



“Contagious diseases stimulate genetic diversity”

The evolutionary effects of contagious diseases

*An analysis using the
Susceptible – Infected – Susceptible (SIS) model*

Key words: contagious diseases, KtW, SIS model, evolution, diversity, herd immunity.

Guest Lecture on October 20, 2022 by: Henk-Jan van der Molen,
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Whoami

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1961



1984



1998



Inspectie Leefomgeving en Transport
Ministerie van Infrastructuur en Waterstaat

2006



Gemeente Haarlemmermeer



1979



1990



2002



2013 – 2022: CISO @

Ministerie van Veiligheid en Justitie



RAAD VOOR ACCREDITATIE



Ministerie van Volksgezondheid,
Welzijn en Sport



Ministerie van Infrastructuur
en Waterstaat

$$\mathcal{F}(\omega) = \frac{1}{\sqrt{2\pi}} \int_{-\infty}^{\infty} f(t) e^{-i\omega t} dt$$



Agenda

1. Introduction: biodiversity paradox
2. From *Predator – Prey* to the *SIS-model*
3. Evolutionary survival: avoid extinction
4. Biodiversity in the homogeneous SIS-model
5. Diversity in the heterogeneous SIS-model
6. Conclusions, open questions & discussion



My questions

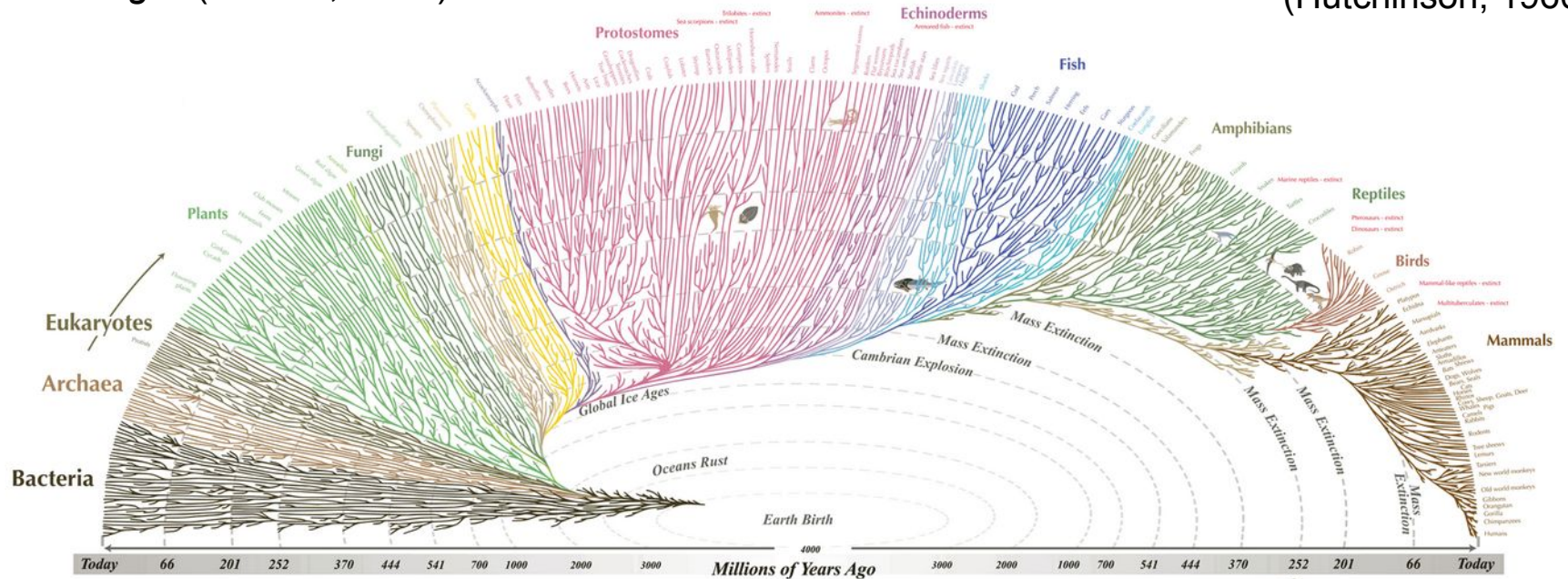
- Do you question the logic presented?
 - E.g. definition of diversity
 - Using two subpopulations in a population
- Does the title match the mathematical evidence?
- Any other concerns?

1. Introduction – Biodiversity paradox

“It is not the strongest of the species that survives, nor the most intelligent.

