Risk of extinction and bottleneck effect in Penna model

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1 Introduction

A species becomes **extinct** when the last existing member of that species dies. Extinction therefore becomes an extreme event after which no surviving specimens are able to reproduce and create a new generation. There have been at least five mass extinctions in the history of life in which many species have disappeared in a relatively short period of geological time.

1.1 “Big Five”

- 444 (End Ordovician),
- 367 (Late Devonian),
- 255 (End Permian),
- 200 (End Triassic)
- and 65 (End Cretaceous) million years ago.

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- impact events,
- climate changes,
- volcanism,
- γ-ray burst
- and plate tectonics

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- impact events,
- climate changes,
- volcanism,
- γ-ray burst
- and plate tectonics
- or the mixtures all of them.

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During End Permian extinctions 96% of marine species and 70% of land ones (including plants, insects and vertebrates animals) were killed.

1.2 Overpopulation

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- Thomas Malthus argued that if left unrestricted, human populations would continue to grow until they would become too large to be supported by the food grown on available agricultural land

1.3 Mutational meltdown

The Darwinian evolution theory predicts genetic modification of individuals genome via mutation process and slow change one species to another. This change (called **speciation**) and the newly created species will be accepted by Nature through the natural selection procedure.

In this way mutations may become crucial for new species creation and evolution.

However, sometimes too many genetic modifications yield genetic death of the individual.

1.4 The Penna model

The Penna model of biological ageing is devoted to reproduce single-species population dynamics for genetically heterogeneous individuals represented only by their genotype — the N_{bit} long binary computer word:

- accumulation theory: random hereditary deleterious mutations accumulate over several generations in the species genomes.

- bad mutations are represented as “1” in the genome.
- the time is measured by discrete variable t.
- in each time step, for each individual of age a, the number of bits set to one in the first a positions in the genome is calculated.
- these “1” in position $1 \leq i \leq a$ are treated as active mutations: if the number of active mutations $\geq T$ — an individual dies.

- individuals compete among themselves for resources: each of them may be removed from the population with probability $N(t)/N_{\mathrm{max}}$ — to avoid the Malthus catastrophe.

- we feel that the well-fitted individuals should be more resistant for random removing — which mimics competition — that ill-fitted ones.

- to keep the population finite and avoid accidentally killing the best-fitted organisms, the Verhulst factor may act only on newly born babies and not on adult ones (reducing $b \rightarrow b[1-N(t)/N_{\mathrm{max}}]$)

- if $R \leq a \leq E$ individual clones itself with probability b producing B offspring.

- during replication parent's genome is exposed to harmful mutations (“0”$\longrightarrow$“1”) which occur with probability m at M randomly selected positions in genome.
- the length of genome N_{bit} restricts maximal age of individuals.

1.5 The aim

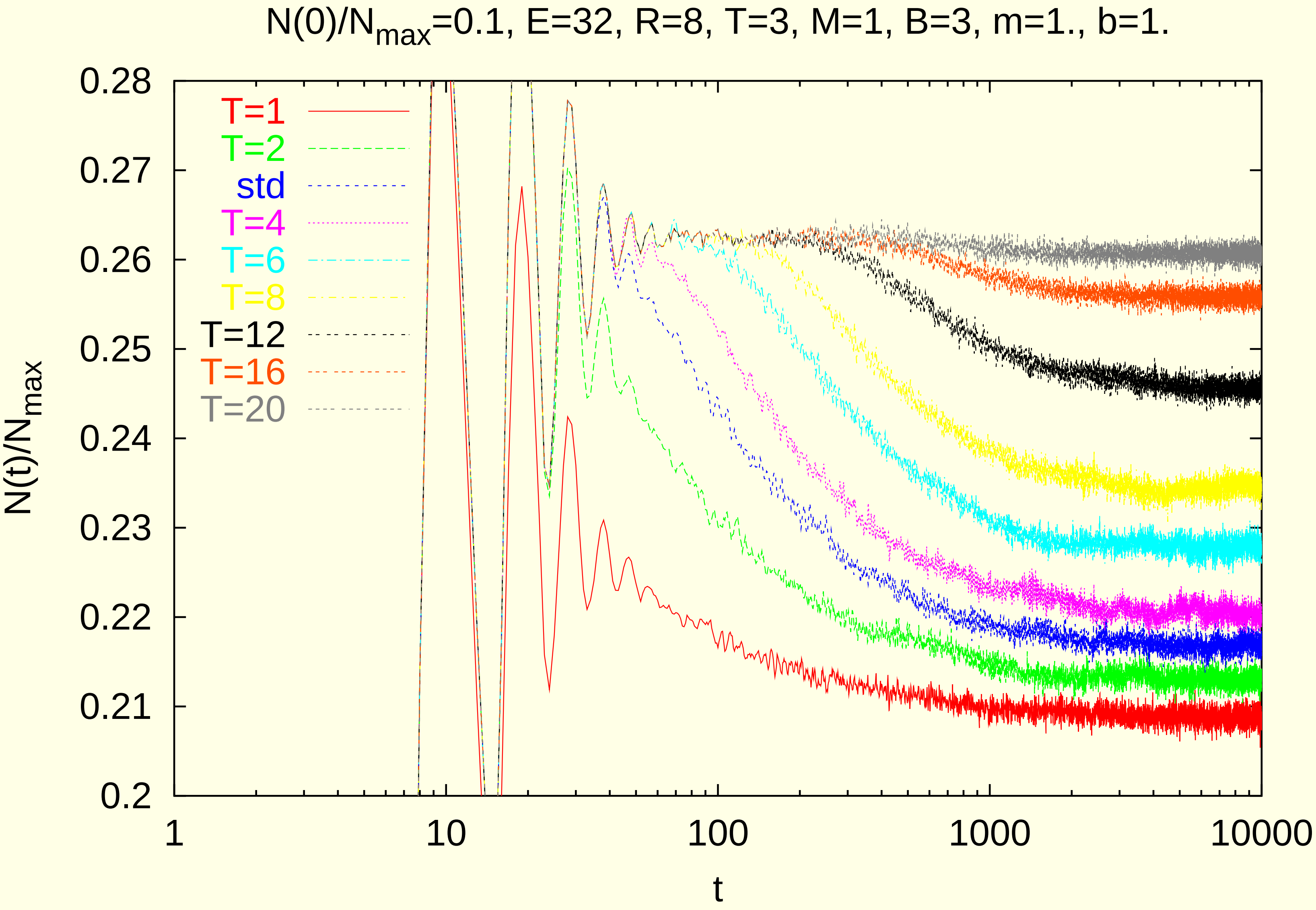
- to draw a phase diagrams in the space of the model control parameters which for initially large populations separate survival from extinction,
- to search for the bottleneck effects (when the populations were drastically decreased after equilibrium was established, and then allowed to increase again).

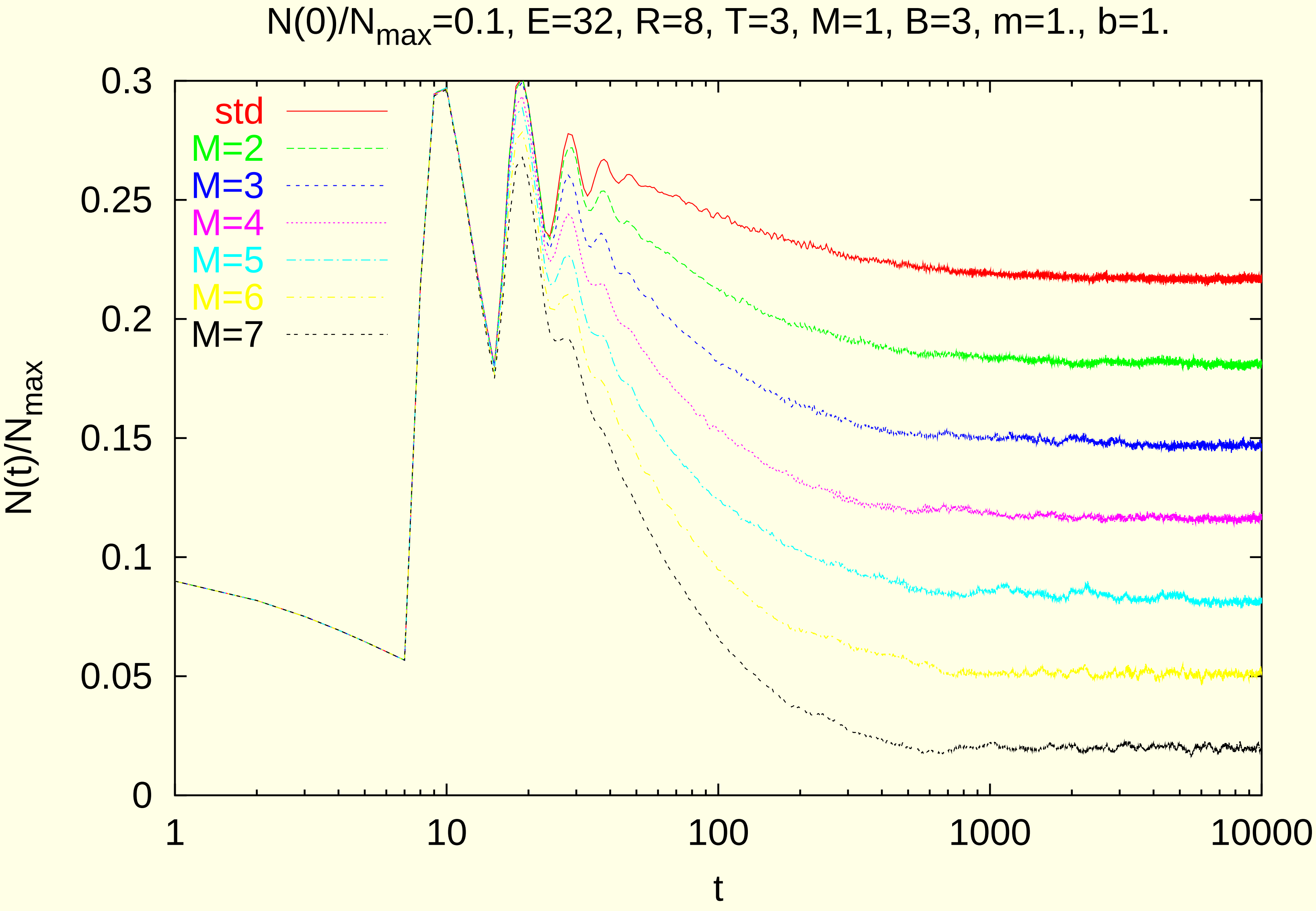
2 Size of population [1]

