# Desgrete Models for Molegular Sumulations Forulation at the

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# MOTIVATION:

- Making the process of simulation of ecological or evolutionary process better understandable for a biologist
- Obtaining the results of a simulation in a form which would correspond directly to the outcome of an experiment

# Logistic growth with competition and mutations – adaptive dynamics

$$\frac{dN(x,t)}{dt} = r \cdot N(x,t) \cdot \left[ 1 - \int C_{x}(x-\chi)N(\chi,t)dy \middle/ K(x) \right]$$

## Here x – ecological character defined by polygene

$$\boldsymbol{K}(\boldsymbol{x}) = \boldsymbol{K}_0 \exp\left[-\frac{(\boldsymbol{x} - \boldsymbol{x}_0)^2}{2\sigma_{\boldsymbol{K}}^2}\right], \quad \boldsymbol{C}_{\boldsymbol{X}}(\boldsymbol{z}) = \exp\left[-\frac{\boldsymbol{z}^2}{2\sigma_{\boldsymbol{X}}^2}\right]$$

## From: On the origin of species by sympatric speciation Ulf Dieckmann & Michael Doebeli, Nature, 1999

#### «Useless» simulation



# Individual-based representation



### Useful simulation, the result is in comfortable format

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ec1733	MAVRI	ECG.	AT.	HR	TD
ec455	MAVRI	ECG.	AT.	DR	TD
ec954	MAVRI	ECG.	AT)	ΗP	ΥN
ed829	MAVRI	ECG.	AT)	HR	LH
ed899	MAVRI	ECG.	AT.	DR	WD
ec1617	MAVRI	ECG.	AT	DR	WD
ed672	MAVRI	ECG.	AT)	ΗP	ΥN
ec1233	MAVRI	ECG.	AT)	HR	TD
ec1274	MALRI	ECG.	AT(	ΩI	TD
ec654	MTVR	ECG.	AD)	ΗW	TS
ed463	MAV <mark>R</mark> I	ECG.	AT.	DR	TD
ec1010	MTVR	ECG.	AD)	ΗW	TS
ec1128	MAV <mark>R</mark> I	E <mark>T</mark> G,	AT)	HR	ΤH
ec1736	MAVRI	ECG.	AT(	ΩI	QD
ec1201	MAVRI	ECG.	AT(	ΩI	ТP
ed947	YAV <mark>r</mark> i	ECG.	AV.	HR	HD
ec210	MAV <mark>R</mark> I	ECG.	ΑT	DR	TD
ec1411	MAV <mark>RI</mark>	RIG	AT]	HR	ТΥ
ed316	MAV <mark>R</mark> I	ECG.	AT	DR	TD
ed955	MAV <mark>R</mark> I	ECG.	AHI	HW	QA
20699	MAVDI	FCC	$\Delta T'$	nт	OD

423 <mark>G<mark>TC</mark>TT</mark>	GICCCGCC	T <mark>AATA</mark> TC	CGCTC
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498 <mark>GTCTT</mark>	GICCCC	T <mark>AATA</mark> TC	CGCTC
169 <mark>GTCTT</mark>	GTCCCCC	T <mark>AATA</mark> TC	
291 <mark>G<mark>TC</mark>TT</mark>	GICCGC	T <mark>AATA</mark> TC	ICG C TO
1037 <mark>AACTC</mark>	GTCCCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
453 <mark>AACTC</mark>	GTCCCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCTZ
782 <mark>IC</mark> AGC	ATCCCCC	AATTGCC	CCCT.
1739 <mark>AA</mark> CTC	Gracecc	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
1006 <mark>AACTC</mark>	GICCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
599 <mark>Aacte</mark>	GICCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
650 <mark>Gaatt</mark>	GICCACCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
1299 <mark>AACTC</mark>	GICCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
1609 <mark>6 a a t t</mark>	GICCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCGT
769 <mark>AACT</mark> C	GICCCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
7 <mark>AACT</mark> C	GTCCCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
995 <mark>AACTC</mark>	GICCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
1121 <mark>GTC</mark> TT	GICCGCC	T <mark>AAT</mark> ATC	CCC
336 <mark>GTCTT</mark>	GICCGCC	T <mark>AATA</mark> TC	CCC
1606 <mark>GTC</mark> TT	GICCGC	T <mark>AATA</mark> TC	CCC
285 <mark>G<mark>aa</mark>tti</mark>	GICCCCC	AAA <mark>T</mark> A <mark>T</mark> C	ICCG TO
781 <mark>AACTC</mark>	GICCCCC	AAA <mark>T</mark> A <mark>TC</mark>	CCCT
1796 <mark>AACTC</mark>	GICCCCC	AAA <mark>T</mark> AT <mark>C</mark>	CCCT

## Motivation: explaining evolution of species flocks

Species flock is a group of species which evolved in confines of the same eco-system from a single ancestor

Species flocks are peculiar to ancient giant freshwater lakes like lake Baikal and Lake Tanganyika, where the most famous and species-rich is set of flocks of ciclids





# Tanganyika



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Pip. 2. - Cleopetre Initaliale Geamann, 1905.