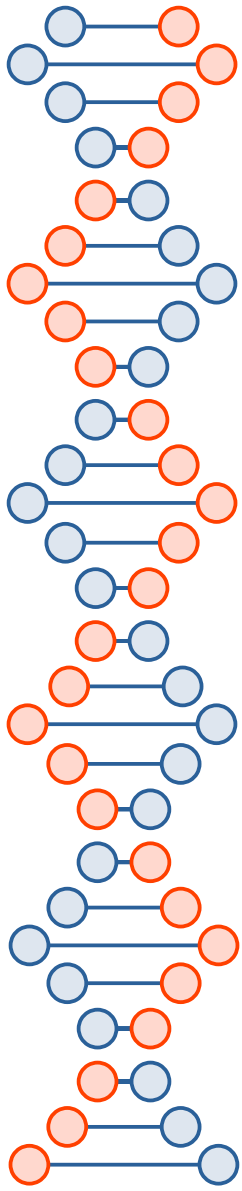
It is the one that is most adaptable to change” (Darwin, 1859)

“Why do so many species coexist that feed on the same nutrients, instead of one species out-competing all the others” (Hutchinson, 1960)



All the major and many of the minor living branches of life are shown on this diagram, but only a few of those that have gone extinct are shown. Example: Dinosaurs - extinct

Concerns on biodiversity

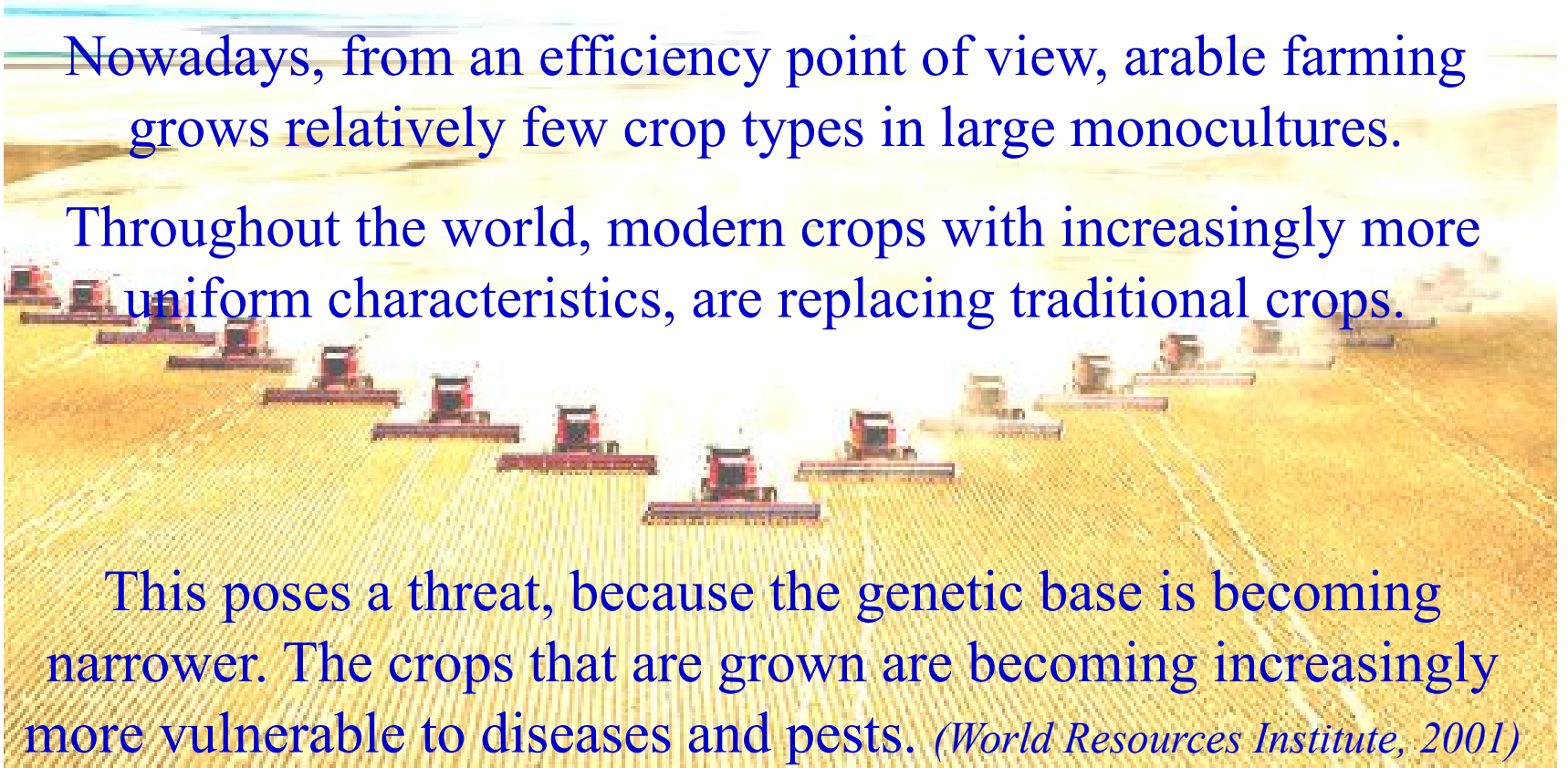
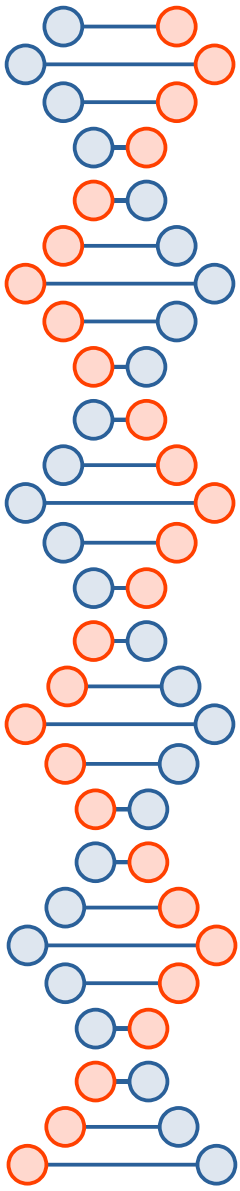