influeance of model control parameter

$$(N_0/N_{\mathsf{max}}, T, B, b, M, m, R, E)$$

on the population size


N(0)/N_max=0.1, E=32, R=8, T=3, M=1, B=3, m=1., b=1.
N(t)/N_max
t
0.28
0.27
0.26
0.25
0.24
0.23
0.22
0.21
0.2
1
10
100
1000
10000
T=1
T=2
std
T=4
T=6
T=8
T=12
T=16
T=20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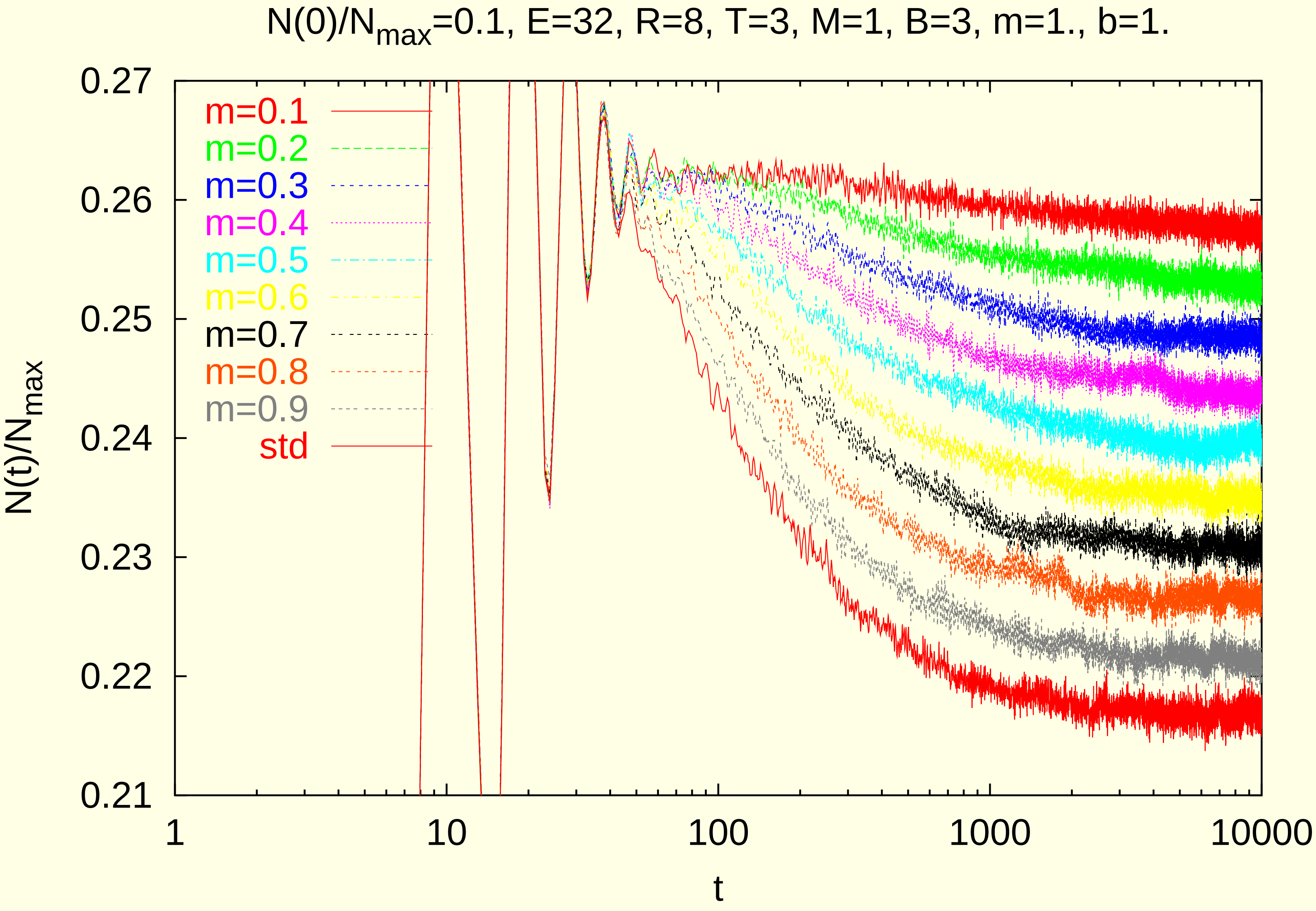
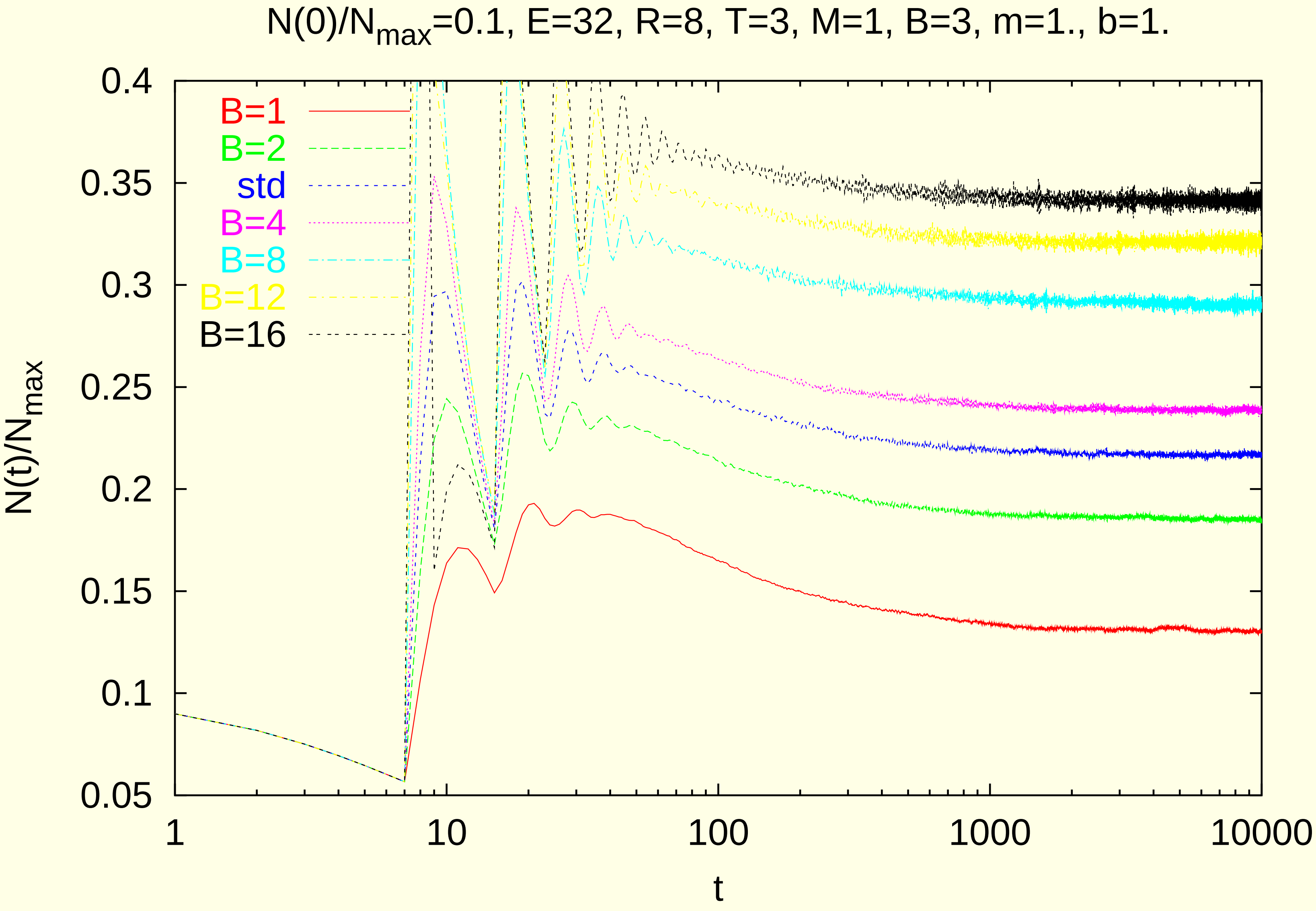
N(t)/N_max
t
std
M=2
M=3
M=4
M=5
M=6
M=7
0
0.05
0.1
0.15
0.2
0.25
0.3
1
10
100
1000
10000


$N(0)/N_{max}$=0.1, E=32, R=8, T=3, M=1, B=3, m=1., b=1.
$N(t)/N_{max}$
0.27
0.26
0.25
0.24
0.23
0.22
0.21
1
10
100
1000
10000
t
m=0.1
m=0.2
m=0.3
m=0.4
m=0.5
m=0.6
m=0.7
m=0.8
m=0.9
std



