

Optimal immune systems

Andreas Mayer (delivered by Aleksandra M Walczak)

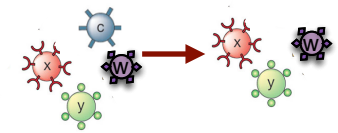
Laboratoire de Physique Théorique - ENS, CNRS



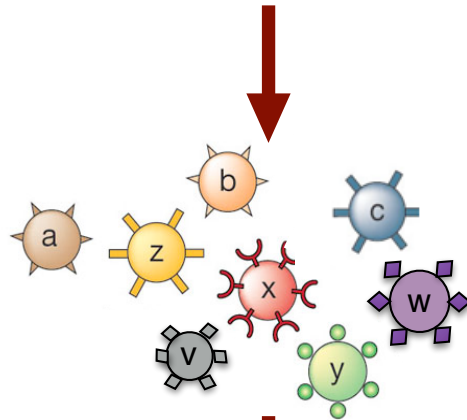
European Research Council
Established by the European Commission

work with
Andreas Mayer, ENS
Vijay Balasubramanian, UPenn
Olivier Rivoire, Grenoble
Thierry Mora, ENS

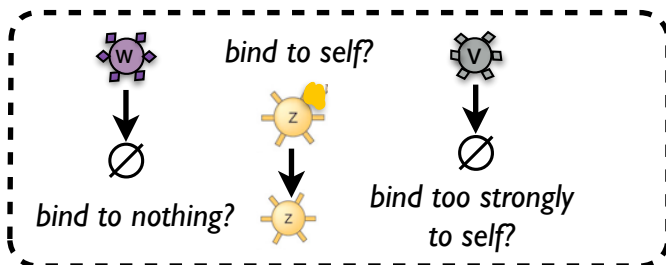
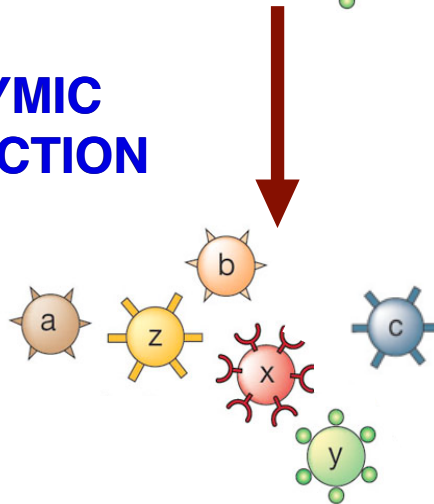
Receptor sharing



RECEPTOR GENERATION



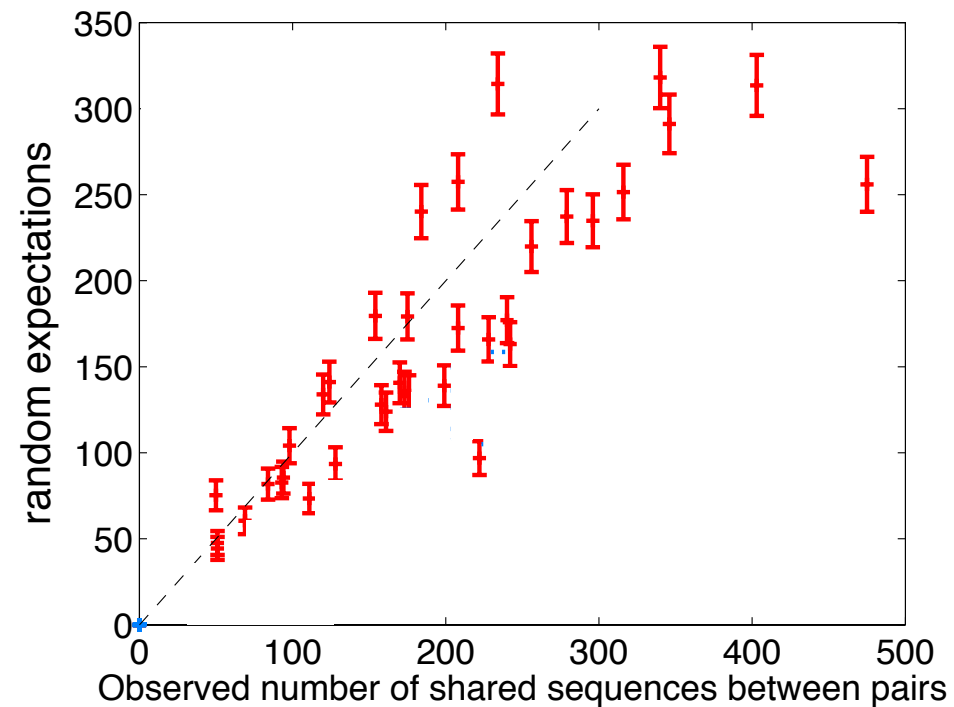
THYMIC SELECTION



- quantify using selection factors

$$Q(\{\sigma\}) = \frac{P_{\text{post-sel}}(\{\sigma\})}{P_{\text{gen}}(\{\sigma\})}$$

- how many shared receptors between 2 people?



→ close to random expectations

Receptor distributions



pathogens
(viruses, bacteria)

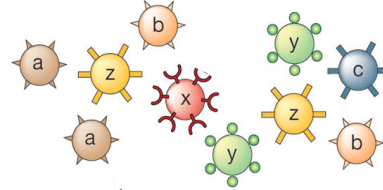
2010
FLU EUROPE
FLU ASIA
COLD 2011

HSV 2011
B19 2011

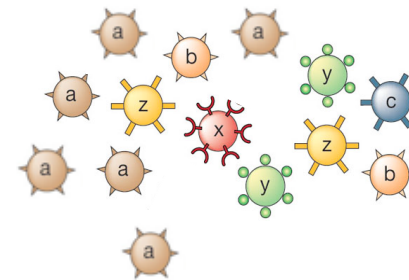
FLU 2011
EUROPE
FLU 2012
ASIA

FLU 2012
EUROPE
B19 2012
COLD 2012

receptor
statistics

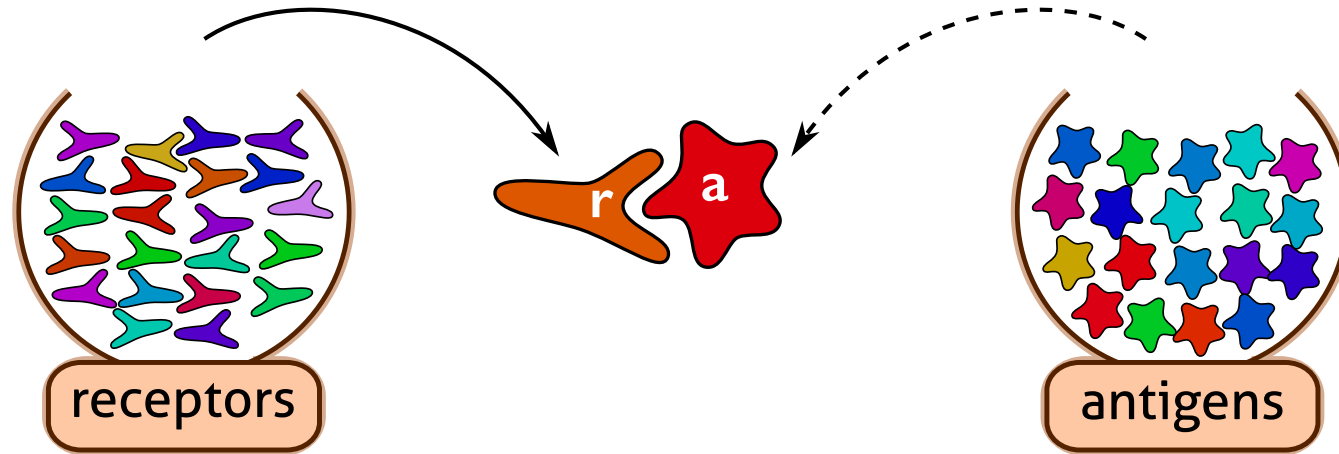


OR



optimal distribution ?

The trade-off



limited number of encounters

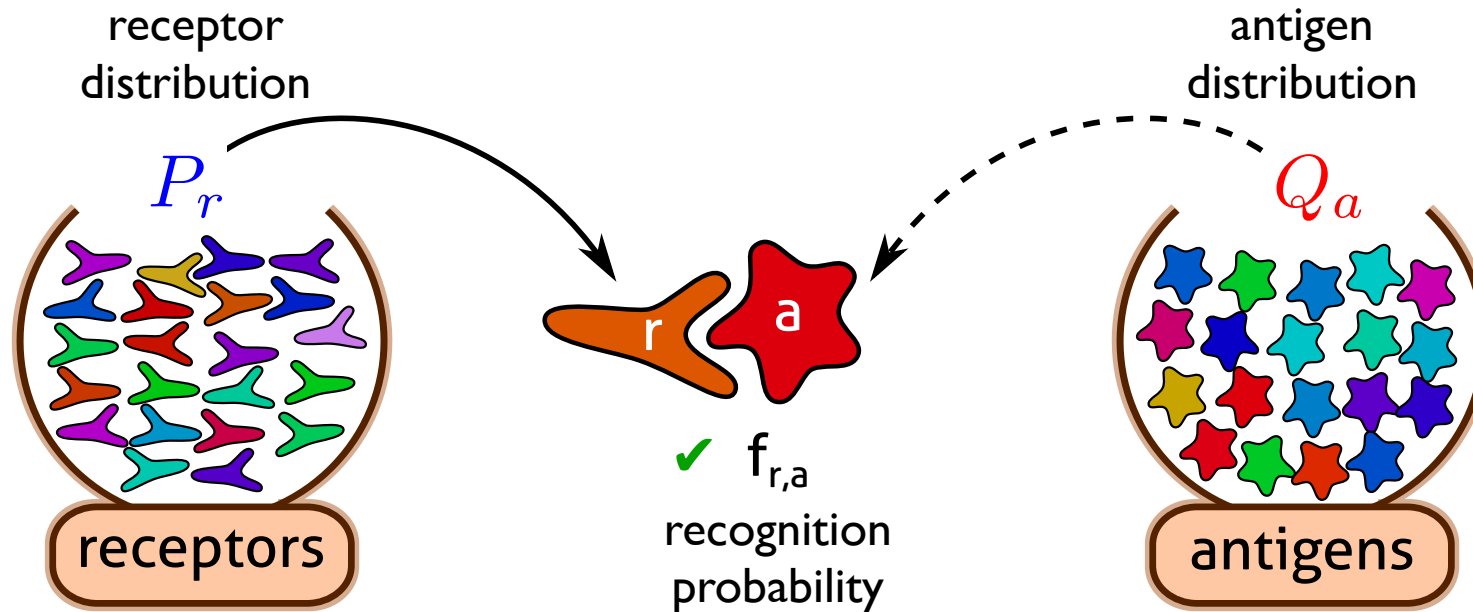
**How should immune receptors be distributed
to minimize harm from infections?**