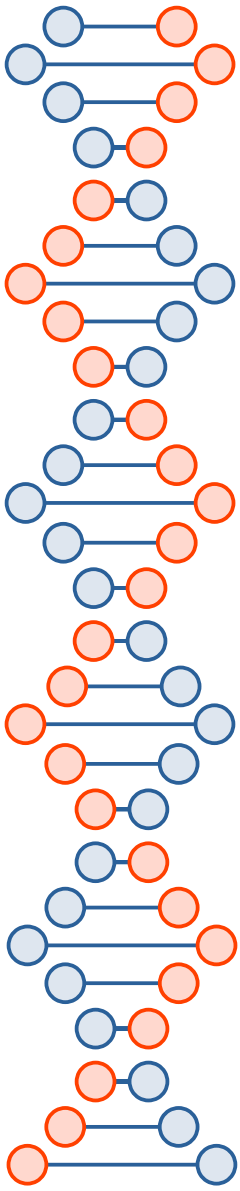
Mono-cultures are vulnerable

Nowadays, from an efficiency point of view, arable farming grows relatively few crop types in large monocultures.

Throughout the world, modern crops with increasingly more uniform characteristics, are replacing traditional crops.

This poses a threat, because the genetic base is becoming narrower. The crops that are grown are becoming increasingly more vulnerable to diseases and pests. *(World Resources Institute, 2001)*



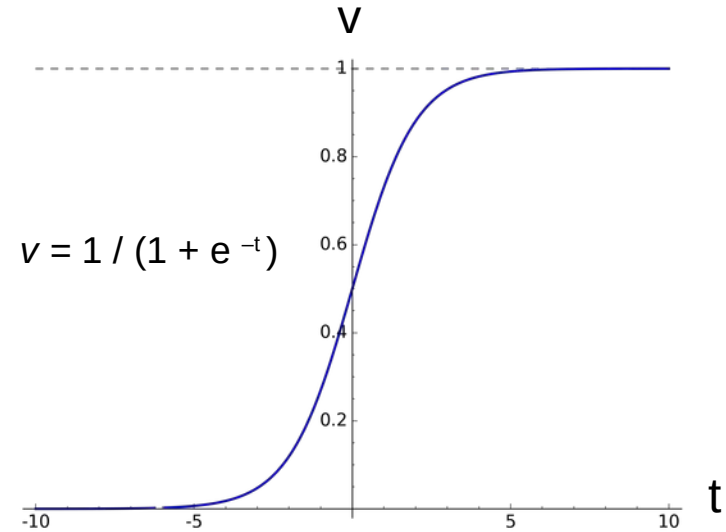
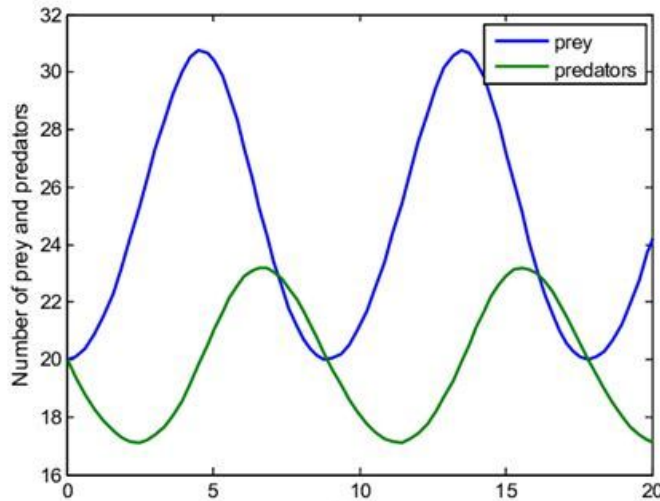


2. From *Predator – Prey* to *SIS* model

$$\text{Predator } (x): \frac{dx}{dt} = ax + bxy$$

$$\text{Prey } (y): \frac{dy}{dt} = cx - dxy$$

$$\frac{dv}{dt} = v - \beta v^2$$





3. Evolutionary survival: avoid extinction

“Species change through the gradual **failure of some lineages** to reproduce, resulting in a subtle but steady drift in the species' genetic make-up towards that of lineages that are more successful.