# Baikal



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Microsporidia parasiting on Baikalian amphipods comprise the first fully parasitic species flocks. The main surprise here is absolute lack of evidence for any co-evolution between host and parasite. Another problem is coexistence of several parasite species on a single host species: this must cause ultimate extinction of the latter





![](_page_12_Picture_1.jpeg)

Baicalia carinata

B. dybowskiana

B. turriformis

## Baicaliidae example

![](_page_13_Figure_1.jpeg)

Some evolutionary relations within a flock cannot be represented correctly by a tree

![](_page_14_Figure_1.jpeg)

# Shackleton cycles: evolution in changing environment

![](_page_15_Figure_1.jpeg)

![](_page_16_Figure_1.jpeg)

![](_page_17_Figure_1.jpeg)

![](_page_18_Figure_1.jpeg)

![](_page_19_Figure_1.jpeg)

![](_page_20_Figure_1.jpeg)

In Lake Baikal there are no strict specialists, at least close to surface, where impact of environmental changes is more dramatic.

Are there specialists in the abyssal zone? It is not yet known, but this zone is relatively young.

# Shackleton cycles: evolution in changing environment

![](_page_21_Figure_1.jpeg)

![](_page_22_Picture_0.jpeg)

Subdivision in *Gmelinoides fasciatus* (Environmental changes are not the only cause of species subdivision)

![](_page_22_Figure_2.jpeg)

![](_page_23_Picture_0.jpeg)

Are different populations separate species? How could this pattern occur?

![](_page_23_Picture_2.jpeg)

![](_page_23_Figure_3.jpeg)

## **Coordinated evolution of amino acid sequences**

## Some features of proteins preserved in evolution involve more then single amino acid residue

- •There is no obvious transition from one state to another: intermediate state is deleterious
- •Numerous physical or/and chemical properties of amino acid residues may be conserved, as the consequences the values of these properties appear to be highly correlated in evolution
- •More then two residues may take part in a group
- •Correlated groups are quite common in proteins

![](_page_25_Picture_5.jpeg)

![](_page_26_Picture_0.jpeg)

•To elucidate the population mechanism allowing coordinated evolution of amino acid residues;

•Using computer simulation of microevolutionary events, to find the conditions favouring coordinated evolution

•To design statistical tests allowing one to study coordinated evolution or/and take it into account when necessary

#### Model

#### Organism

Hermaphroditic, but during the same reproduction cycle may have only one gender
Diplod and has maternally transferred («mitochondrial») DNA
Has age limit measured in reproductive cycles

- •Fitness depends on one protein coding gene and
- population density limited
- resource)
- •Number of progeny is Poisson distributed

#### Mitochondrial marker

 $x_i \in A, C, G, T$ 

- Single vector
- •No recombination
- •Transfered from mother to all her progeny
- •Does not affect fitness
- •All substitutions (mutations) are equiprobable

1176<mark>C</mark> 498 <mark>G</mark> 169. 291 1037 782 1739 1006599 650 995. 1121<mark>G</mark> 336 <mark>G</mark> 1606<mark>G</mark> 285 G CCCCCC

#### Nuclear gene

- •Sequence consists of 20 «amino acids»
- •Each substitution is equiprobable;
- •Each residue has property, which changes from 0 to 19
- •Each sequence consists of 2 parts: «the neutral one, where sequences does not affect fitness of the organism, and **non-neutral one,**where fitness is function of the sum of properties:  $f = \sum (x_i - s_i)$