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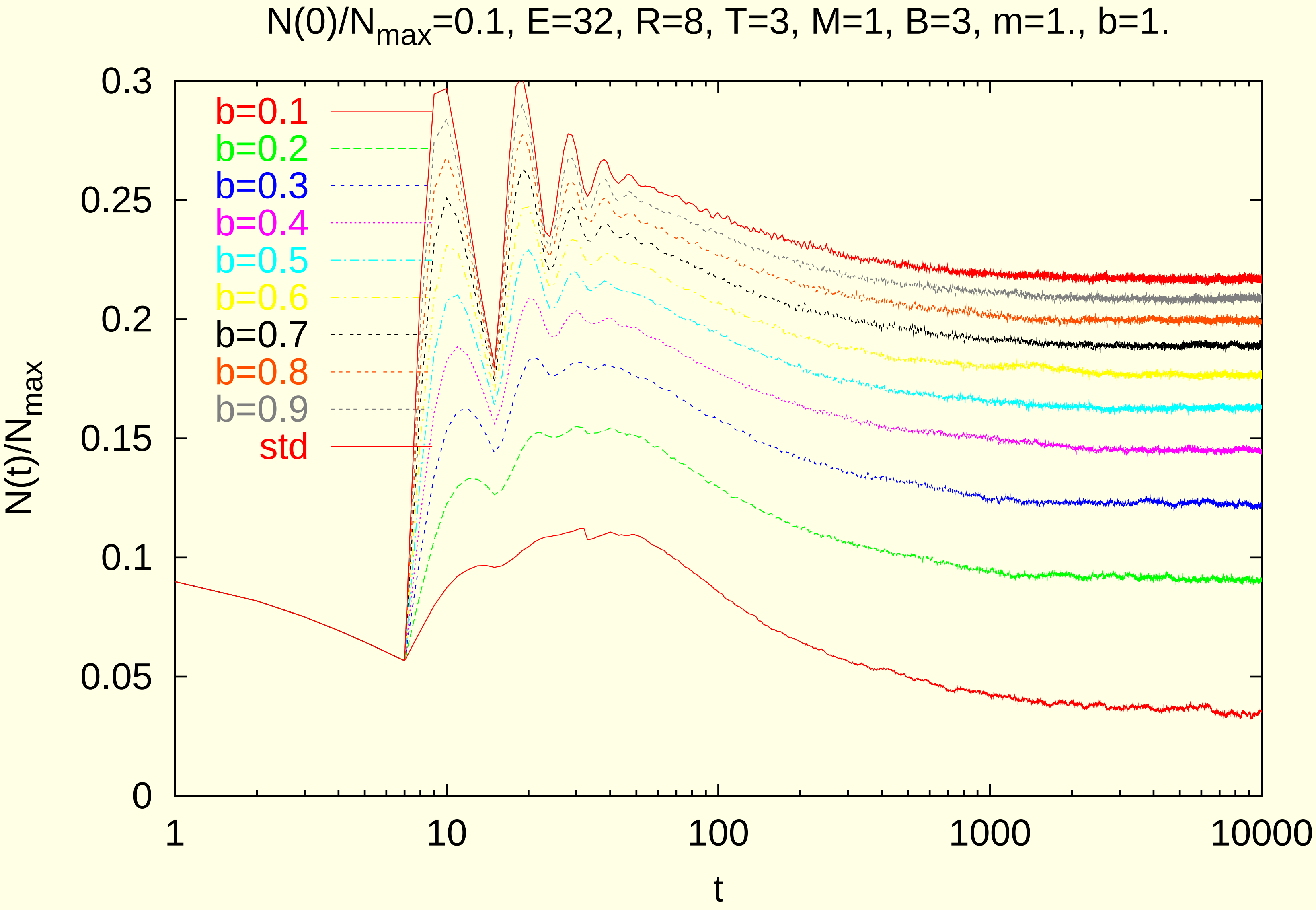
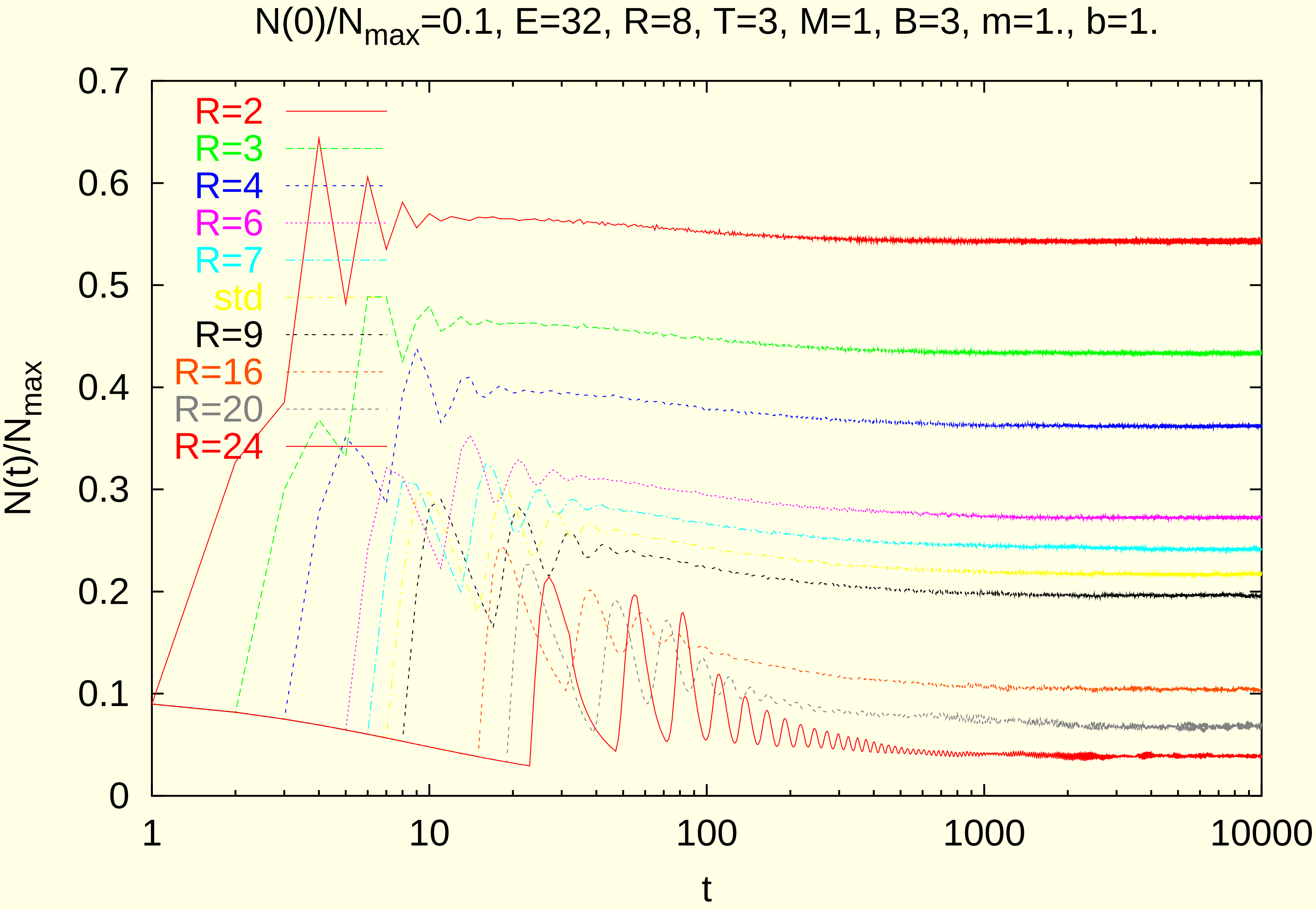
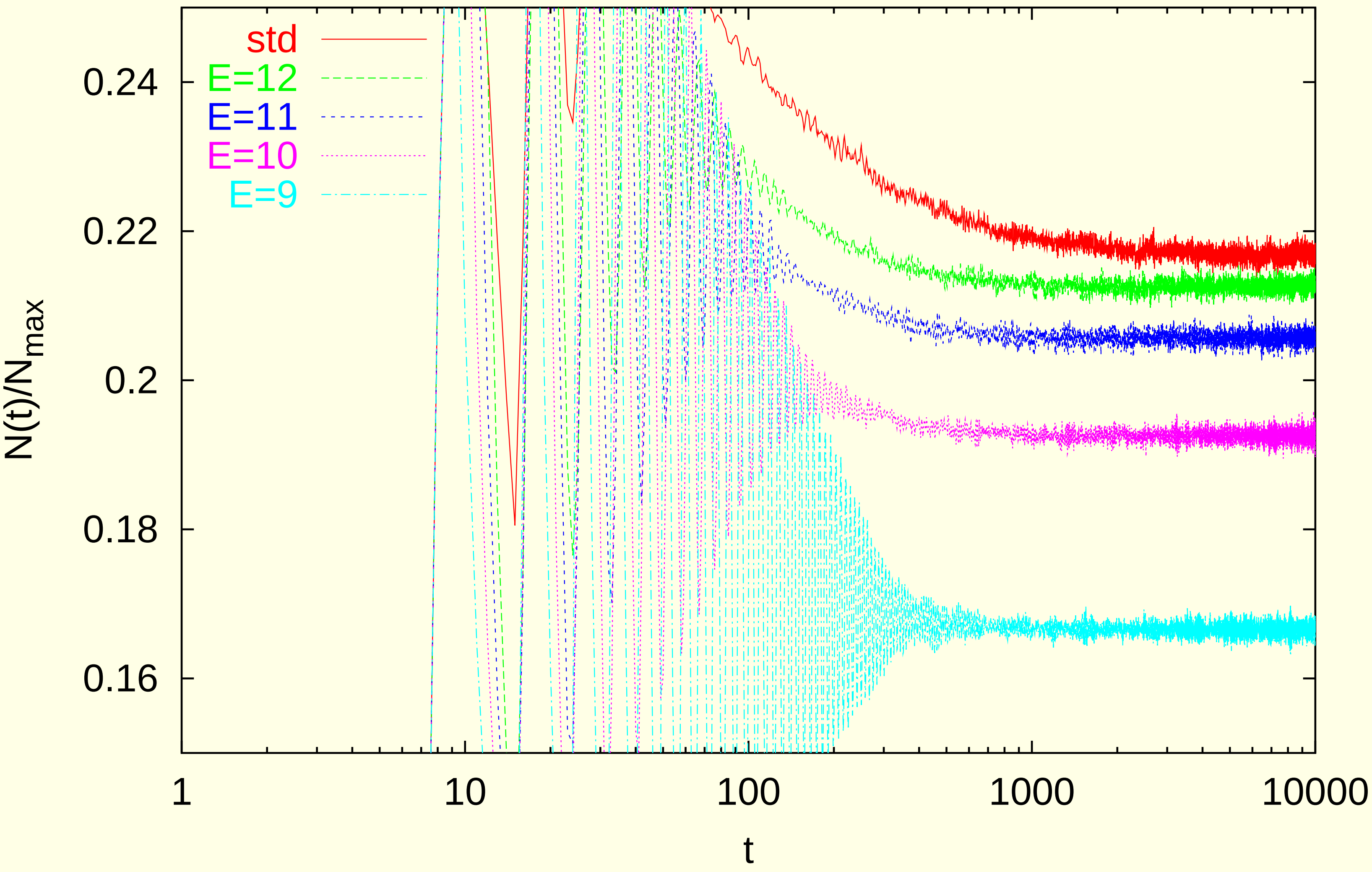

N(0)/N$_{max}$=0.1, E=32, R=8, T=3, M=1, B=3, m=1., b=1.
0.3
0.25
0.2
0.15
0.1
0.05
0
N(t)/N$_{max}$
b=0.1
b=0.2
b=0.3
b=0.4
b=0.5
b=0.6
b=0.7
b=0.8
b=0.9
std
1
10
100
1000
10000
t


N(0)/N_max=0.1, E=32, R=8, T=3, M=1, B=3, m=1., b=1.
R=2
R=3
R=4
R=6
R=7
std
R=9
R=16
R=20
R=24
N(t)/N_max
0
0.1
0.2
0.3
0.4
0.5
0.6
0.7
1
10
100
1000
10000
t

N(0)/N$_{max}$=0.1, E=32, R=8, T=3, M=1, B=3, m=1., b=1.



