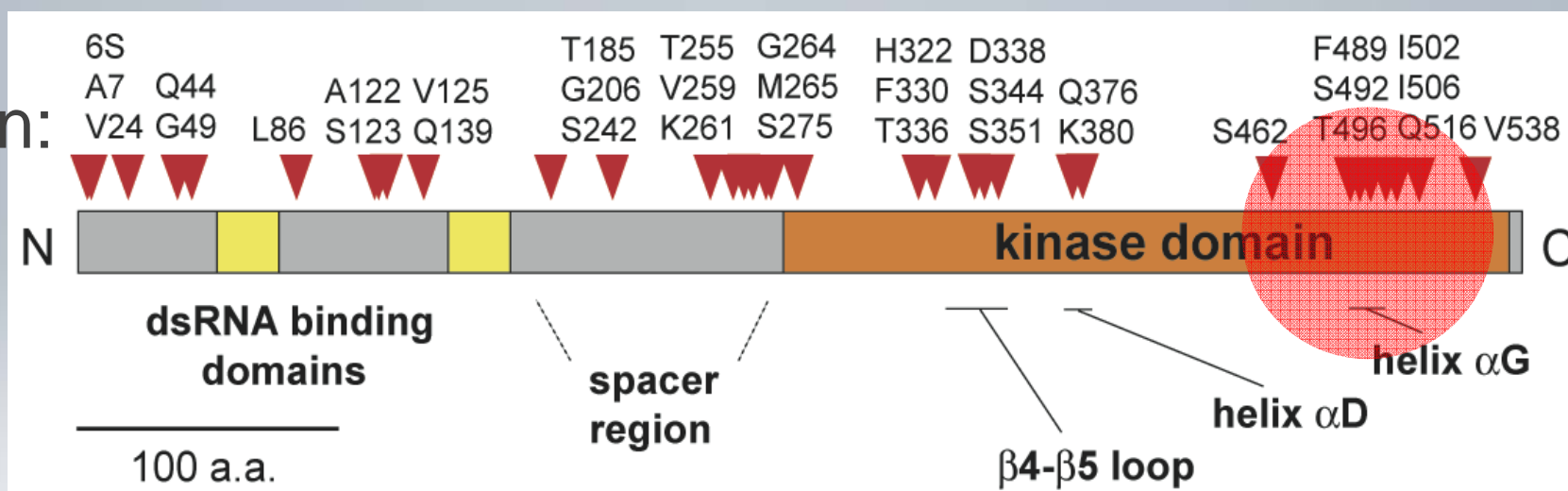
NS5A (HCV)

K3L & E3L

(poxvirus)

RelF2H (ranavirus)

under  
positive selection:



# THE (ART AND) SCIENCE OF SEQUENCE ALIGNMENT

CLUSTAL : [www.ebi.ac.uk/Tools/msa/clustalw2/](http://www.ebi.ac.uk/Tools/msa/clustalw2/)

MUSCLE (multiple sequence comparison by log expectation) : [www.ebi.ac.uk/Tools/msa/muscle/](http://www.ebi.ac.uk/Tools/msa/muscle/)

[L2NAL \(protein alignment to nucleotide alignment\)](http://www.bork.embl.de/pal2nal/)  
[www.bork.embl.de/pal2nal/](http://www.bork.embl.de/pal2nal/)

# SELECTION

PAML : PHYLOGENETIC ANALYSIS BY MAXIMUM  
LIKELIHOOD

ZIHENG YANG (UNIVERSITY COLLEGE LONDON)

[BACUS.GENE.UCL.AC.UK/SOFTWARE/PAML.HTML](http://BACUS.GENE.UCL.AC.UK/SOFTWARE/PAML.HTML)

“DATA MONKEY” : HY-PHY PACKAGE  
[DATAMONKEY.ORG](http://DATAMONKEY.ORG)



UCSD viral evolution group

Sergei Kosakovsky Pond  
Jason Young

Art Poon : UBC Vancouver

Simon Frost : Cambridge University



PARRIS : is their evidence of selection in your alignment?