Although **in most cases these processes are quite slow**, an entire species can go extinct catastrophically if none of its various lineages can reproduce fast enough to offset unusually high levels of mortality.

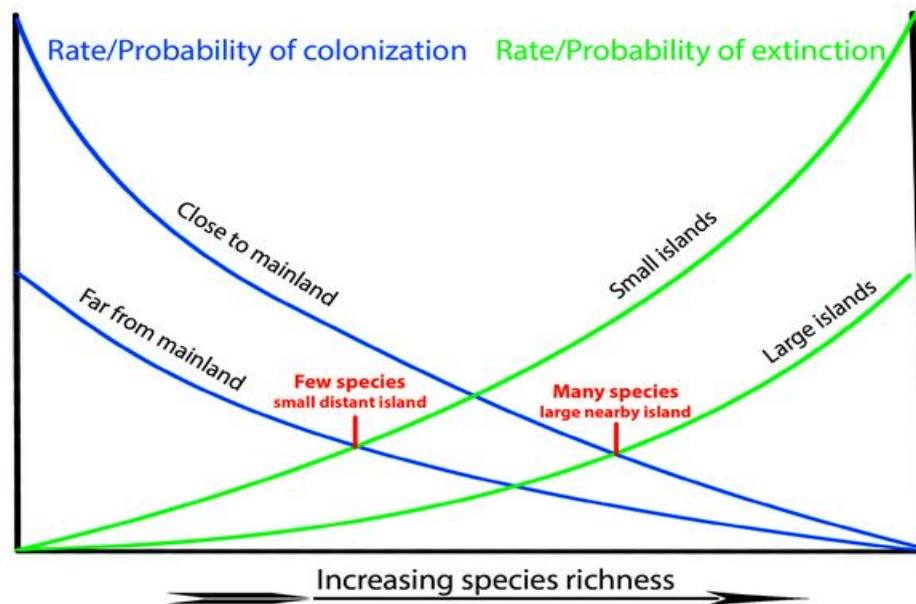
There is always a **steady trickle of such extinctions** over time – there have been literally dozens within our own lineage during the course of our six-million-year evolutionary history.

Sometimes, however, environmental conditions conspire to produce a **rapid burst of extinctions.**” (Robin Dunbar)

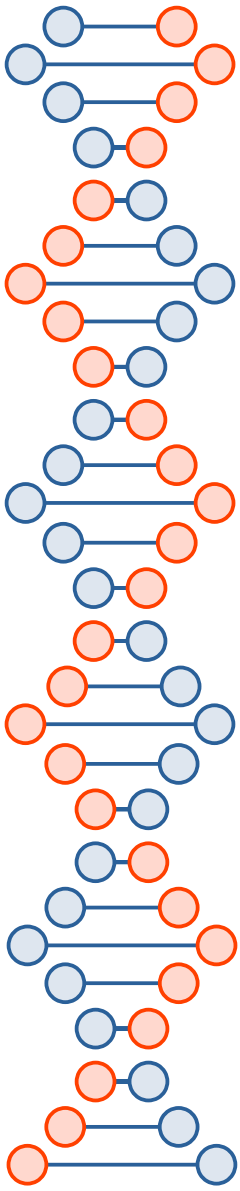
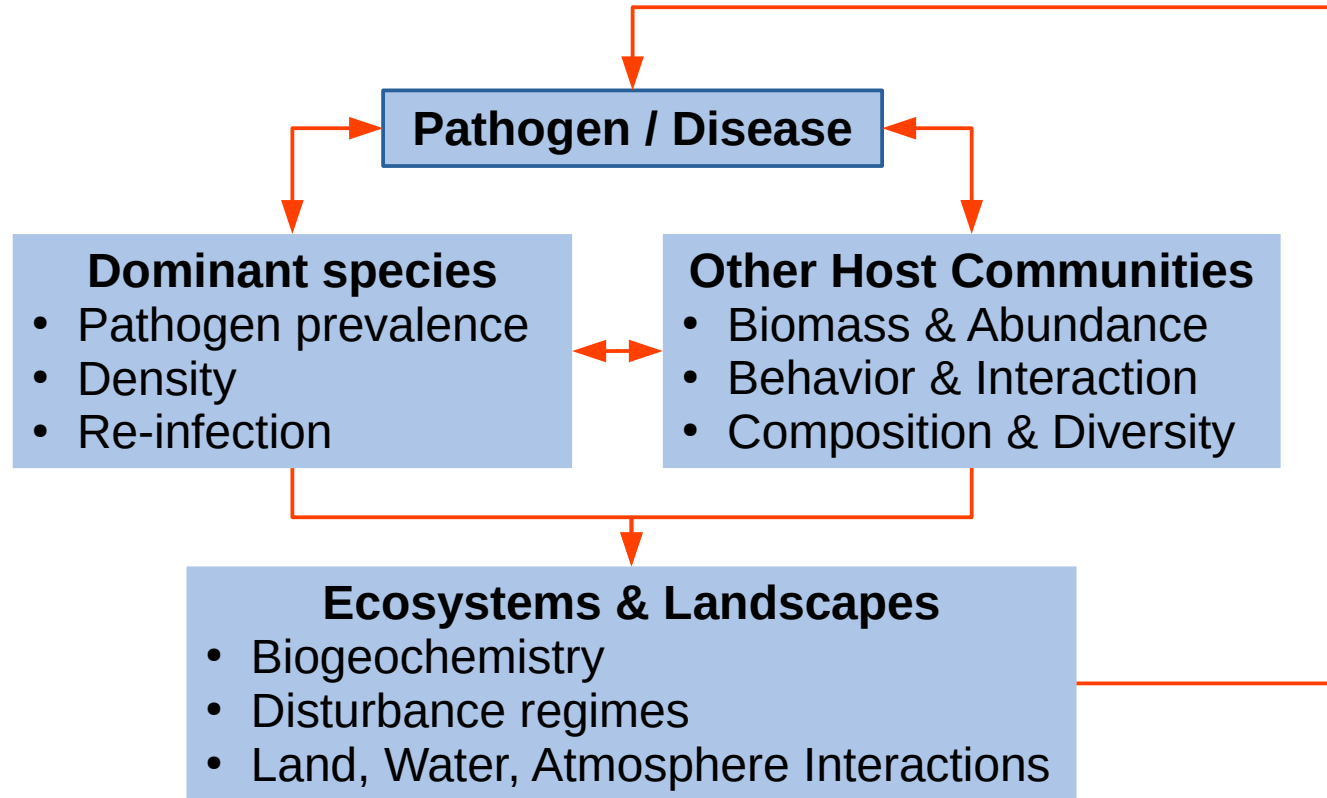
Model for Island Biogeography (MacArthur & Wilson)