lymphocyte
repertoire



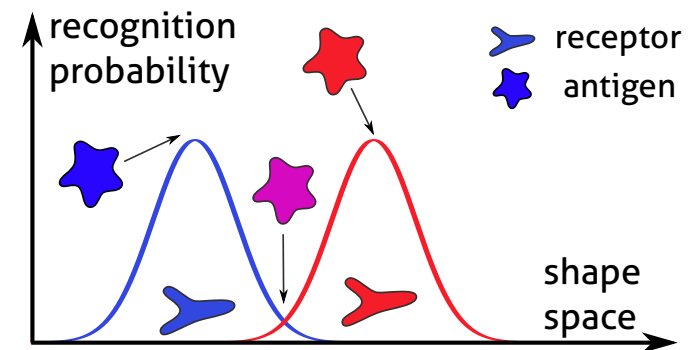
antigenic
environment

Cross-reactivity

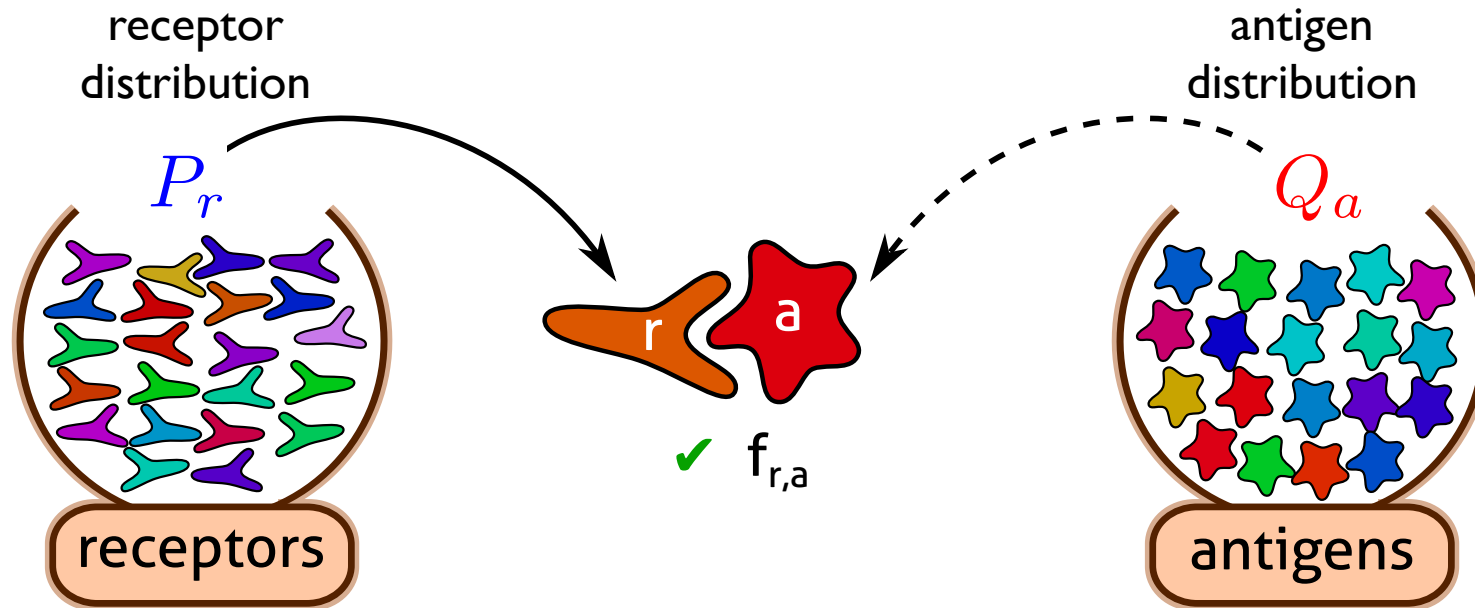


- cross-reactivity - recognition probability
- probability of immune response from encounter with a given antigen

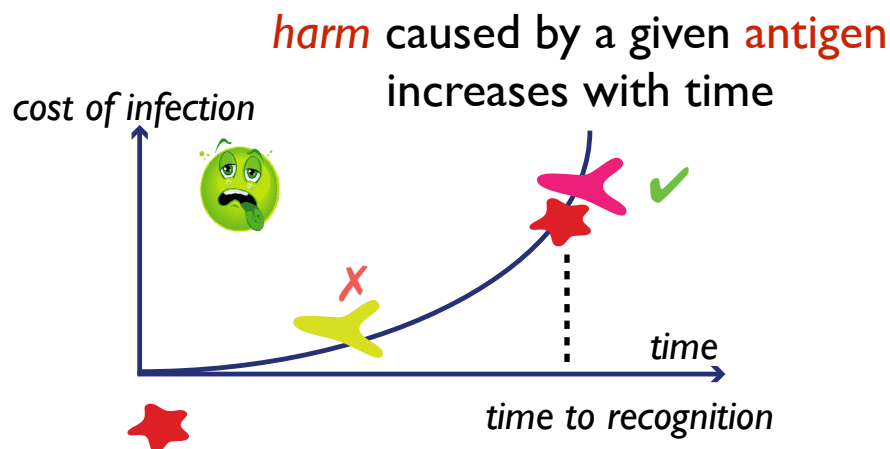
$$\tilde{P}_a = \sum_r f_{r,a} P_r$$



Receptors - antigens interactions



- probability of immune response from encounter with a given antigen $\tilde{P}_a = \sum_r f_{r,a} P_r$
- time measured in mean number of encounters m



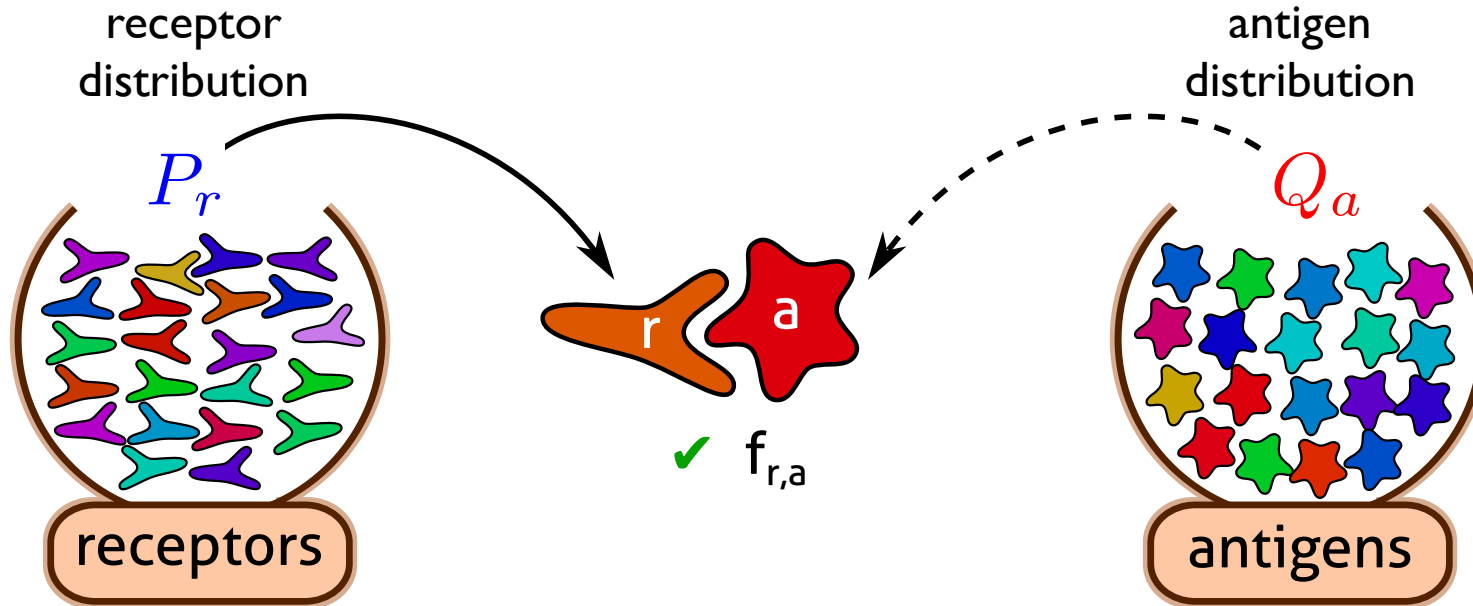
$$\bar{F}_a(P_r) = \mu_a \int_0^{+\infty} dm F_a(m) \tilde{P}_a e^{-m \tilde{P}_a}$$

virulence \downarrow effective cost of infection \downarrow

Poisson distributed recognition \uparrow

$$\text{Cost}(\{P_r\}) = \sum_a Q_a \bar{F}_a(P_r)$$

Cost

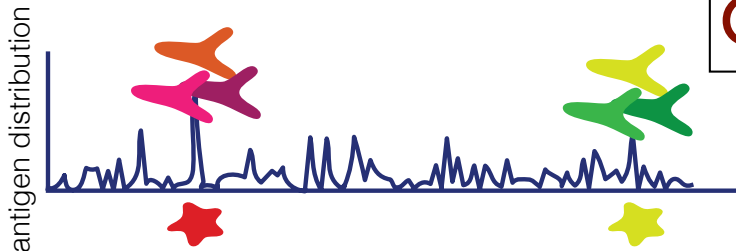


total harm caused by antigen increases with time

$$\text{Cost}(\{P_r\}) = \sum_a Q_a \bar{F}_a(P_r)$$

trade-off: many antigens \leftrightarrow limited resources

Optimal repertoire?



→ minimize cost given fixed antigen distribution

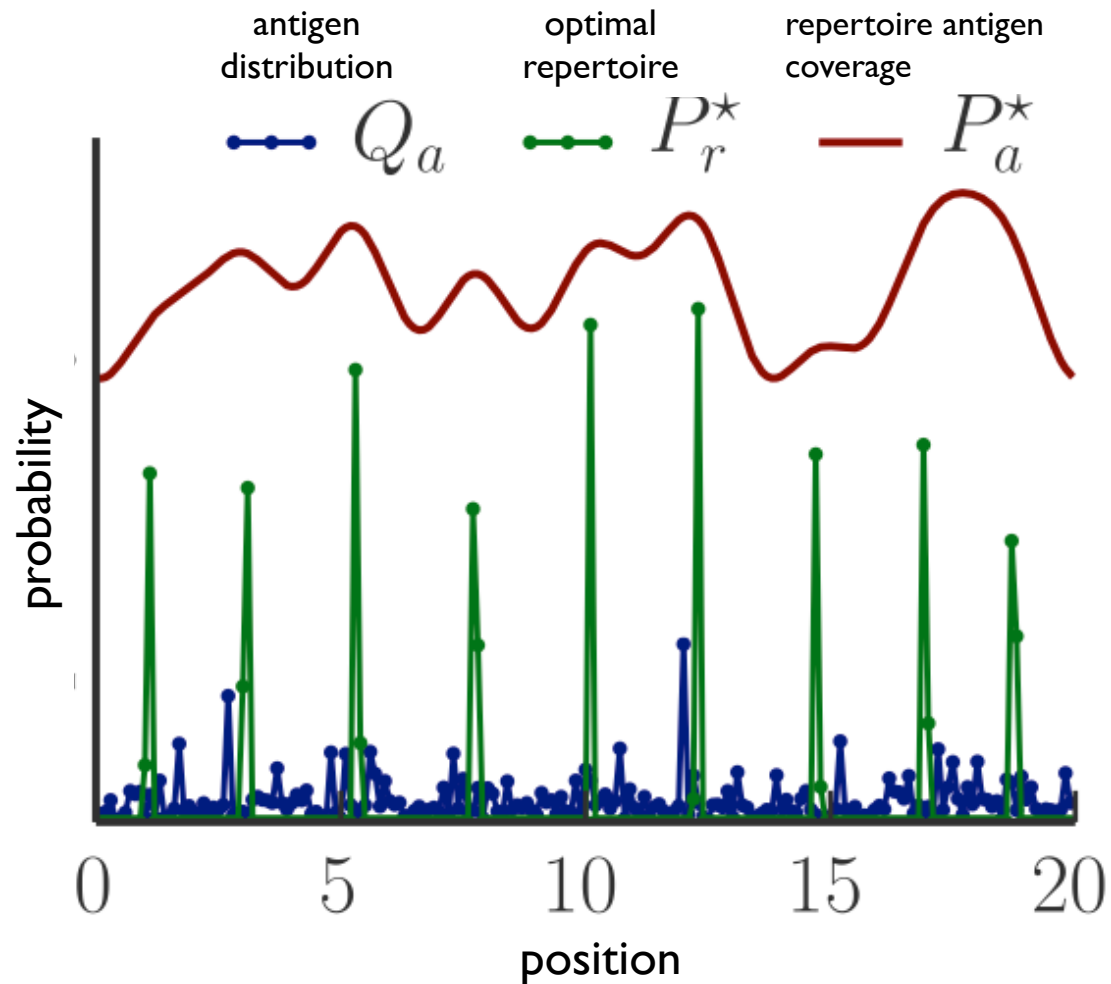
Peaked optimal repertoires



- exponentially expanding antigen population + exponentially growing cost in time $F(m) = m$