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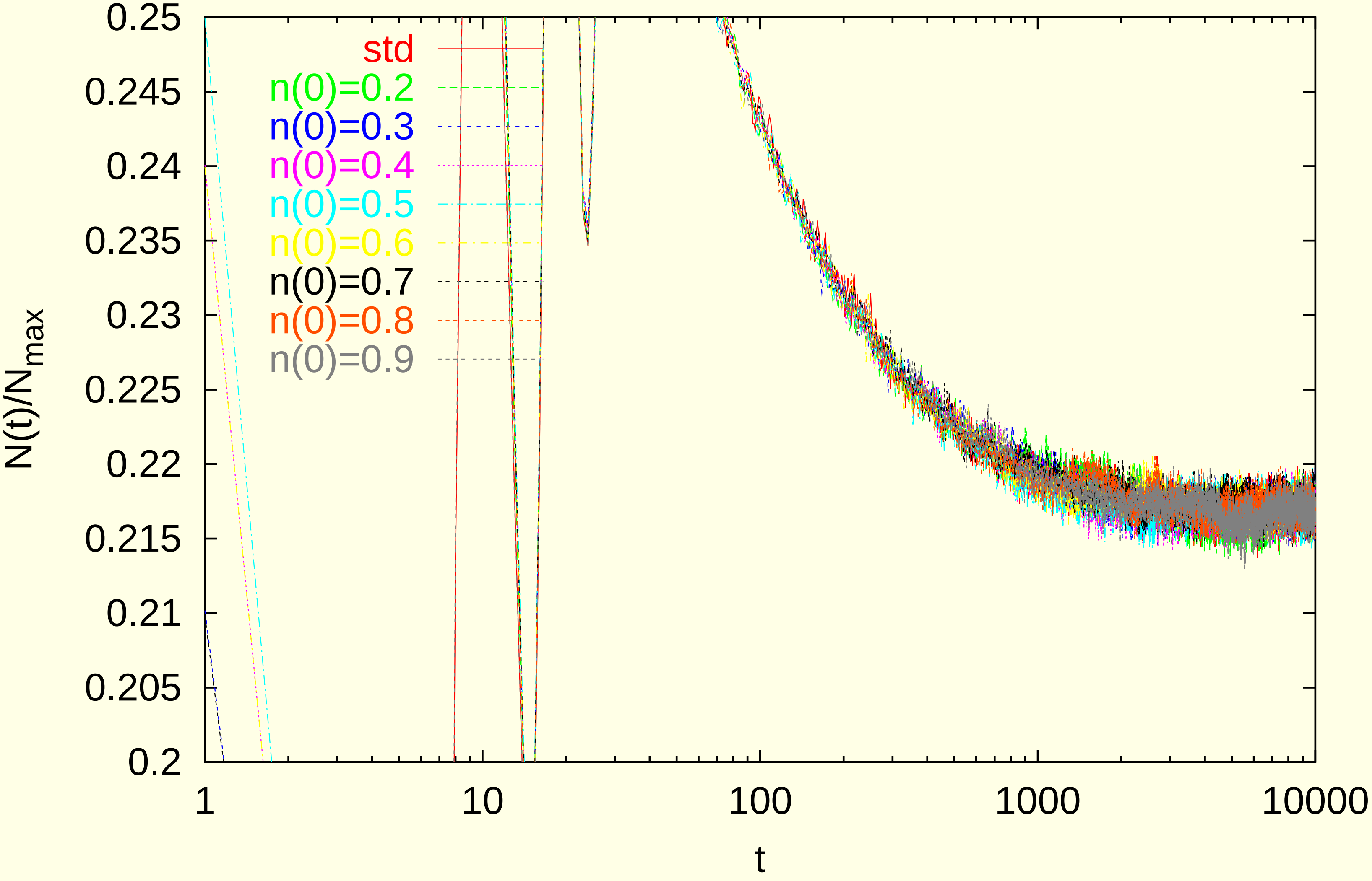
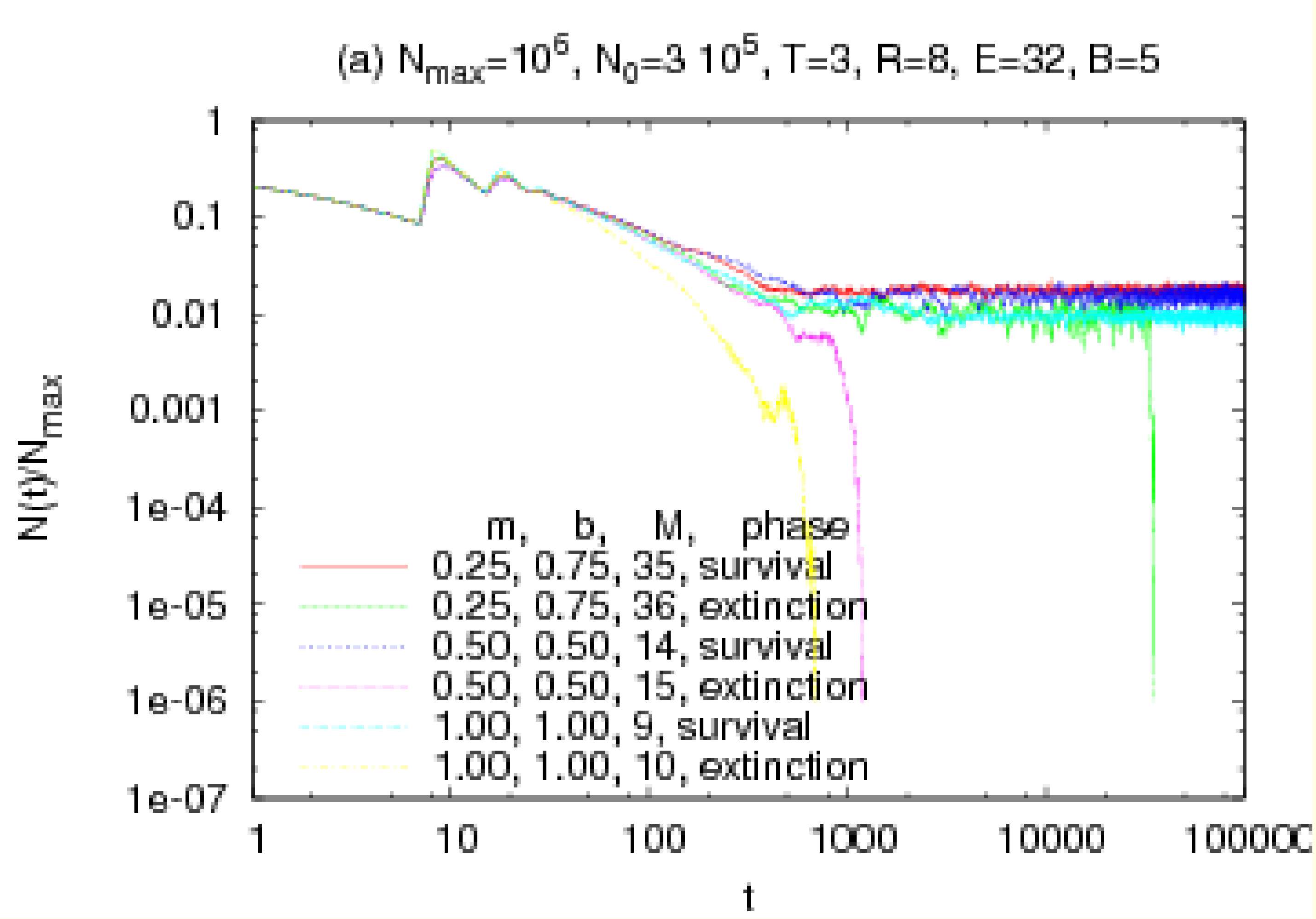