- S = #species on the island
- P = #of potential immigrant species
- λ = immigration rate per species
- μ = extinction rate per species

$$\frac{dS}{dt} = \lambda(P - S) - \mu S = 0 \rightarrow S = \frac{\lambda P}{\lambda + \mu}$$



Relation Pathogens to Host Communities and Ecosystems



Classes of contagious diseases with
Basic Reproduction Number (R_0)
and *Herd Immunity Threshold (HIT)*

Infection	Class	Diversity	R_0	HIT(%)
Influenza H1N1	A	High	1.3 - 2	23 - 50
SARS	A	High	2 - 4	50 - 75
STD: HPV	B	High	0.5	0
Mumps	C	Low	4 - 7	75 - 86
Polio	C	Low	5 - 7	80 - 86
Rubella	C	Low	6 - 7	83 - 86
Pertussis	C	Low	12 - 17	92 - 94
Measles	C	Low	12 - 18	83 - 94



4. Steady State of the homogeneous SIS model

$$\frac{dv}{dt} = \beta v(1-v) - \delta v = \delta(R_0 v(1-v) - v) = 0 \rightarrow v = 1 - \frac{1}{R_0}$$

- v = % Infected; $(1 - v)$ = % Susceptible
- β , δ = Infection rate, curing rate
- R_0 = Basic Reproduction Number = β/δ

Diversity in the homogeneous SIS model

$$\frac{dv}{dt} = \delta(R_1 v(1 - n_2 - v) - v) = 0 \rightarrow v = 1 - n_2 - \frac{1}{R_1}$$

- n_1 (remains susceptible) + n_2 (becomes immune) = 1
- Diversity $D = 2n_1n_2R_1 / R_0$; $D = [0..1]$ if $\{0 \leq n_1, n_2 \leq 1/2\}$
- R_0 must remain constant $\rightarrow R_1 = R_0 / n_1 \rightarrow D = 2n_2$

$$v' = \frac{dv}{dD} = \frac{1}{2} \frac{dv}{dn_2} = -\frac{1}{2} \left(1 - \frac{1}{R_0}\right)$$



5. Steady State of the heterogeneous SIS model

$$\frac{dv_i}{dt} = \delta_i (R_i v (1 - v_i) - v_i); \quad \sum_{i=1}^m (n_i) = 1; \quad v = \sum_{i=1}^m (n_i v_i); \quad R_0 = \sum_{i=1}^m (n_i R_i)$$

- v_i , $(1 - v_i)$ = %Infected, %Susceptible for subpopulation i
- β_i , δ_i = Infection rate, curing rate for subpopulation i
- R_i = Basic Reproduction Number for subpopulation i
- m = #subpopulations

$$\frac{dv_i}{dt} = 0 \rightarrow v_i = \left(\frac{R_i v}{R_i v + 1} \right); \quad v = \sum_{i=1}^m n_i v_i = v \sum_{i=1}^m \left(\frac{n_i R_i}{R_i v + 1} \right) \rightarrow$$

$$\{\forall v \neq 0\} \sum_{i=1}^m \left(\frac{n_i R_i}{R_i v + 1} \right) = 1$$