- peaked distributions
- tile space

- coverage follows antigen distribution
- but not exactly



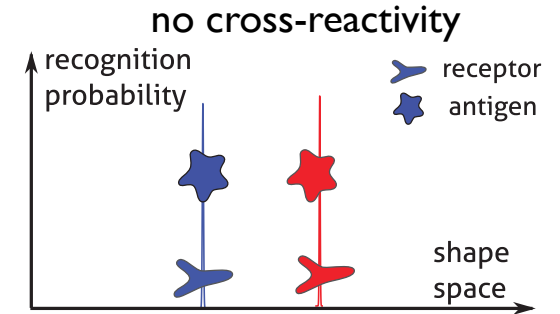
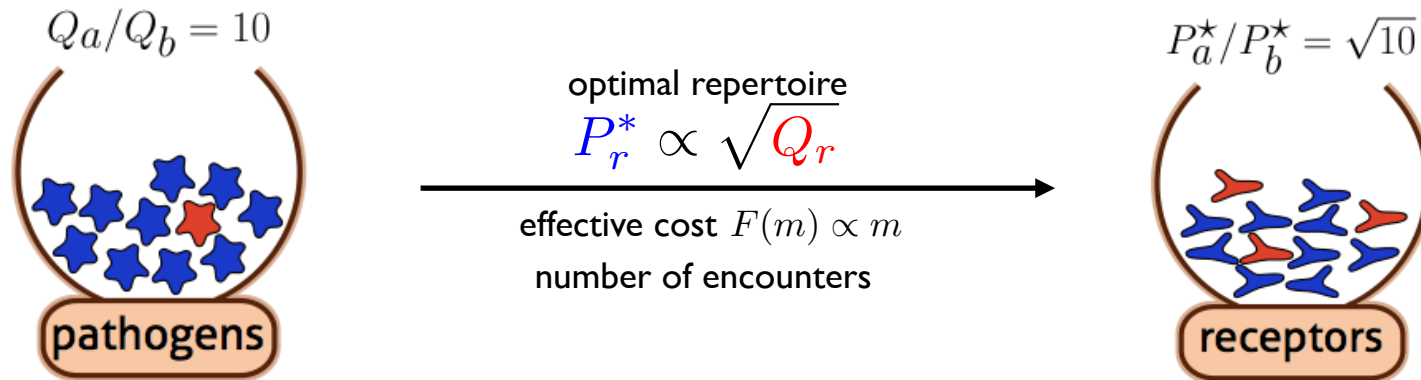
Covering rare pathogens



How many resources aimed at common/rare antigen?

depends on cost of late recognition → effective cost function

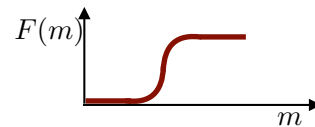
- exponentially expanding antigen population



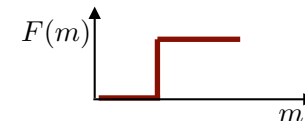
- exponentially expanding antigen population + exponentially growing cost in time

$$F(m) = m^\alpha \quad \rightarrow \quad P_r^* \propto Q_r^{1/(1+\alpha)}$$

- saturated cost → low frequency cut-off

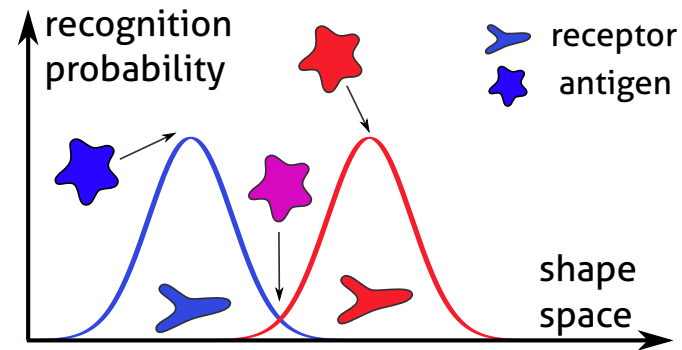


- harm past threshold → flattened receptor distribution

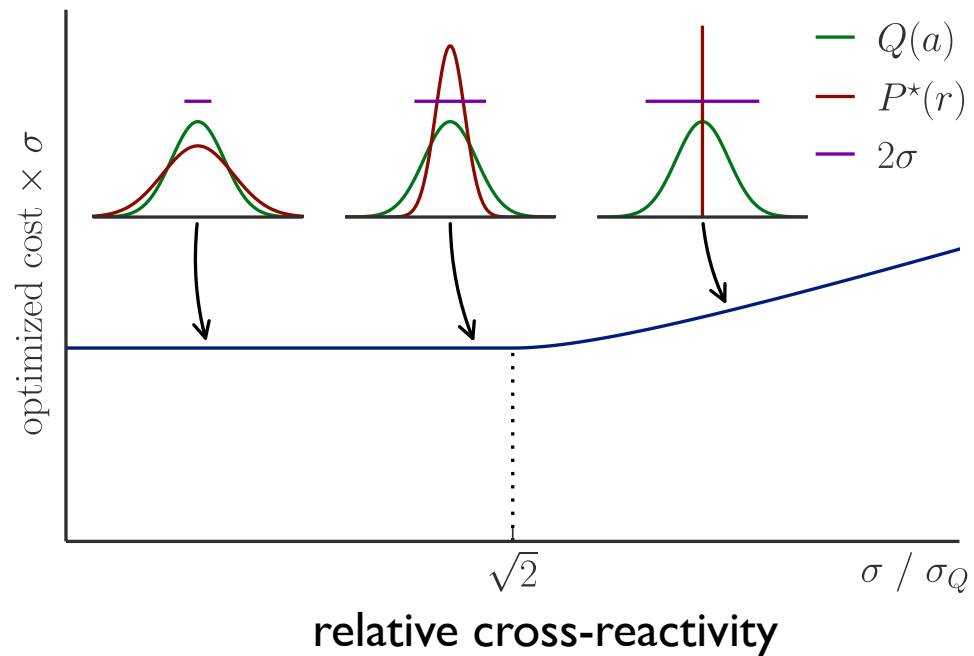


- $P_r^* \propto Q_r \Leftrightarrow$ very slowly increasing cost $F(m) \propto \ln m$

Cross-reactivity

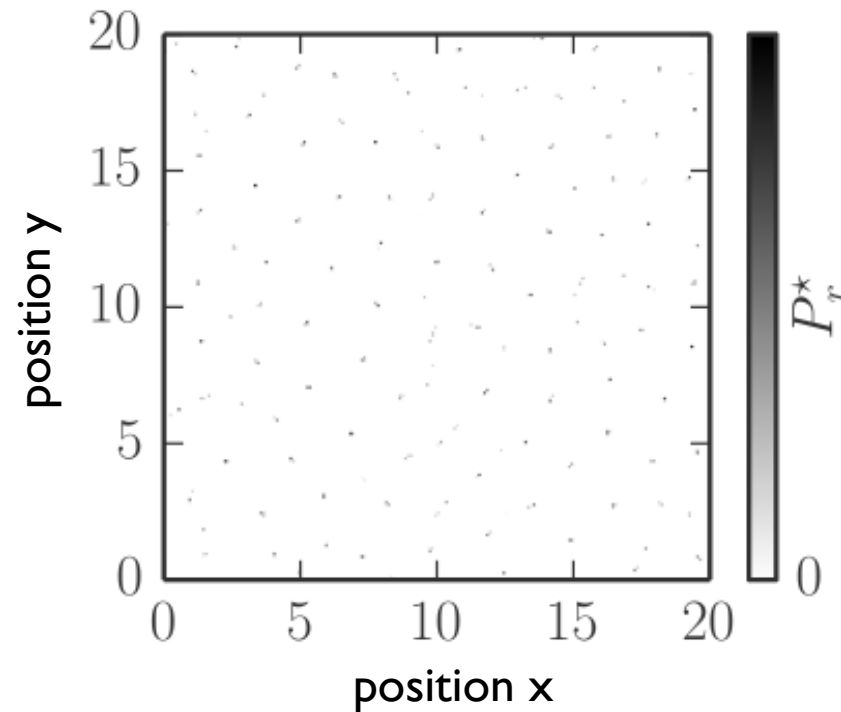
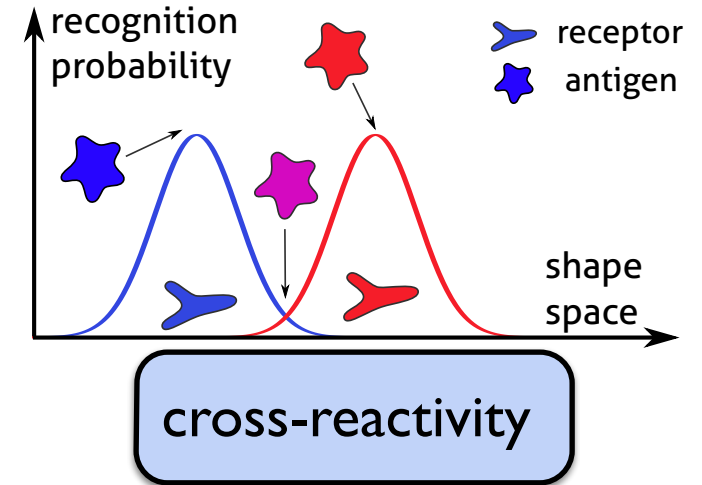
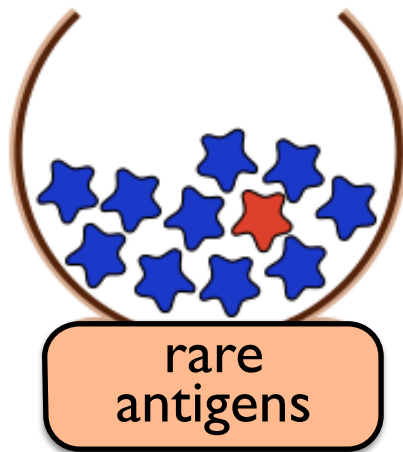