3 Survive/extinction phase diagram [2]

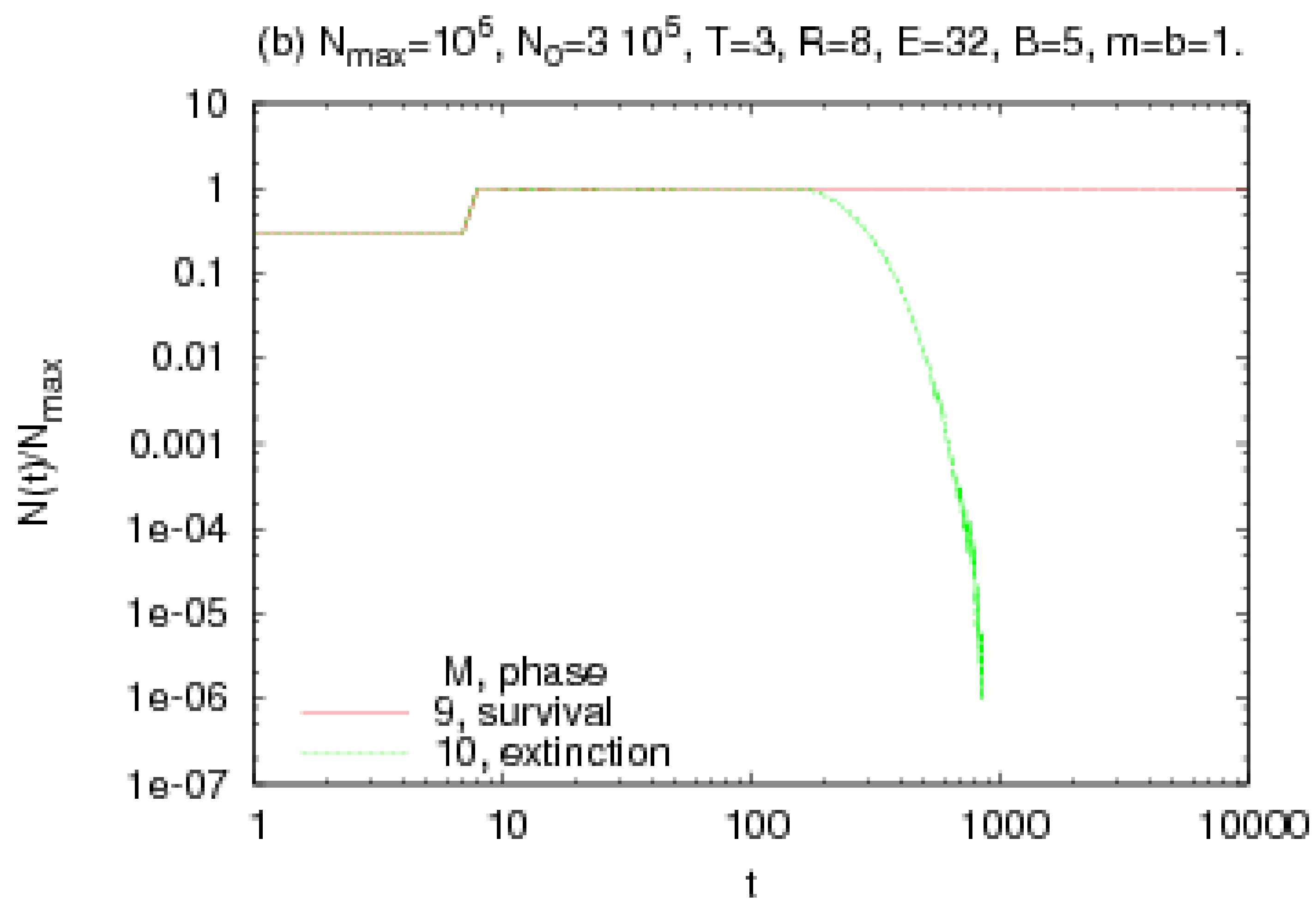
The extinction phase may be caused by **either mutational meltdown or overpopulation**.

When the Verhulst factor is responsible for removing only newly born babies and does not act on adults the overpopulation is avoided and only genetic factors may lead to species extinction.

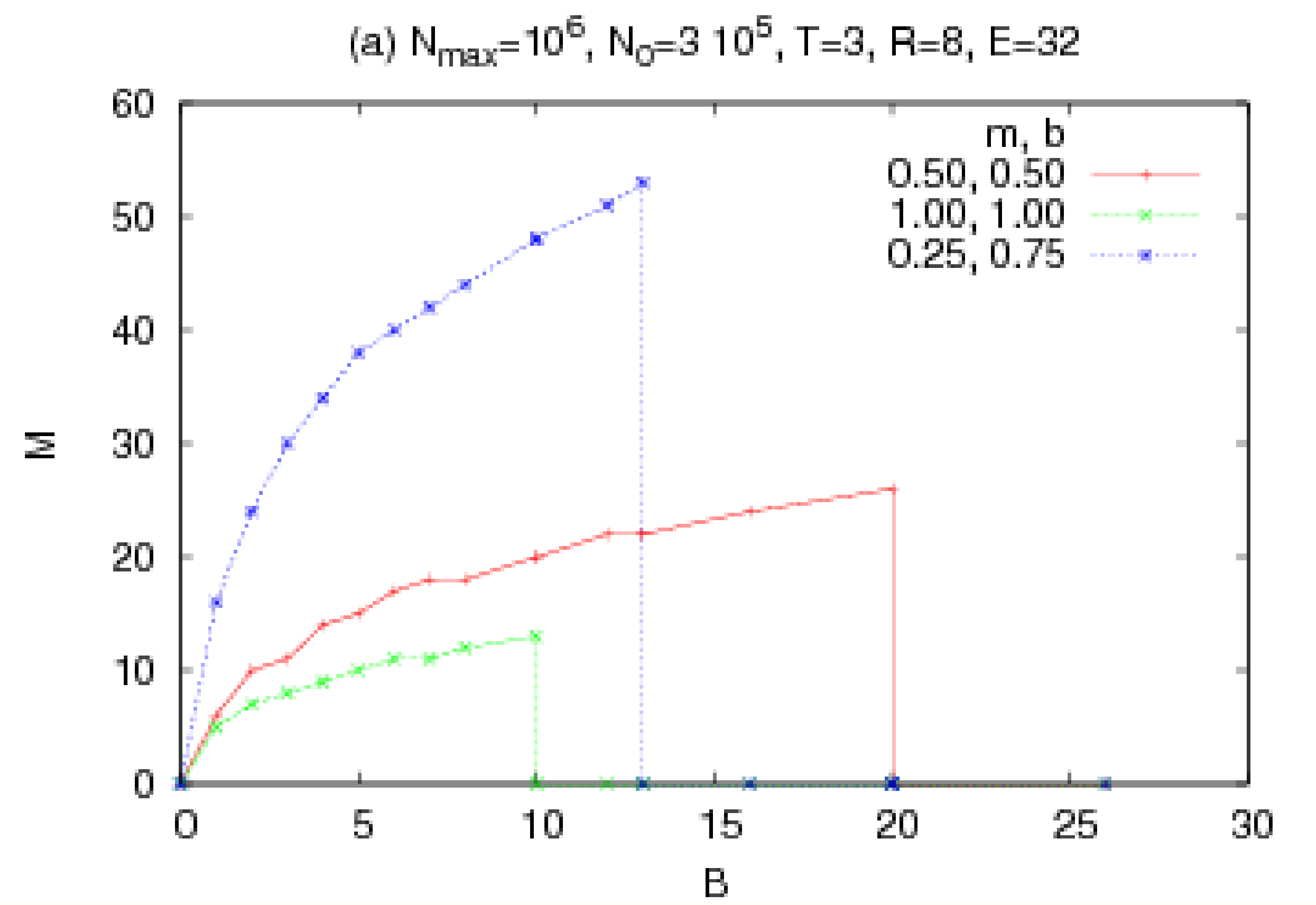
The subsequent pairs of curves have identical set of parameters except of mutation rates which are M and $M+1$.



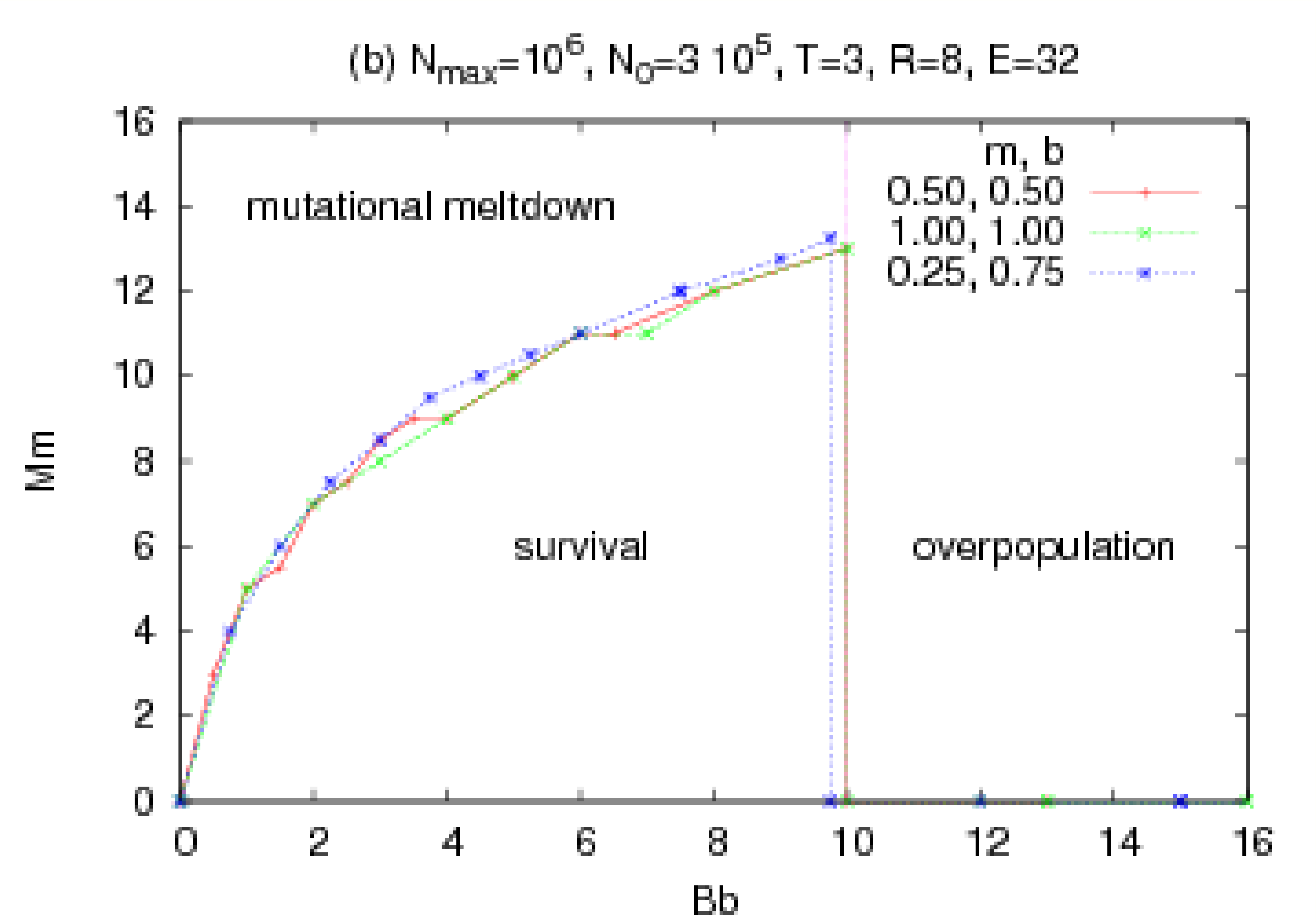
The Verhulst's factor applies either to all individuals or... only to newly born babies.