Diversity in the heterogeneous SIS model (m=2)

$$\left(\frac{n_1 R_1}{R_1 v + 1} + \frac{n_2 R_2}{R_2 v + 1} \right) = 1 \rightarrow av^2 + bv + c = 0 \rightarrow v = \frac{-b + \sqrt{d}}{2a}$$

$$a = R_1 R_2; \quad b = R_1 + R_2 - R_1 R_2; \quad c = 1 - n_1 R_1 - n_2 R_2; \quad d = b^2 - 4ac$$

- $R_0 = n_1 R_1 + n_2 R_2 = \text{constant} \rightarrow 2R_0 = R_1 + R_2$
- $D = 2n_1 n_2 |R_1 - R_2| / R_0 \rightarrow \{0 \leq D \leq 1\}$
- Reduce complexity: $n_1 = n_2 = 1/2$;
- $\{R_0 \leq R_1 \leq 2R_0\} \rightarrow D = (R_1 - R_0) / R_0 \equiv R_1 / R_0 \rightarrow$

$$v' = R_0 \frac{dv}{dR} = 2 R_0^2 (R - R_0) \frac{(R^2 - 2 R_0 R + 2 R_0^2 - R_0 \sqrt{d})}{R^2 (R - 2 R_0)^2 \sqrt{d}}$$



Sagemath calculations

- Sign of derivative $dv/dD < 0 \rightarrow$
- Derivative of v for Diversity:

```
# plot v, dv as functions of D = (R - R_0)/R_0 →  
# R = R_0(D+1) with R_0 = 2, 5, 9  
# v can be normalized with the factor: R_0 / (R_0 - 1)  
# Run in load("Plot_v_dv_using_D.sage")
```

```
R_0, D = var('R_0 D')  
R_0=2  
print("Plotting v, dv in green for R_0 =",R_0)
```

```
a=(1-D^2)*R_0^2  
b=2*R_0-a  
c=1-R_0  
d=b*b-4*a*c
```

```
v2=(sqrt(d)-b)/(2*a)  
dv2 = v2.diff(D)
```

```
p_v2 = plot(v2,0,1, color='green', gridlines='minor',  
legend_label='R0 = 2')  
p_dv2 = plot(dv2,0,1, color='green', gridlines='minor')  
p_v2.axes_labels(['Diversity', 'v'])  
p_dv2.axes_labels(['Diversity', 'dv'])
```

```
# Negative slope dv/dD using D  
sage: R, R_0, D = var('R R_0 D')
```

```
sage: a=(1-D^2)*R_0^2  
sage: b=2*R_0-a  
sage: c=1-R_0  
sage: d=expand(b^2 - 4*a*c)
```