- antigen distribution + cross-reactivity Gaussian



→ large cross-reactivity concentrates distribution

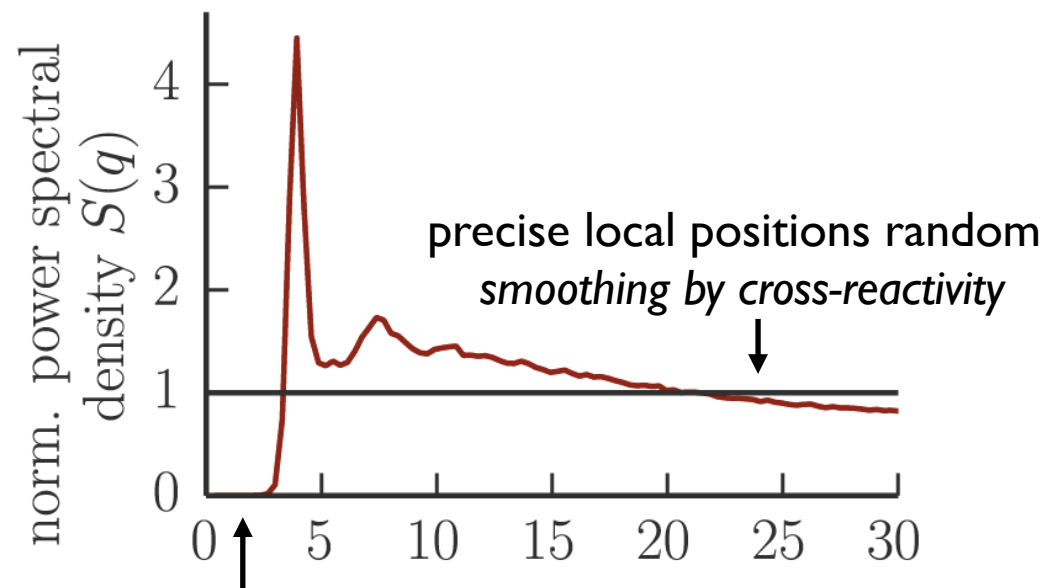
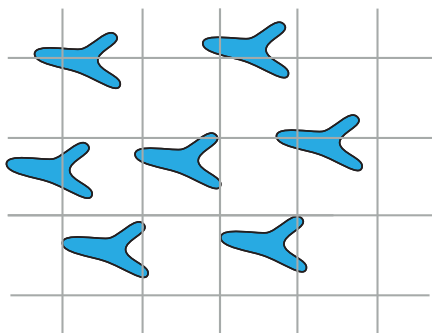
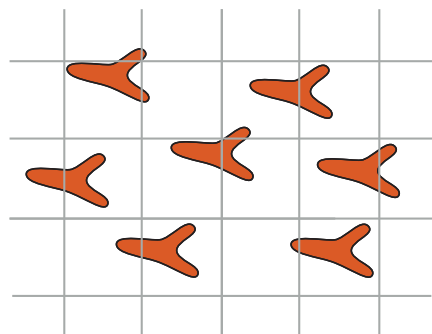
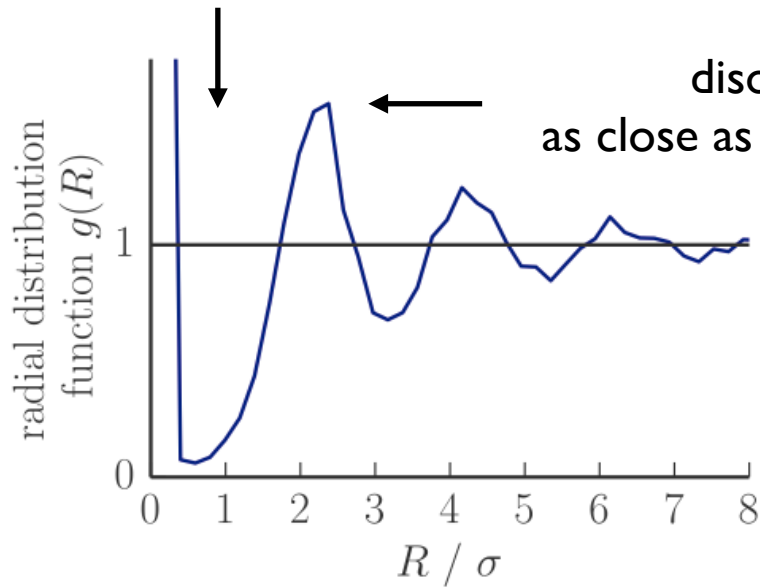
Peaked optimal repertoires



Disordered hyperuniformity



receptors cannot be close to each other

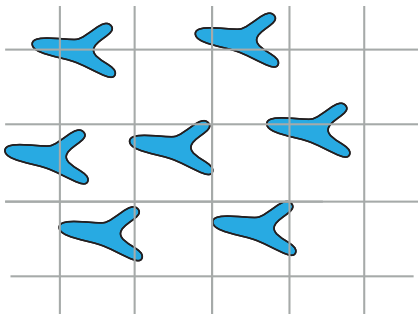
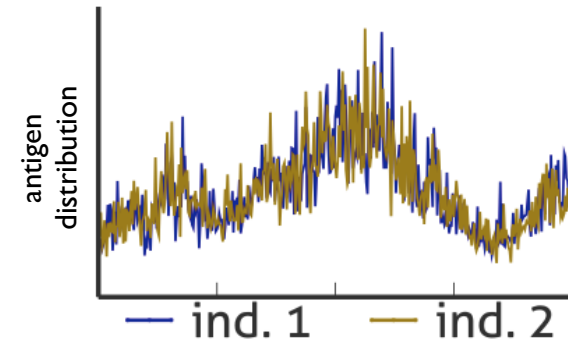


reproducible number of receptors in large space
tracking of antigen

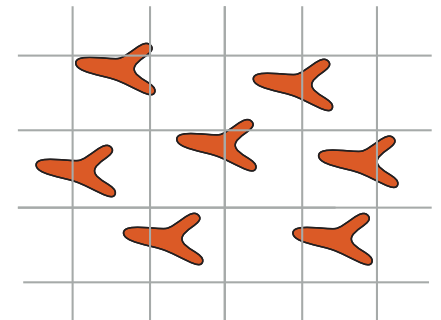
Personalized responses



two individuals see the environment slightly differently



→ very different repertoires



Self-organized dynamics

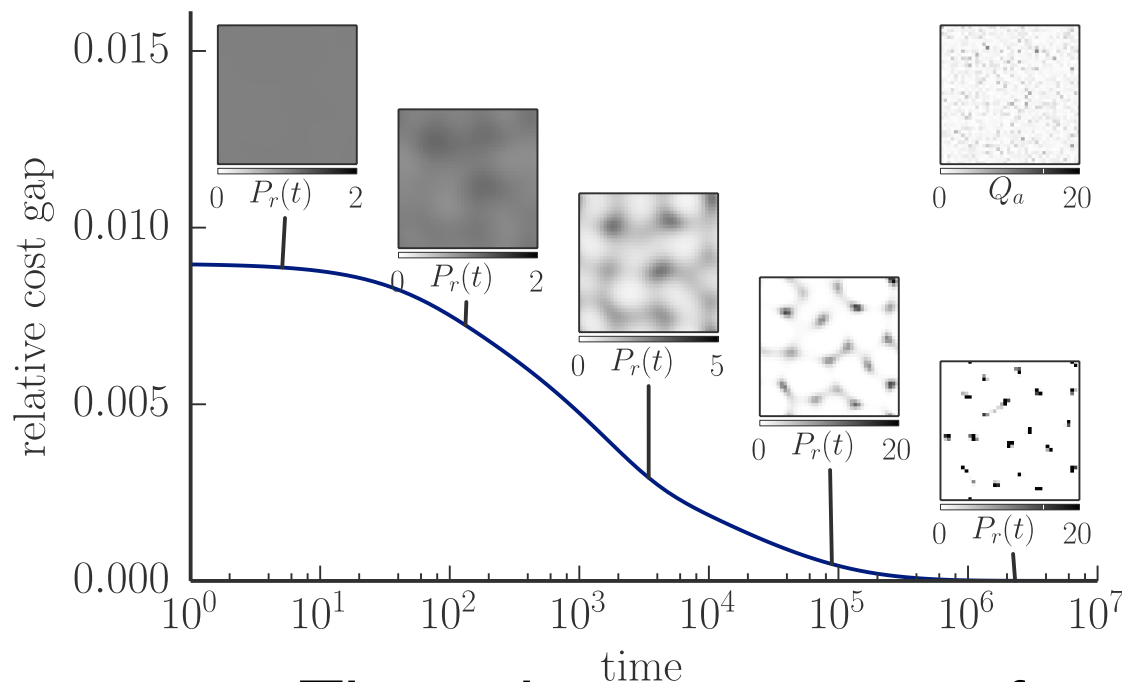
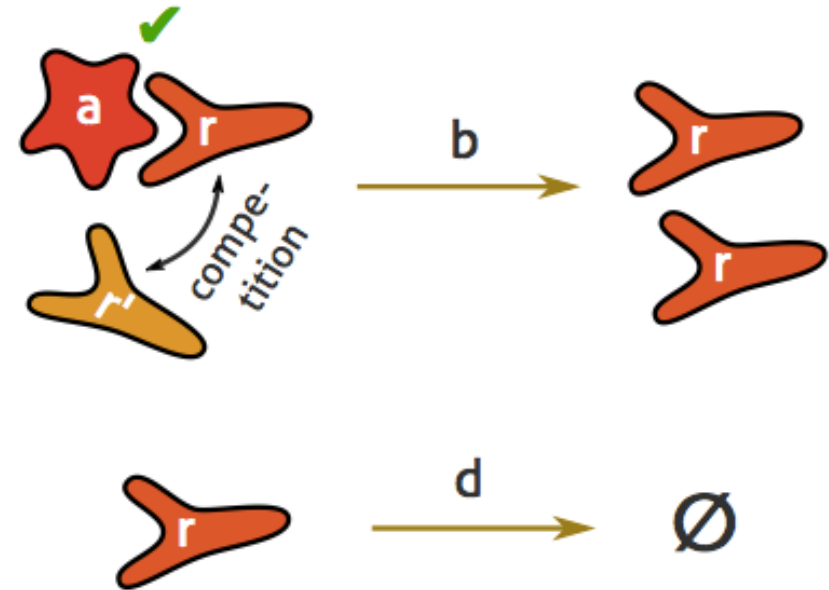


Can optimal repertoires be reached via dynamics?

$$\dot{N}_r = N_r \left[b \sum_p Q_p f_{r,a} A \left(\sum_{r'} N_{r'} f_{r',a} \right) - d \right]$$

population size \nearrow N_r
 proliferation rate \nearrow b
 detectable pathogen \nearrow $\sum_p Q_p f_{r,a}$
 availability of pathogen \rightarrow reduced by competition \nearrow $A \left(\sum_{r'} N_{r'} f_{r',a} \right)$
 death rate \nearrow d

e.g. $A(\tilde{N}_a) = \frac{1}{(1+\tilde{N}_a)^2}$



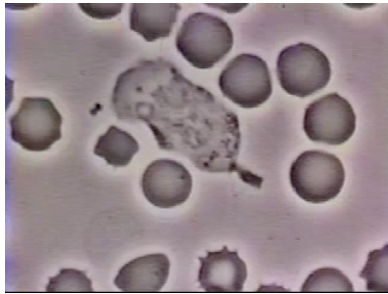
→ Through competition of receptors for antigen