GARD : has recombination acted in your sequence

GA-BRANCH : does selection vary along lineages

REL, FEL, SLAC : which codons are under selection

REL : random effects likelihood

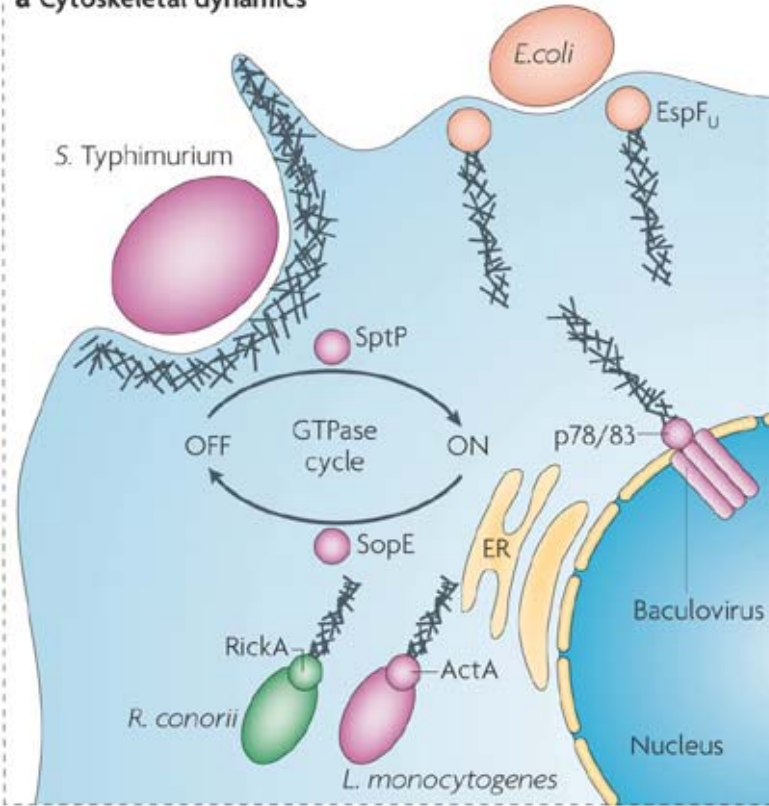
FEL : fixed effects likelihood

# datamonkey demo

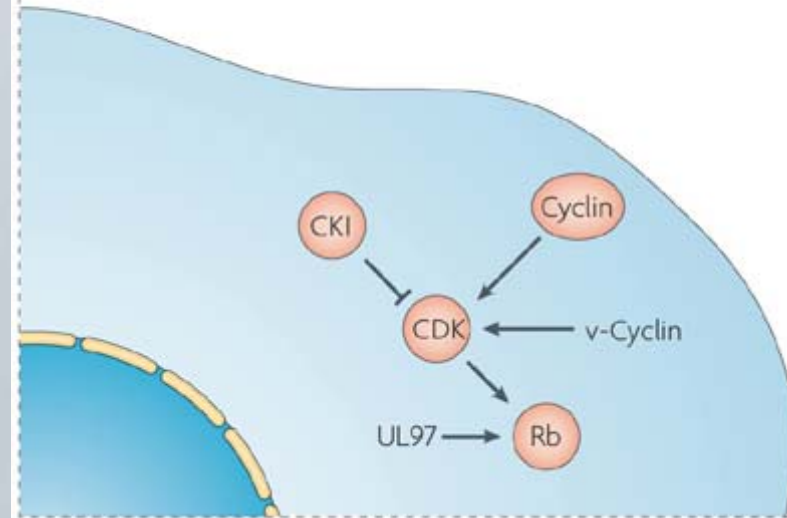
<http://hyphy.ucsd.edu/cgi-bin/Datamonkey2007/jobStatus.pl?file=upload.747341901319036.1>