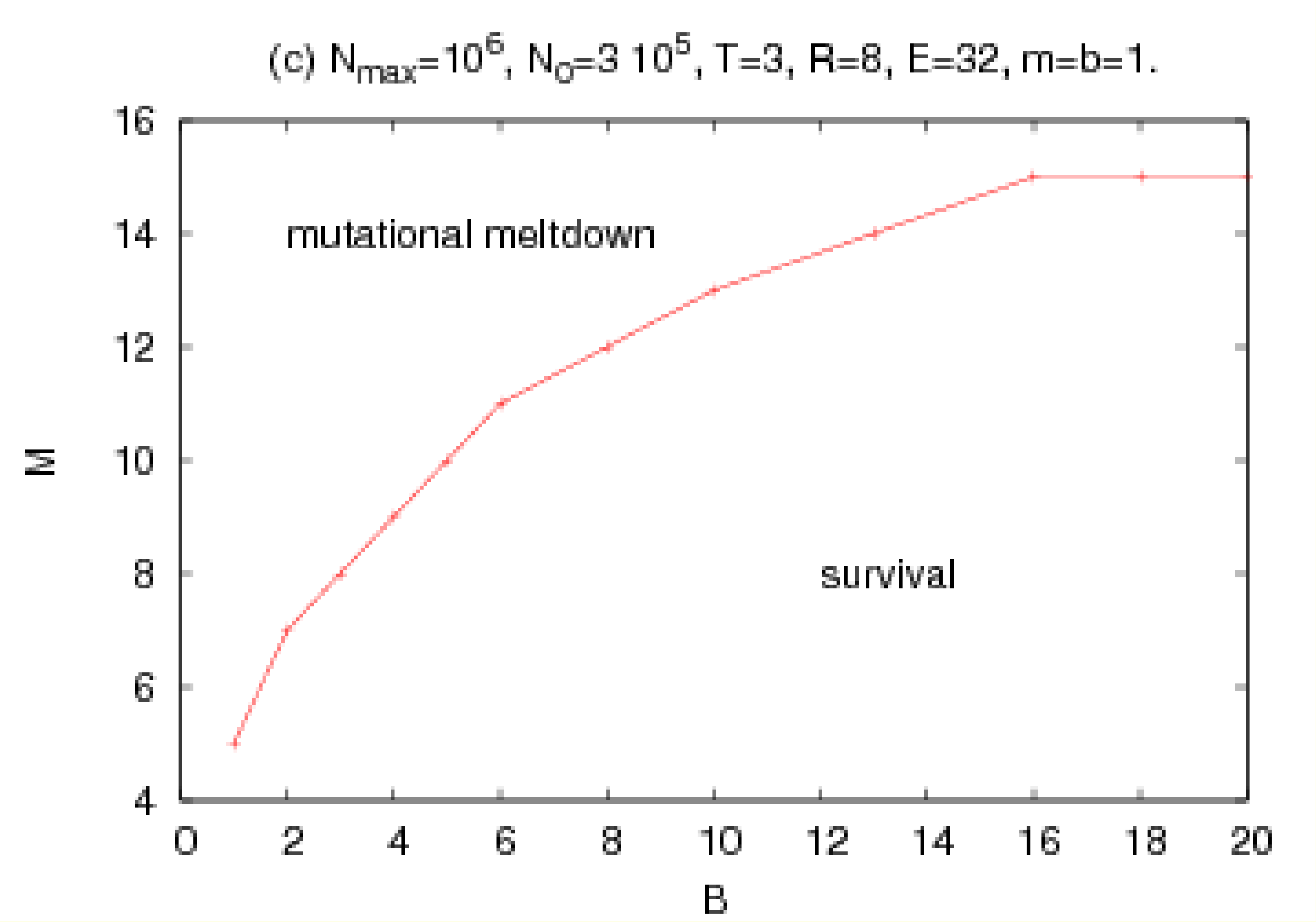
Below arc-like lines the species survival is possible.

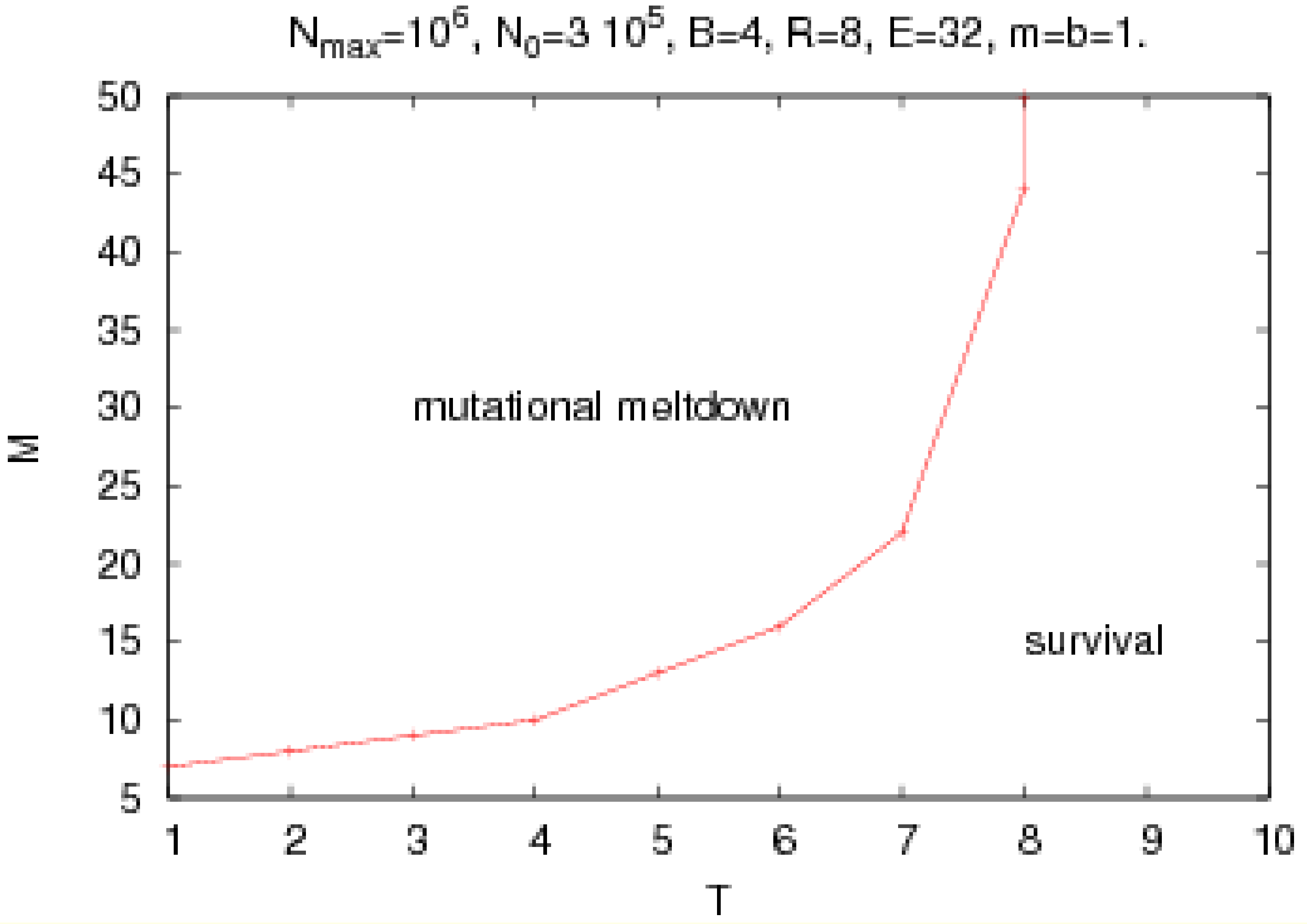


- At and above them individuals die due to too many mutations pumped into their genome.
- On the right side of the vertical line the extinction process is caused by overpopulation.