Different immune strategies



adaptive immunity

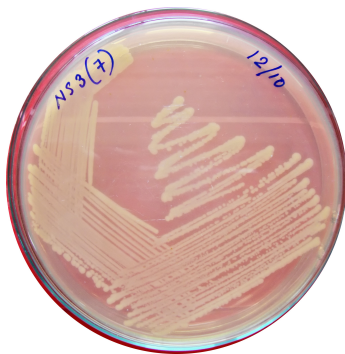
Other immune strategies



innate immunity

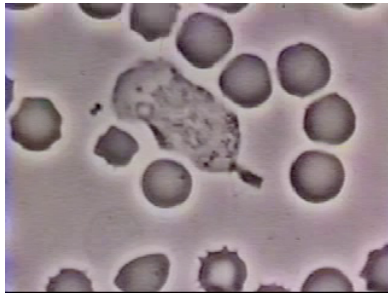


adaptive immunity



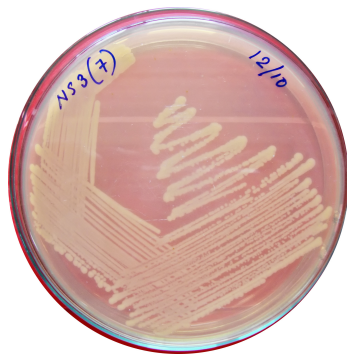
CRISPR immunity

Common strategic choices



innate immunity

heritable



CRISPR immunity

randomly acquired

regulated

adaptive immunity

non-heritable

Processing information about the environment on **evolutionary** timescales

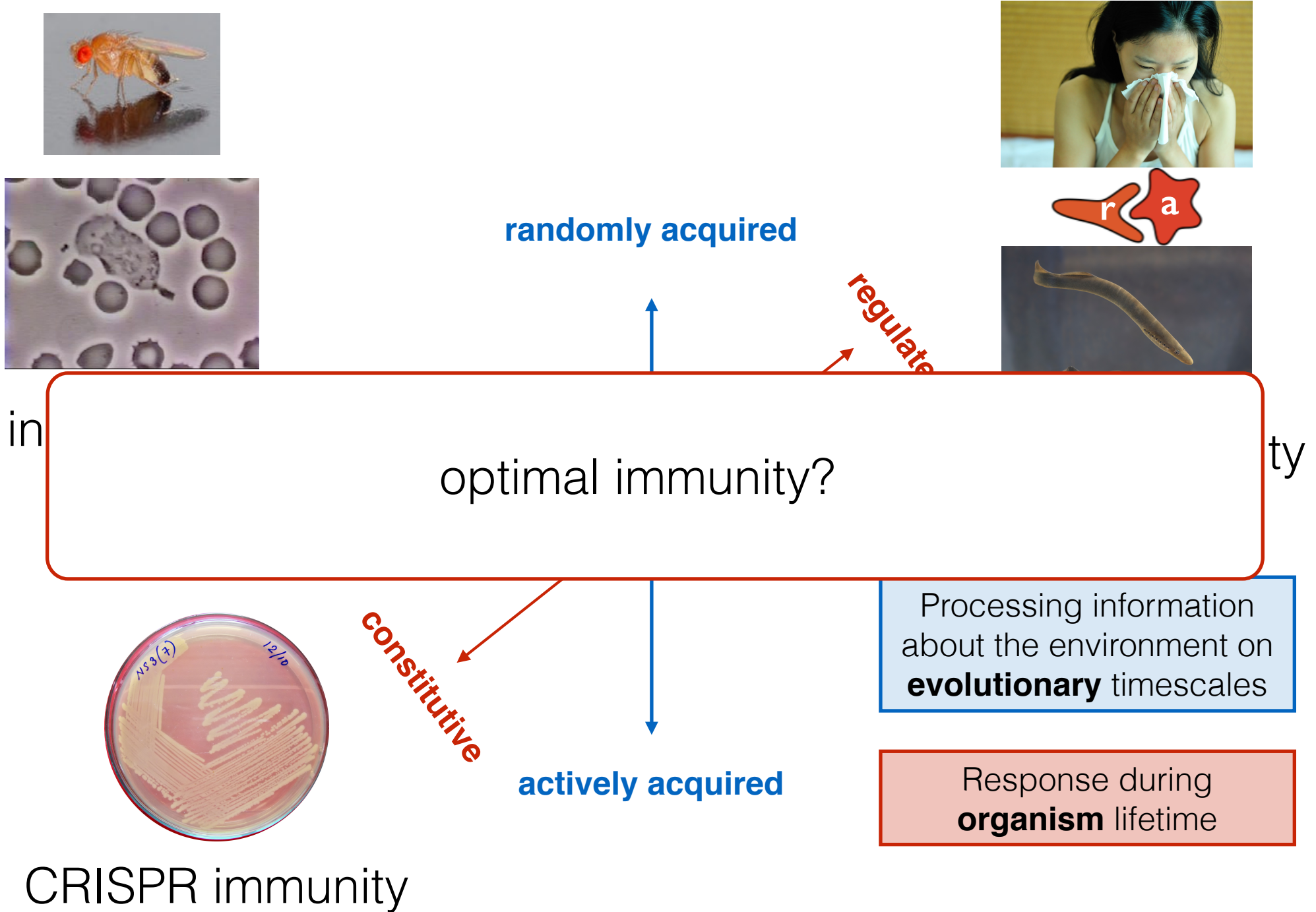
Response during **organism** lifetime



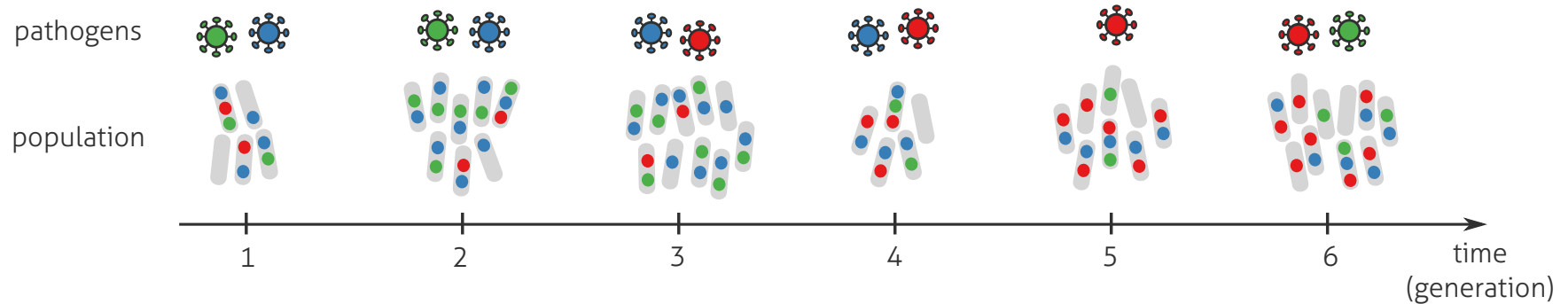
constitutive

actively acquired

Common strategic choices



Optimal immunity

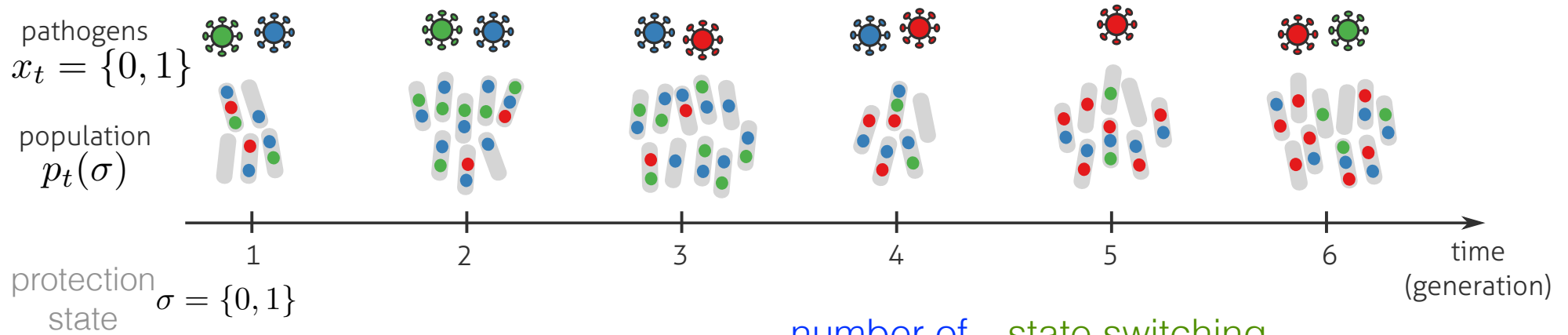


- match environment statistics
- ensure long term population growth

→ immunity as adaptation to pathogen statistics

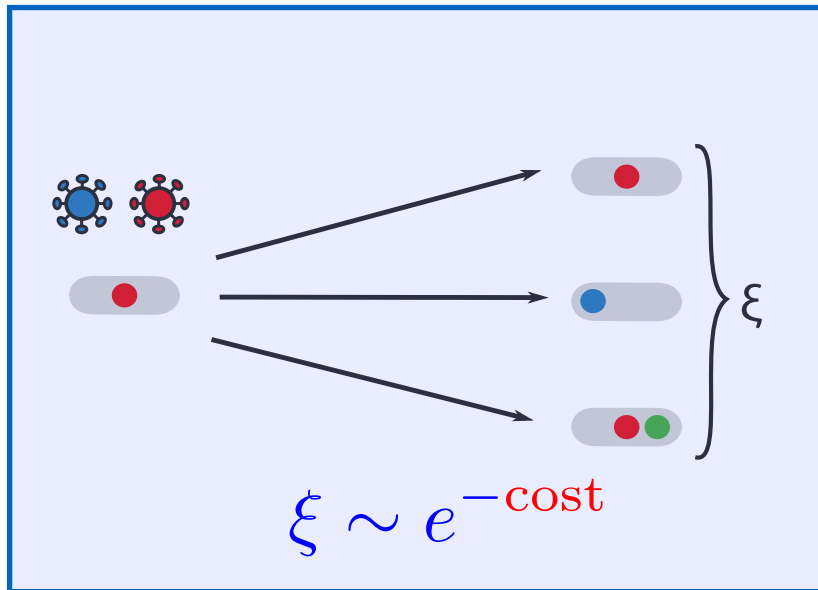
- consider different strategies
- optimize long term population growth

Population growth

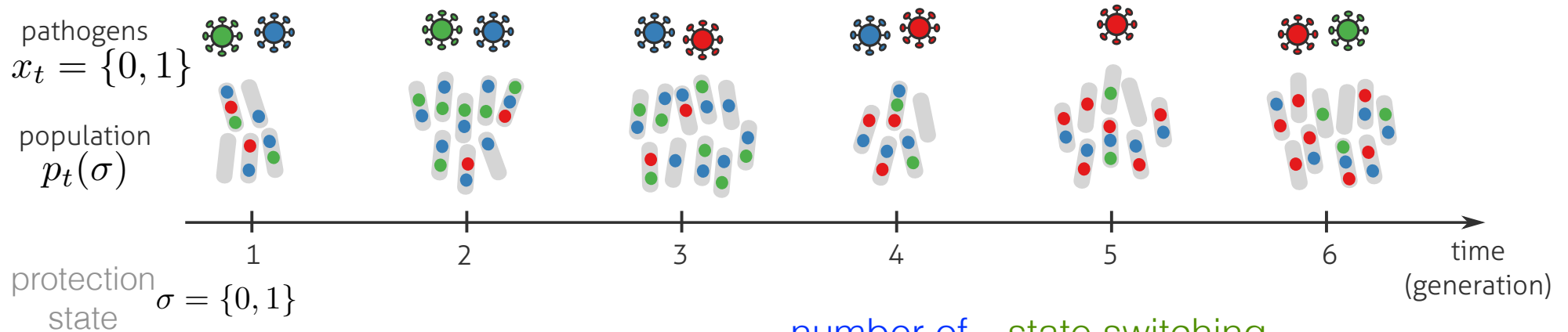


$$p_{t+1}(\sigma) = \frac{1}{Z_t} \sum_{\sigma'} \xi(\sigma', x_t) \pi(\sigma | \sigma', x_t) p_t(\sigma')$$

number of offspring $\xi(\sigma', x_t)$
state switching probability $\pi(\sigma | \sigma', x_t)$



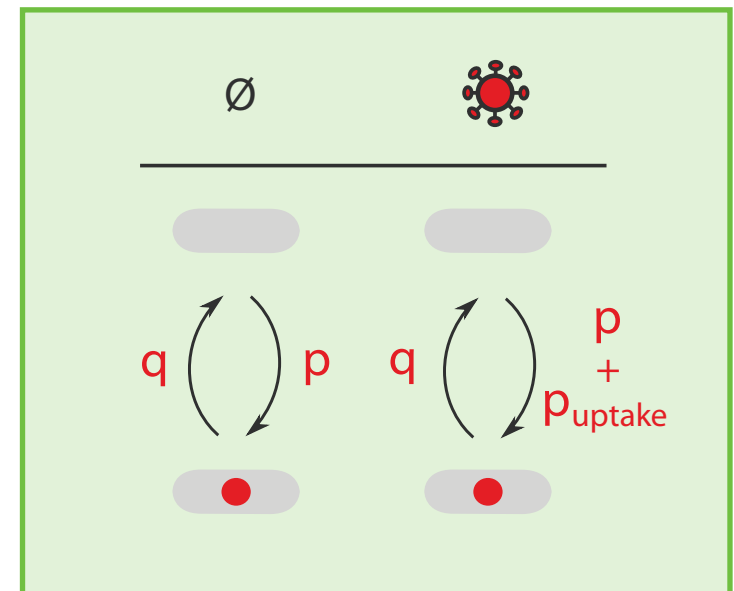
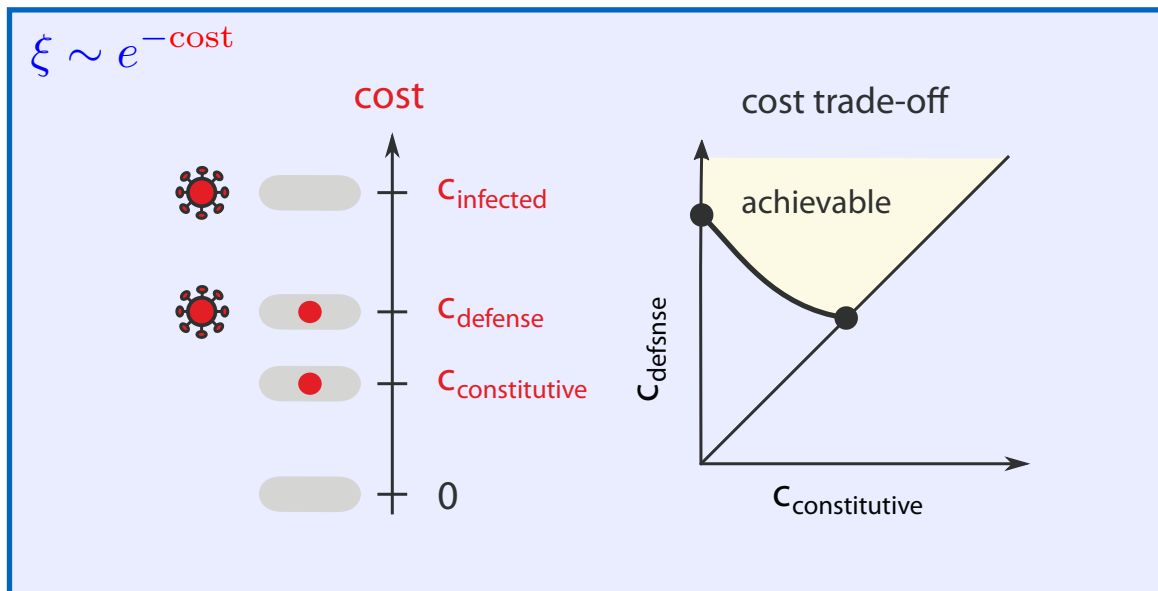
Population growth