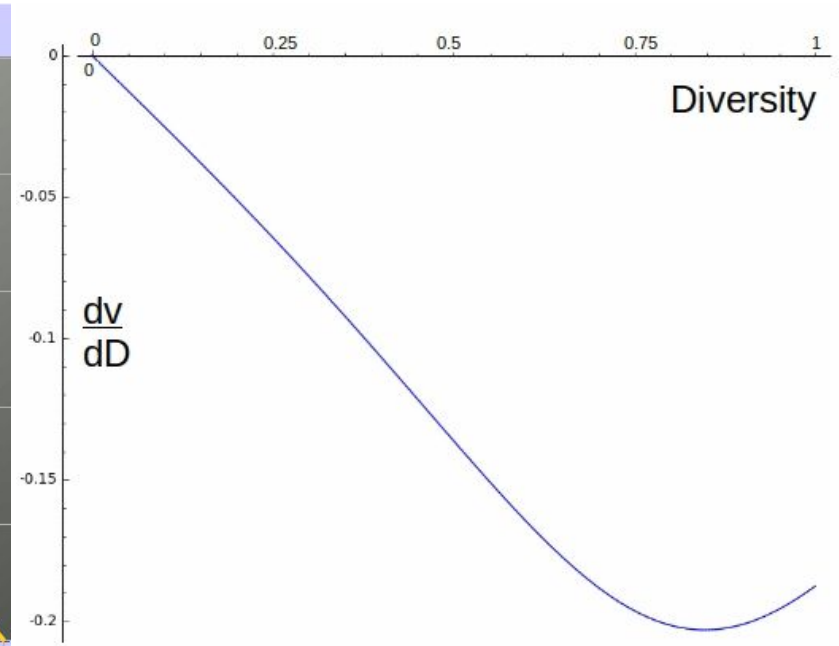
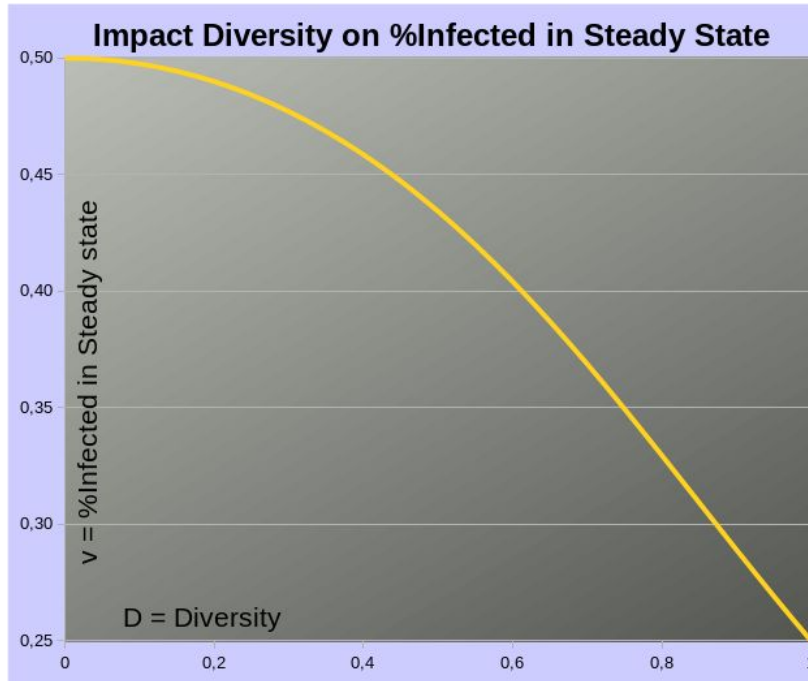
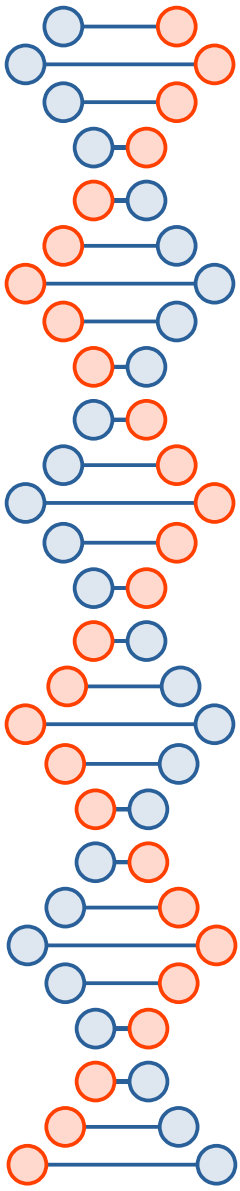
```
sage: da=a.diff(D)  
sage: db=b.diff(D)  
sage: dd=factor(expand(d.diff(D)))
```

```
sage: da  
-2*D*R_0^2  
sage: db  
2*D*R_0^2  
sage: dd  
4*(D^2*R_0^2 - R_0^2 + 2)*D*R_0^2
```