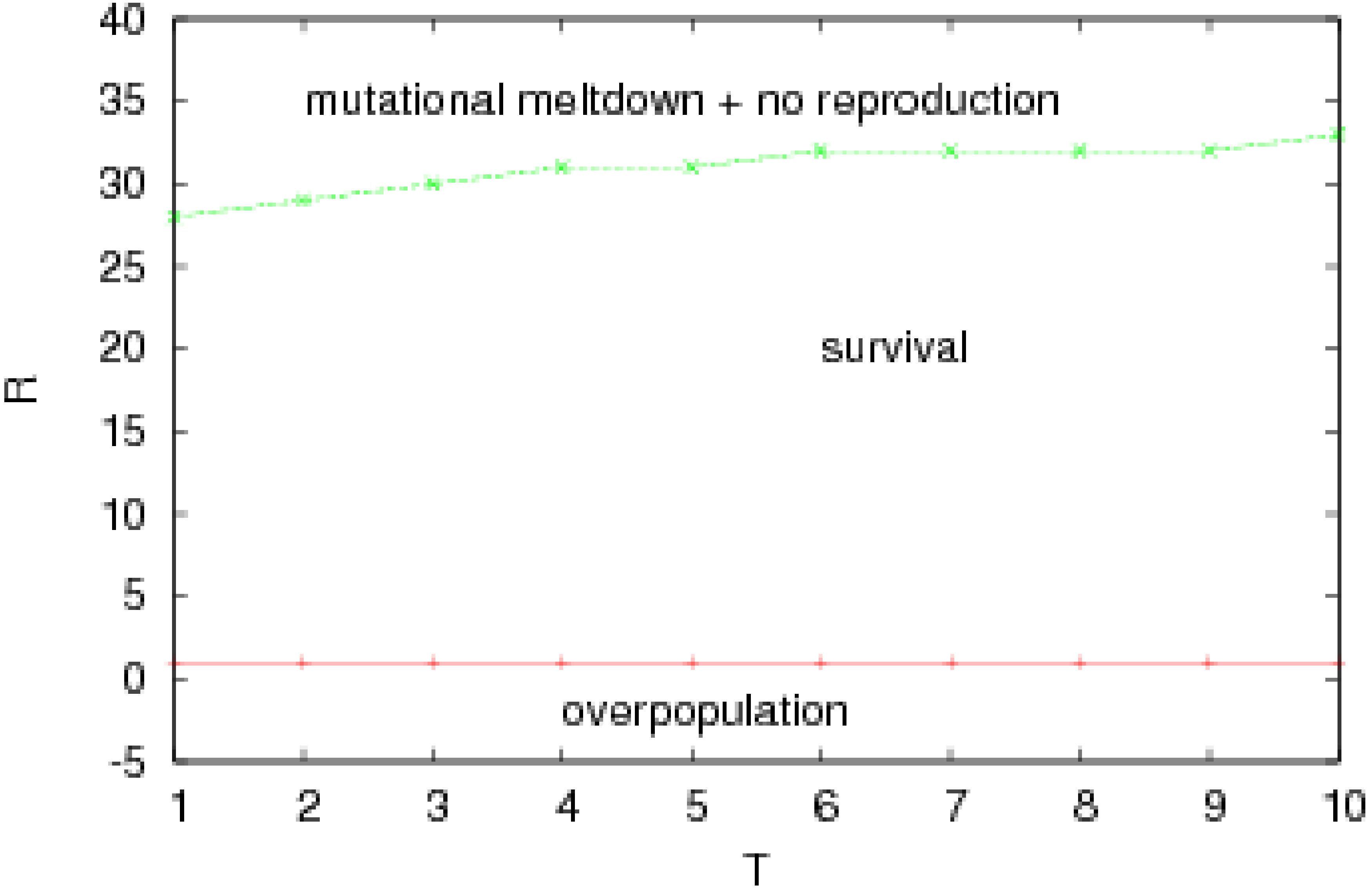

(b) $N_{max}=10^6$, $N_0=3\ 10^5$, T=3, R=8, E=32
mutational meltdown
survival
overpopulation
m, b
0.50, 0.50
1.00, 1.00
0.25, 0.75
Mm
Bb
0
2
4
6
8
10
12
14
16

The latter may be avoided when Verhulst's factor acts only on newly born babies:

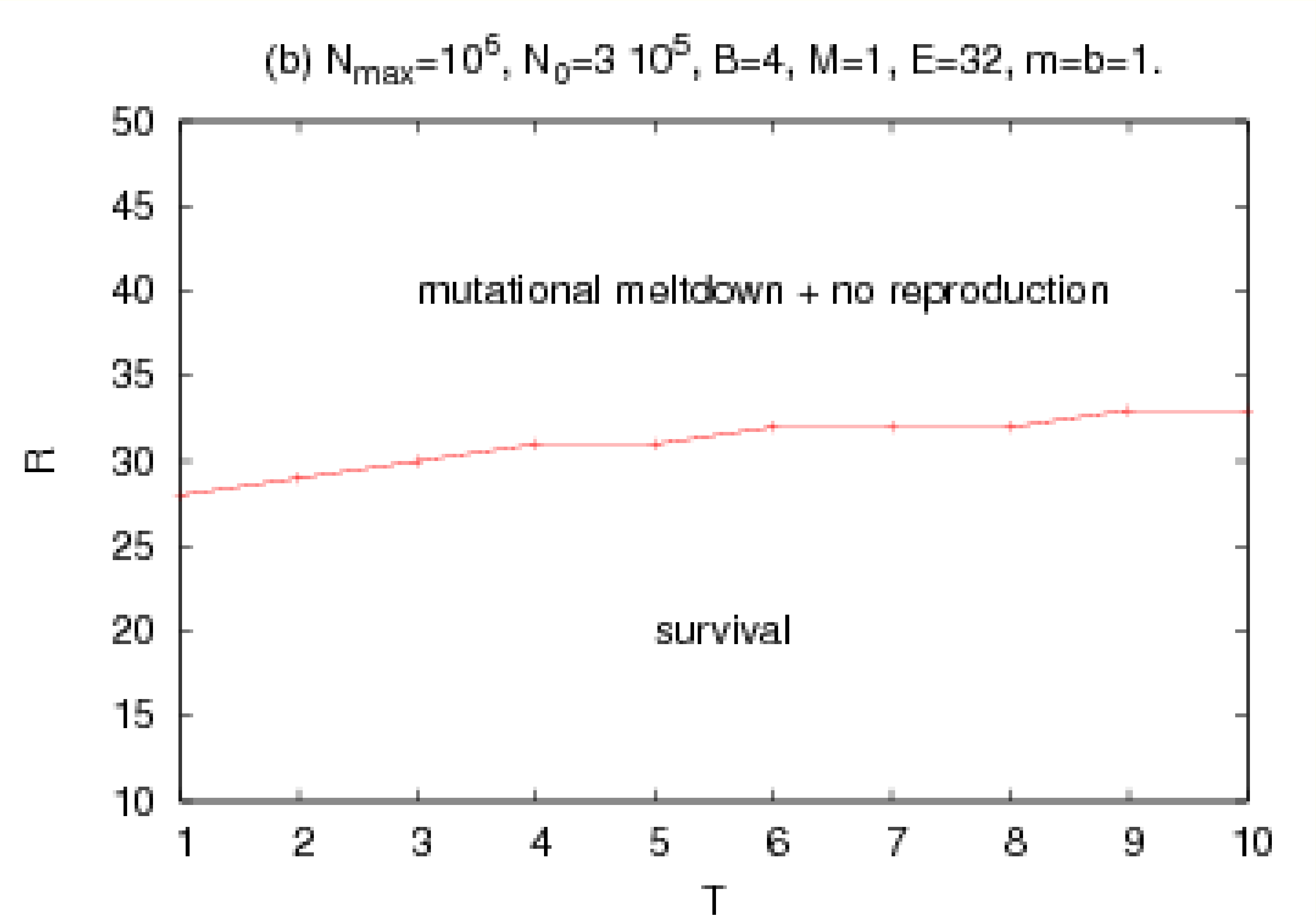



$N_{max}=10^6$, $N_0=3\ 10^5$, B=4, R=8, E=32, m=b=1.
M
50
45
40
35
30
25
20
15
10
5
1
2
3
4
5
6
7
8
9
10
T
mutational meltdown
survival

The phase diagram survival/extinction on (harmful mutation threshold T)/(minimal reproduction age R) plane for Verhulst's factor acting on all individuals and... or only on newly born babies. In the latter case the overpopulation is avoided.



(a) $N_{max}=10^6$, $N_0=3\ 10^5$, B=4, M=1, E=32, m=b=1.


(b) $N_{max}=10^5$, $N_0=3\ 10^5$, B=4, M=1, E=32, m=b=1.
mutational meltdown + no reproduction
survival
R
T
50
45
40
35
30
25
20
15
10
1
2
3
4
5
6
7
8
9
10

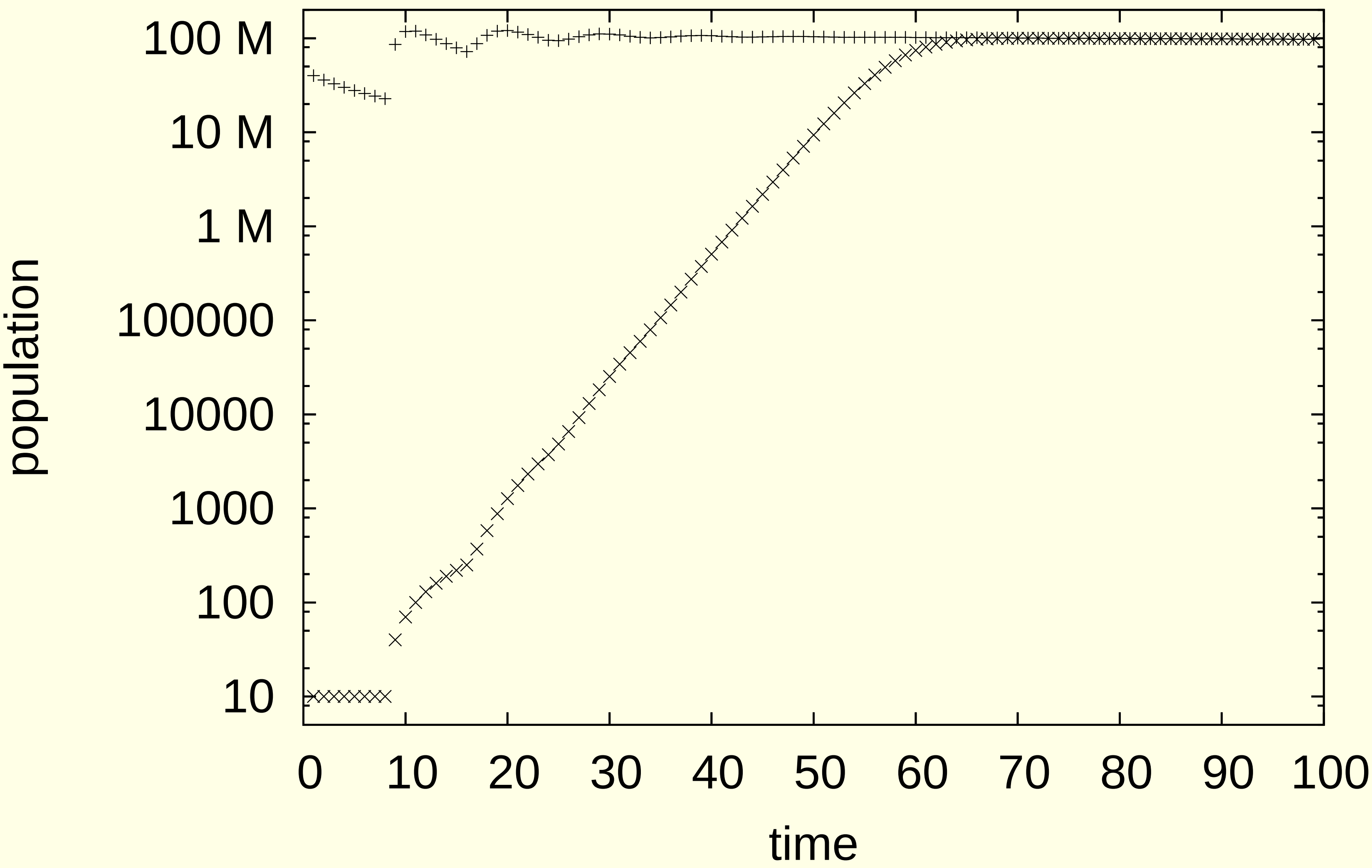
Our results agree with independent work of H. Dudzus, [B.Sc. thesis, Cologne University, 2006], who also found the critical birthrate as