# CELL

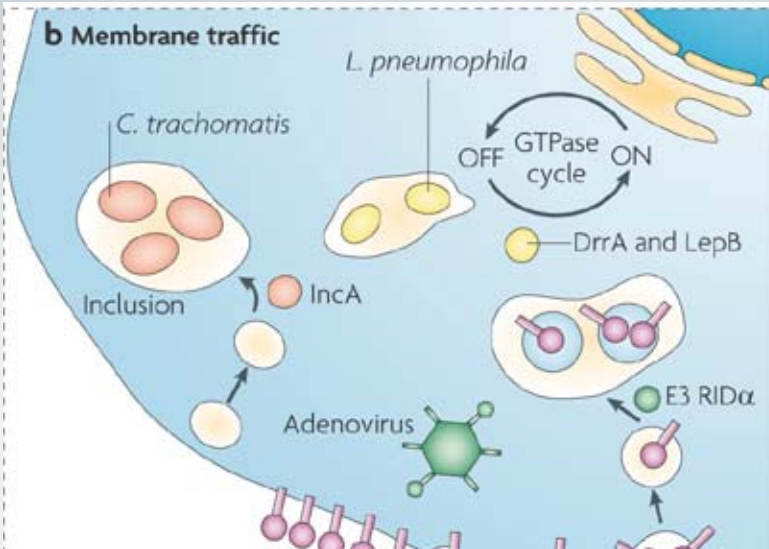
**a Cytoskeletal dynamics**



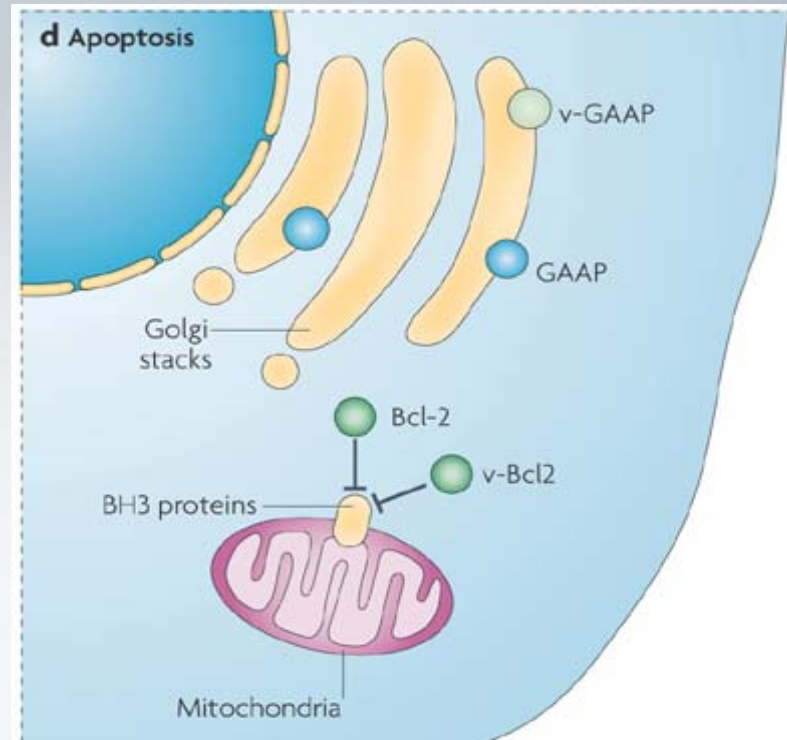
**c Cell cycle**



**b Membrane traffic**



**d Apoptosis**





# MIMICRY RINGS

## a Ecological mimicry ring

### Model



*Vespula vulgaris*  
(common wasp)

### Mimics



*Syrphus ribesii*  
(hoverfly)



*Clytus arietis*  
(wasp beetle)



*Sesia apiformis*  
(hornet moth)

## b Molecular mimicry ring

### Model

Eukaryotic host (WASP)



### Mimics

*Rickettsia conorii* (RickA)



Baculoviruses (p78/83)



*Listeria monocytogenes* (ActA)





model

mimic