1-1	<u> </u>	- D	ey.	Τ.	F
ec1733	MAVRI	ECG	ATH	R'	D
ec455	MAVR	ECG	ATD	R	D
ec954	MAVR	ECG	ATH	P	ZN
ed829	MAVR	ECG	A <mark>T</mark> H	RI	LΗ
ec899	MAVR	ECG	ATD	R	<b>V</b> D
ec1617	MAVR	ECG	ATD	R	Ð
ed672	MAVR	ECG	ATH	P	ΖN
ec1233	MAVR	ECG	A <mark>T</mark> H	R	D
ec1274	MAL	ECG	<mark>a</mark> tq	I'	D
ec654	MTVR	ECG	A <mark>D</mark> H	W.	cs
ed463	MAVR	ECG	ATD	R	CD.
ec1010	MTVR	ECG	A <mark>D</mark> H	W.	cs
ec1128	MAVR	ETG	ATH	R	CH
ec1736	MAVR	ECG	<mark>a</mark> tq	Iς	2D
ec1201	MAVR	ECG	<mark>a</mark> tq	I.	CР
ed947	YAV <mark>R</mark> I	ECG	AVH	RI	ID
ed210	MAVRI	ECG	ATD	R	D
ec1411	MAVRI	RIG	ATH	R'	CΥ
ed316	MAVR	ECG	ATD	R	D
ec955	MAVR	ECG	AHH	WÇ	)A
20699	MAVD	RCC.	$\Delta T \cap$	iτc	<mark>n</mark> D

### Interactions between organisms

1) The organisms who reached maximal age allowed die;

2)Each of the survivors determine it's gender for this round;

3)Density-dependent decrease of survival rate is introduced;

 $f = f\left(1 - \frac{n}{N}\right)$ 

4)Pairs («families» are formed according to the random gender-choice made at stage (2);

5)Each pair «decides» how many children will they have. The number of children is Poisson-distributed;

6) Children are produced (if their number exceed the max. Number, their number is reduced proportionally), They inherit mother's «mitochondrial» marker and one «nuclear» allel from each parent;

7)Progeny fitness according to the group rule is calculated (Full dominance in this study)

8)New density dependent viability is calculated and the unlucky «die», the rest increase their age;

9)Stage (1) occurs. Life goes on.

### Mask size, number of kids etc.

![](_page_30_Figure_1.jpeg)

### Group size influences relaxation curve after a jump

![](_page_31_Figure_1.jpeg)

# Relaxation curves depend on exact start and target values

![](_page_32_Figure_1.jpeg)

![](_page_33_Picture_0.jpeg)

![](_page_34_Picture_0.jpeg)

## **Optimum shift without coordinated evolution**

![](_page_35_Picture_1.jpeg)

# Two optinmal values co-existing do not cause co-ordinated substitutions

![](_page_36_Figure_1.jpeg)

## Double jump

![](_page_37_Figure_1.jpeg)

![](_page_38_Picture_0.jpeg)

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File $\nabla$ Props $\nabla$	Sites ⊽	Species $\nabla$	Foote
sel=3		Seq:2	3 <b>Þ</b> ðs
Spec1119 Spec1530		ILMDQGT	GPCT GPCA
Spec907 Spec34	K WMR	WNMCQGY WLYDQGQ	VPLA VPQA
Spec1324 Spec1742	K WMR K WMS	TLMDRSY WMYDQGY	V <mark>PD</mark> A V <mark>PLA</mark>
Spec228 Spec652	K WMR K WMR	WLYDQGQ WLYDQGQ	VPQA VPLA
Spec1176 Spec1837		WLYDQGQ WLMDLPY	VPLA QPPA
Spec1132 Spec1689		WENDOGY	PYLA VPLA
Spec1147 Spec1864	K WMR	WRMLQGY	PYLA GPCT
Spec1883 Spec2026	K WMR K WMR	WLMHQPY WMYDQGY	VPLA VPLA
Spec344 Spec104	K WMR	WMYDQGY W <mark>R</mark> MEQGY	VPLA IPL <mark>E</mark>
Spec1207 Spec713		WMYDQGY WCMEQGY WLMD <mark>M</mark> CY	VPLA IPLE MIA
Spec1871 Spec727	KWMR	WMYDQGY WKYDYGY	VPLA VPDA
Spec373 Spec1073	K WMR K WMR	W <mark>KMDQ</mark> GY GCMEQGY	EPLE IPLE
Spec390 Spec1107	K WMR K WMR	GCMEQGY ILMWQGT	IPLE GPC <mark>T</mark>
Spec594 Spec1628	K WMR	WLYDQGQ WLYDQGQ	VPLA VPLA
Spec305 Spec995 Spec1223		WLMHQPY	VPDA VPLA APLA
Spec1223		WAMDQGY WLMDOGY	VSAY VVMA
Spec1813	K WMR	WLMDPPY	CPPA
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Double shift of optimal value results in coordinated sunstitutions!

# Repeated change of environment promotes coordinated substitutions

![](_page_40_Figure_1.jpeg)

## Very preliminary conclusions:

Number of group members must be more then 2. Coordinated substitutions become more frequent with the increase of number of group members.
Periodic shift of optimim promotes coordinated substitutions

•New optimal value of a property must be reached at a single mutation