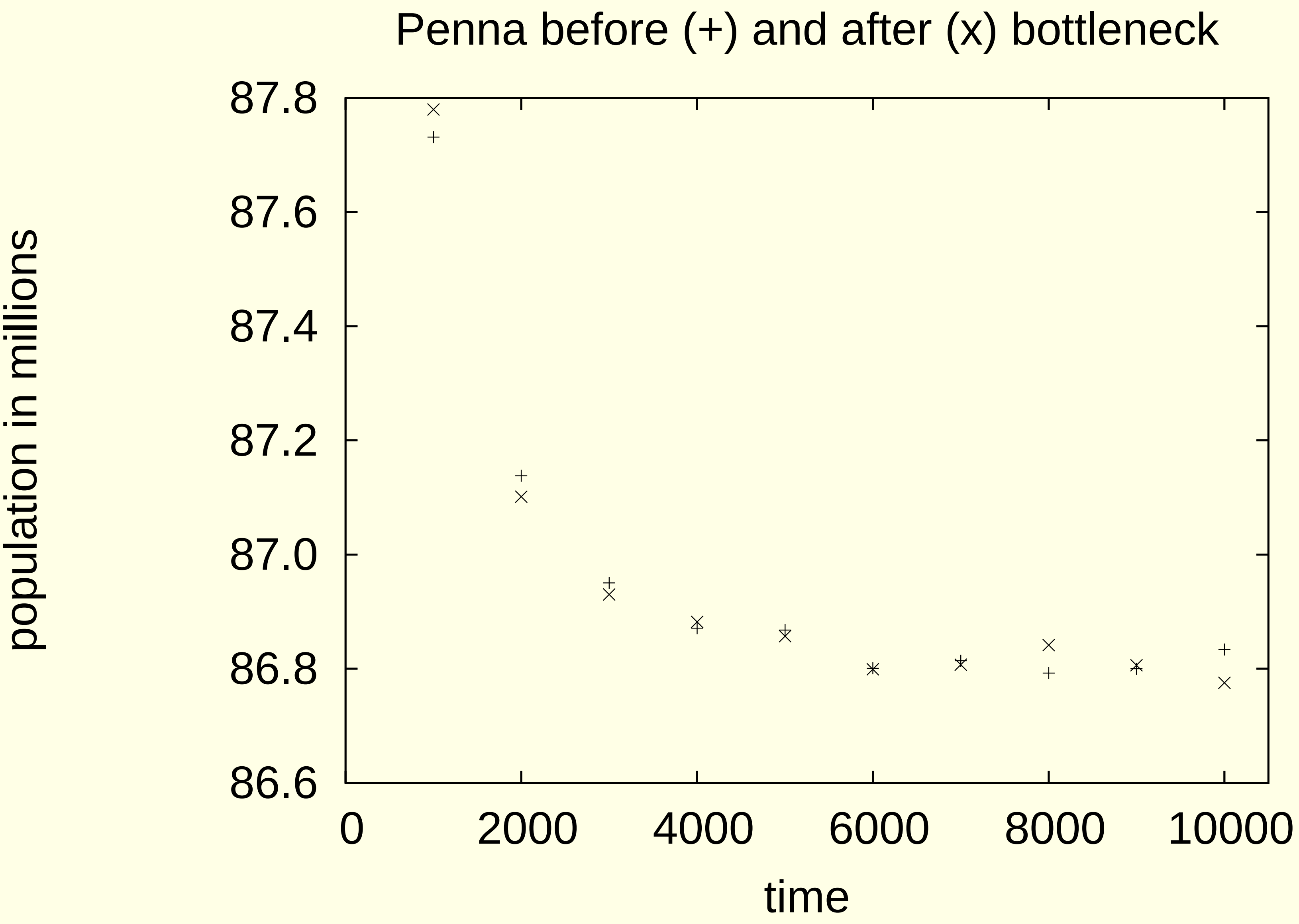
$$B = [32/(31 - R + T)]^M.$$

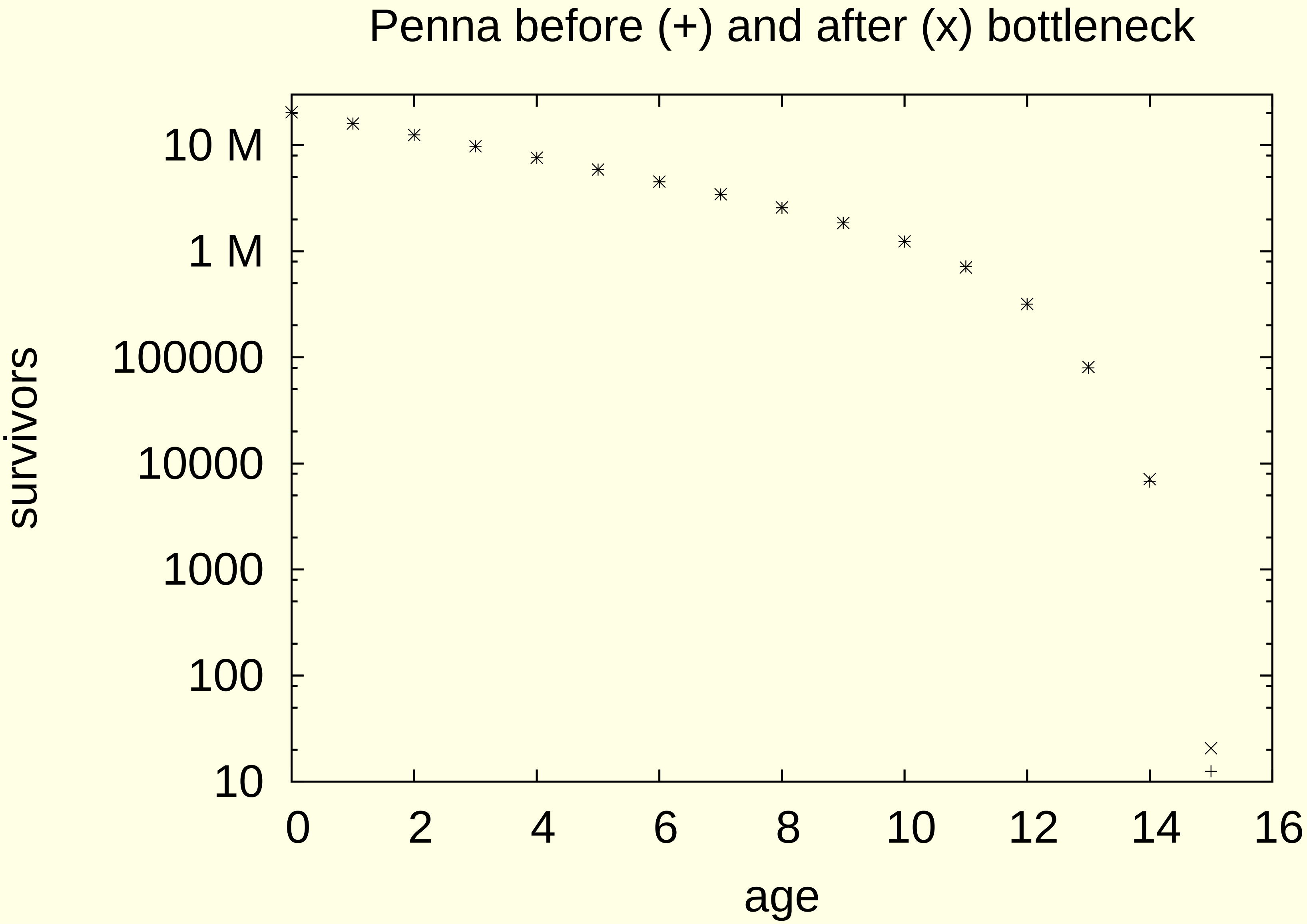
4 (No) bottleneck effect [3]

We made 10,000 iterations (sweeps through the population), then simulated a bottleneck by reducing the population to ten randomly selected individuals, and then made another 10,000 iterations to find the new equilibrium. Then we compare the results after the second half with those after the first half (before the bottleneck).

Penna bottleneck down to 10 at t = 10,000




Penna before (+) and after (x) bottleneck
population in millions
87.8
87.6
87.4
87.2
87.0
86.8
86.6
0
2000
4000
6000
8000
10000
time


Penna before (+) and after (x) bottleneck
survivors
10 M
1 M
100000
10000
1000
100
10
0
2
4
6
8
10
12
14
16
age

- In biology, at a “bottleneck” most of the population dies out e.g. due to an environmental catastrophe, and then the population grows back to about its old size.
- Immediately after this bottleneck, the distribution of genes then is an equilibrium distribution, which in general differs from both a random distribution and the case where all genomes are identical.

- Then, if the system has long-time memory, the final genetic distribution long after the bottleneck can be different from the one immediately before the bottleneck.
- For the Penna ageing model the effects of the bottleneck vanish after several dozen iterations, before even the total population gets its equilibrium value.

- Also in the age distribution of the population after a long time and the distribution of “1” bits among the 32 bit positions no significant difference was found.

References

[1] K.M., et al, Lect. Notes Comput. Sc. **3037** (2004) 638

[2] K.M., Theory Biosci. **125** (2007) 147

[3] K.M., D.Stauffer, Adv. Complex Syst. — in print