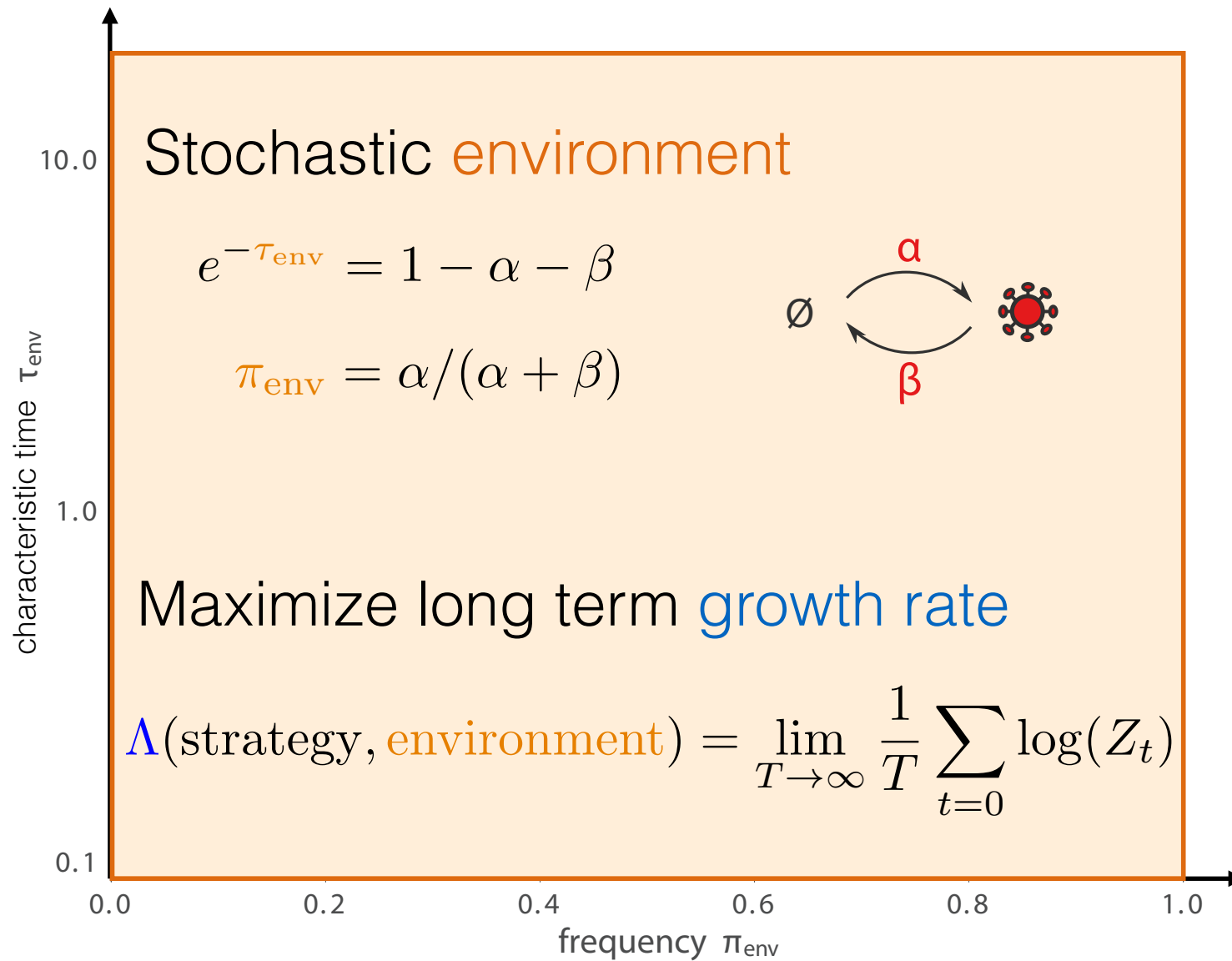
$$p_{t+1}(\sigma) = \frac{1}{Z_t} \sum_{\sigma'} \xi(\sigma', x_t) \pi(\sigma | \sigma', x_t) p_t(\sigma')$$

number of offspring $\xi(\sigma', x_t)$

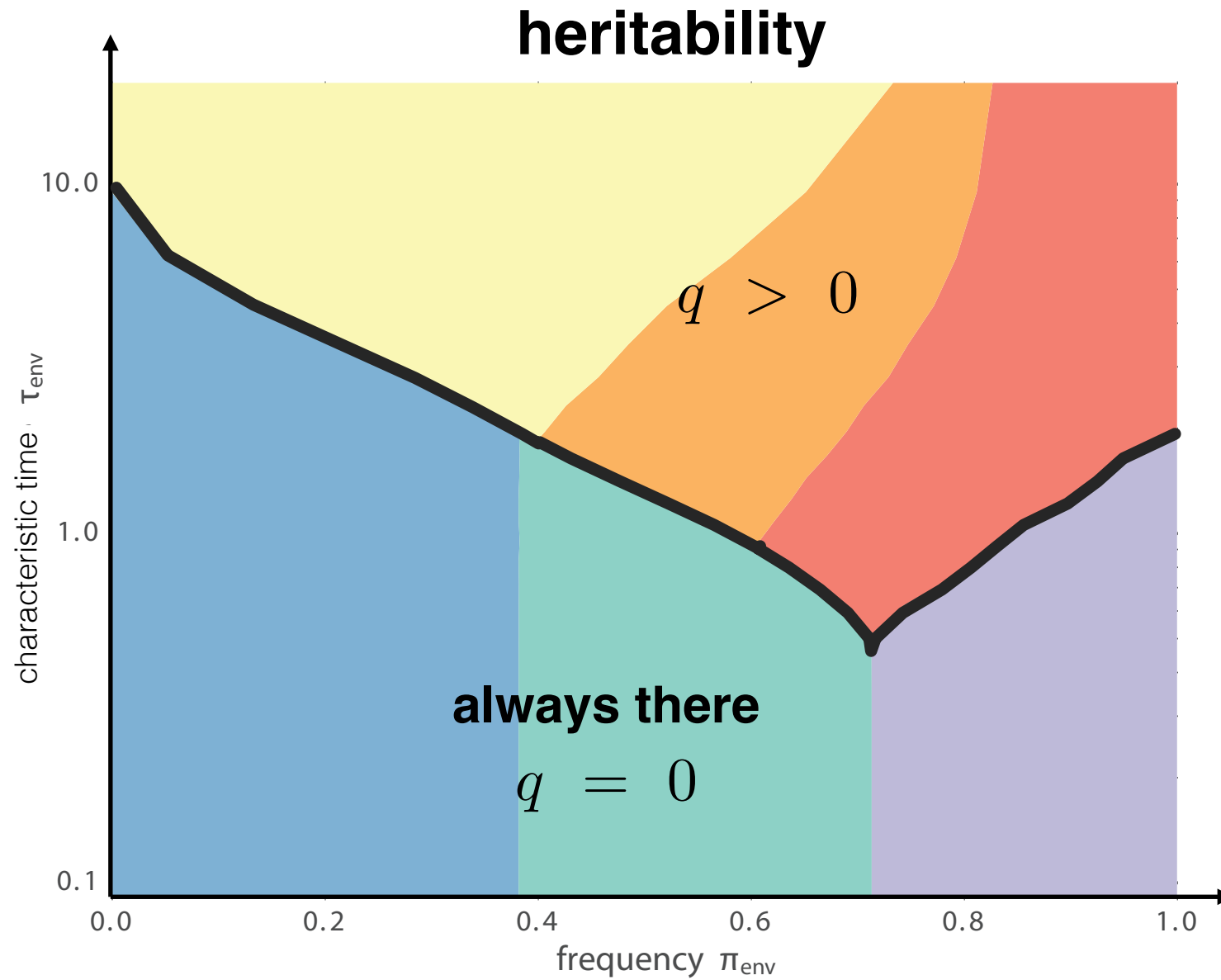
state switching probability $\pi(\sigma | \sigma', x_t)$



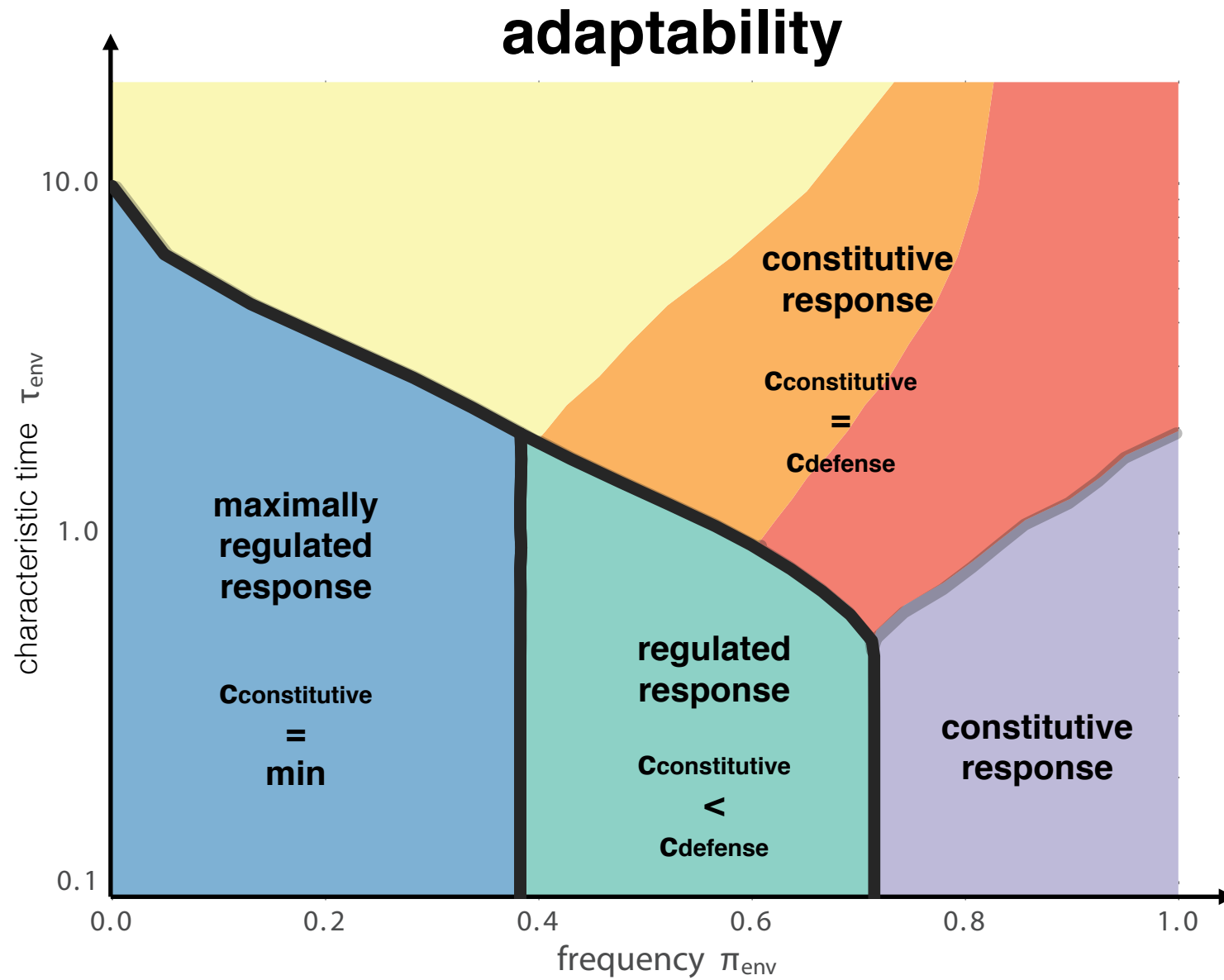
The environment



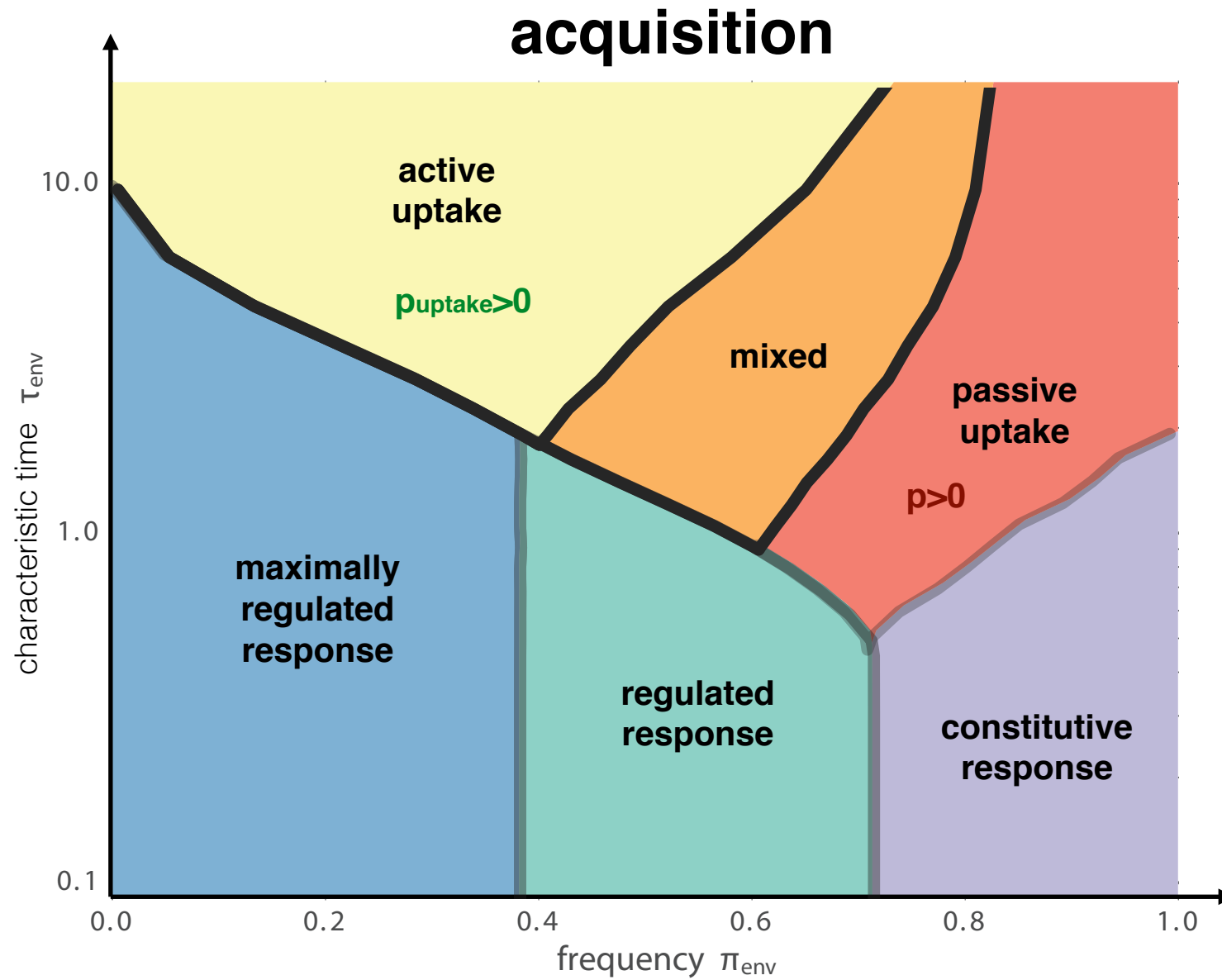
Optimal strategies



Optimal strategies

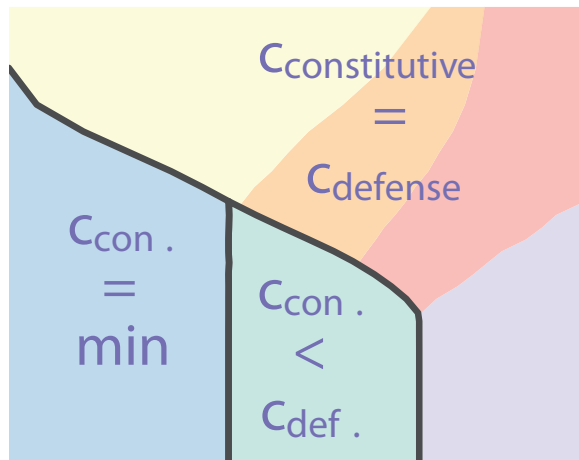


Optimal strategies

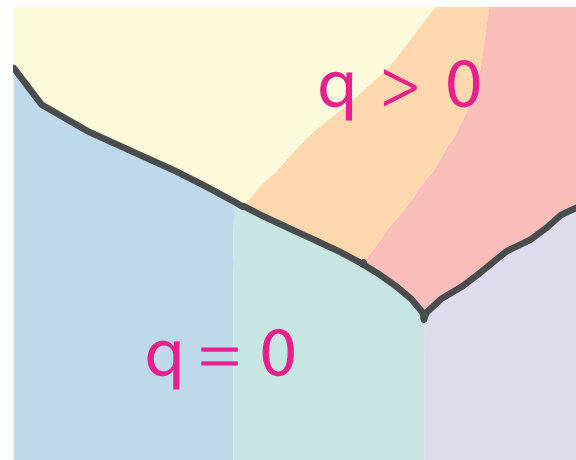


Three strategy axes

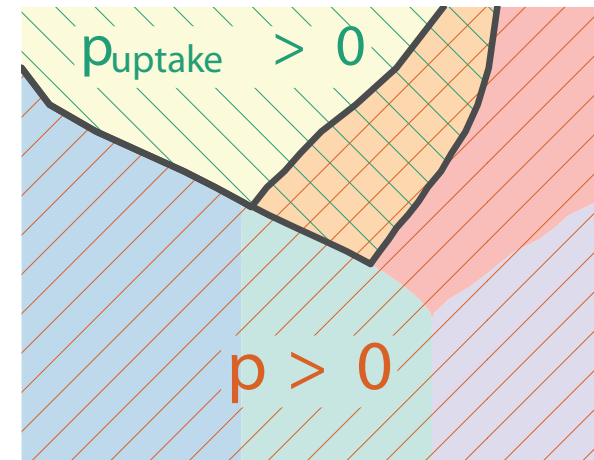
adaptability



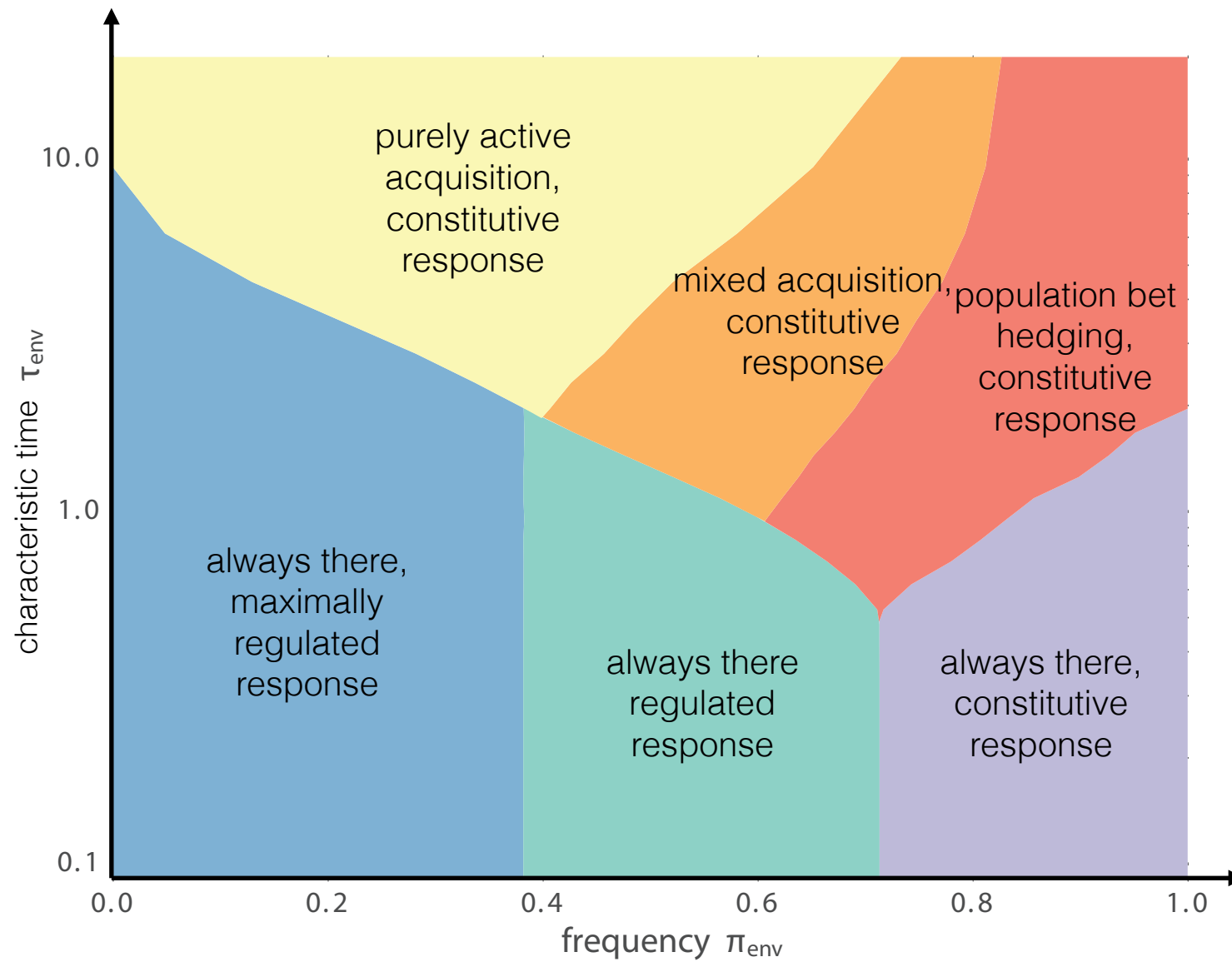
heritability



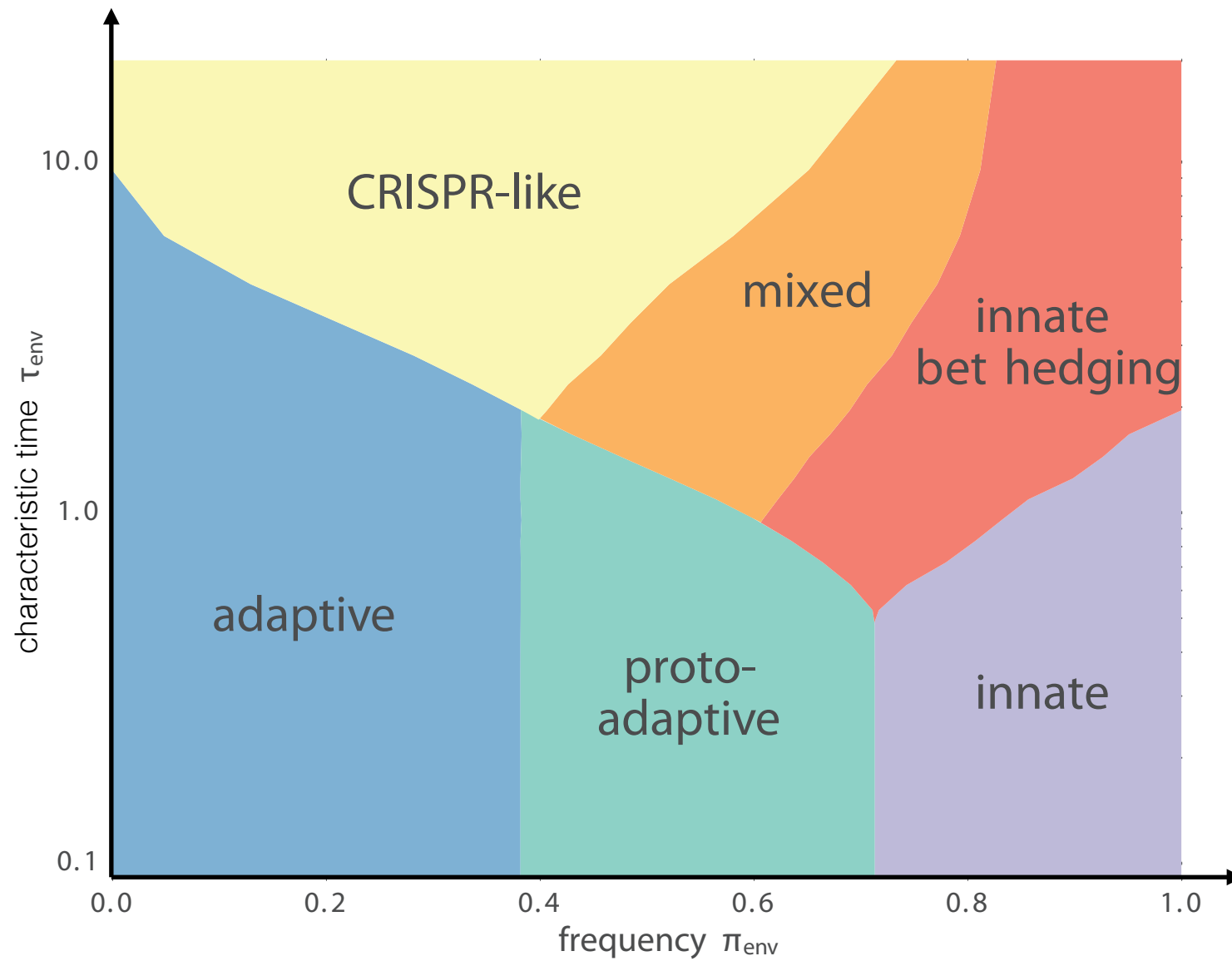
acquisition mode



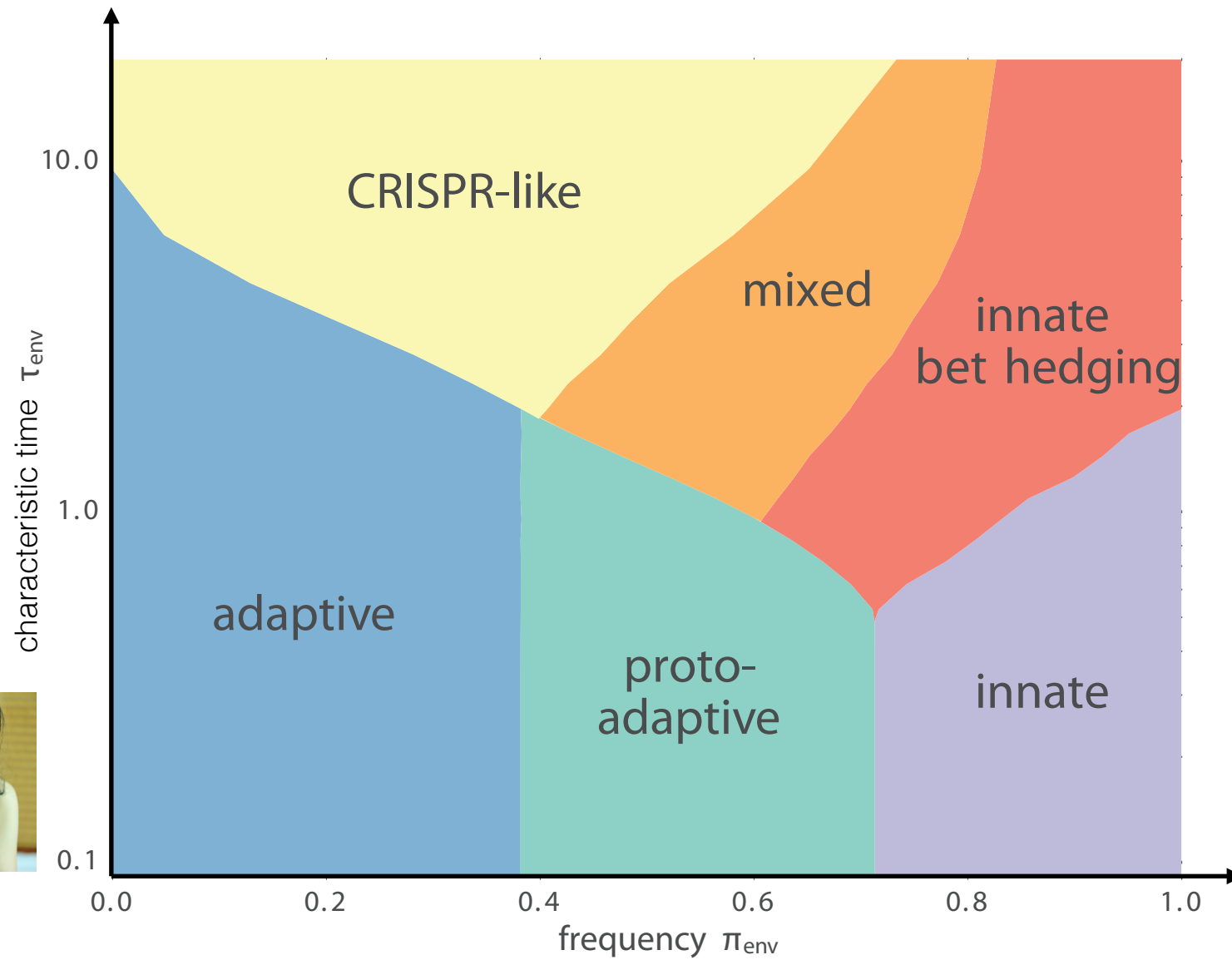
Optimal strategies



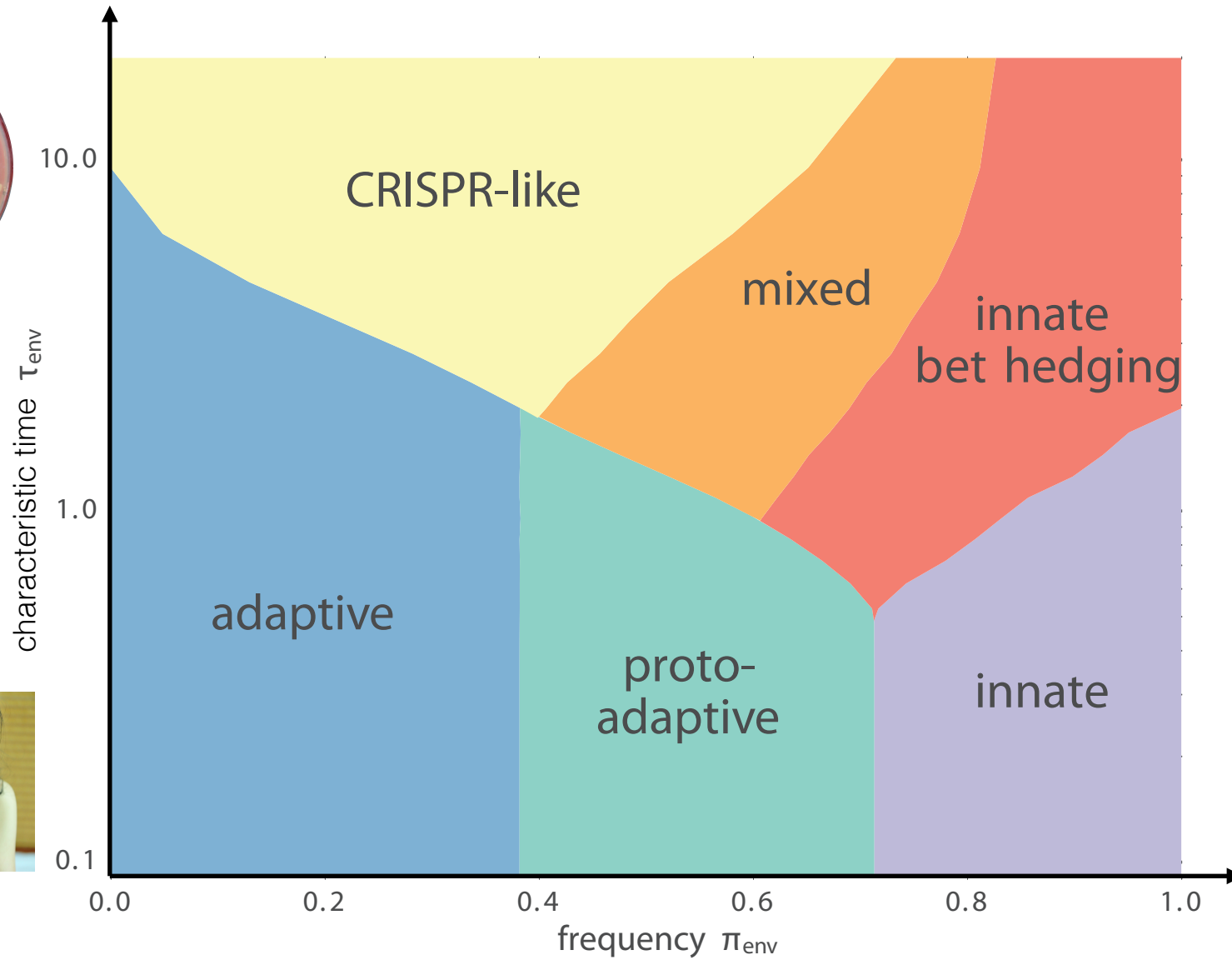
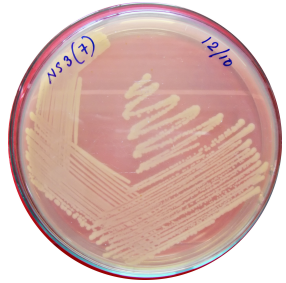
Optimal immune systems



Optimal immune systems



Optimal immune systems





optimal repertoires:

- cover space but are random
- differ in two individuals
- result from competitive receptor dynamics

optimal immunity:

- known immunity from evolutionary constraints
- depends on environment statistic
- reproduces human vs bacterial types of immunity

A Murugan, T Mora, AM Walczak, CG Callan, PNAS (2012)

Y Elhanati, A Murugan, CG Callan, T Mora, AM Walczak, PNAS (2014)

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A Mayer, T Mora, O Rivoire, AM Walczak, qbio/bioarxiv (2015)

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M Pogorelyy, Y Elhanati, Q Marcou et al qbio/bioarxiv (2016)