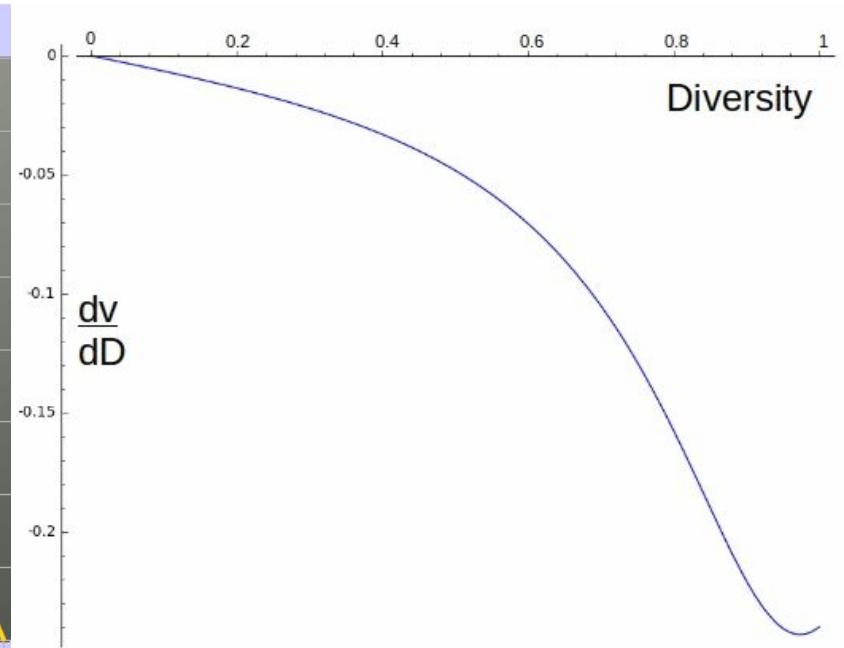
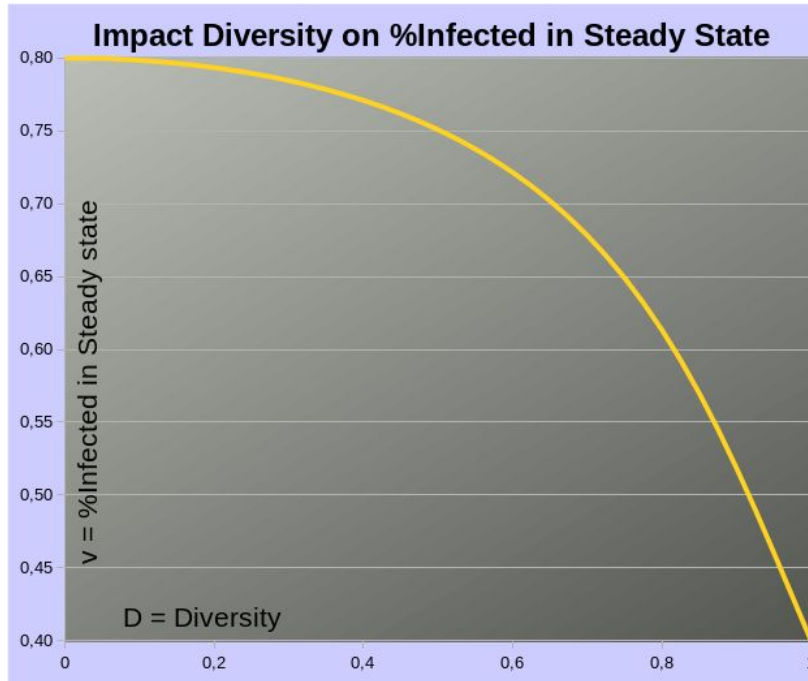
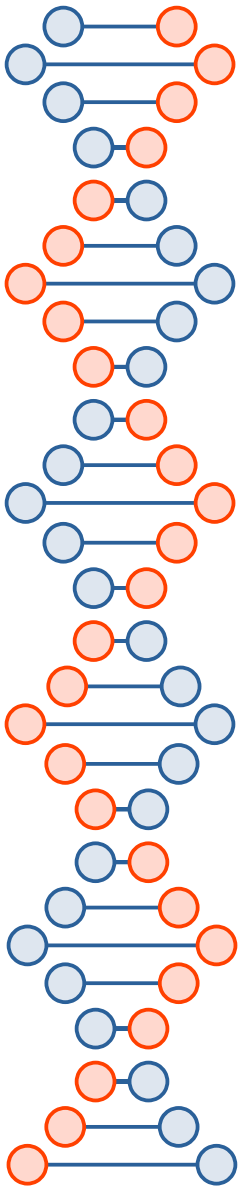
```
sage: factor(expand(2*da*b-2*a*db))  
-8*D*R_0^3  
sage: factor(expand(a*dd-2*da*d))  
8*(D^2 + 1)*D*R_0^4
```

```
sage: f=8*(D^2 + 1)*D*R_0^4  
sage: g=factor(expand(f^2 - d*(8*D*R_0^3)^2))  
sage: print("The slope of dv is negative: ", g)  
-64*(D + 1)^2*(D - 1)^2*D^2*(R_0 + 1)*(R_0 - 1)*R_0^8
```

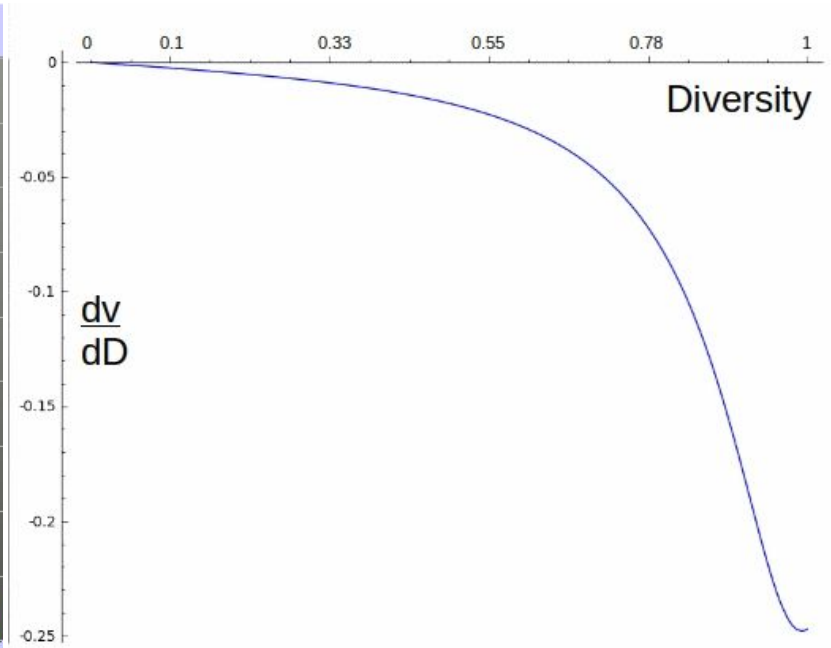
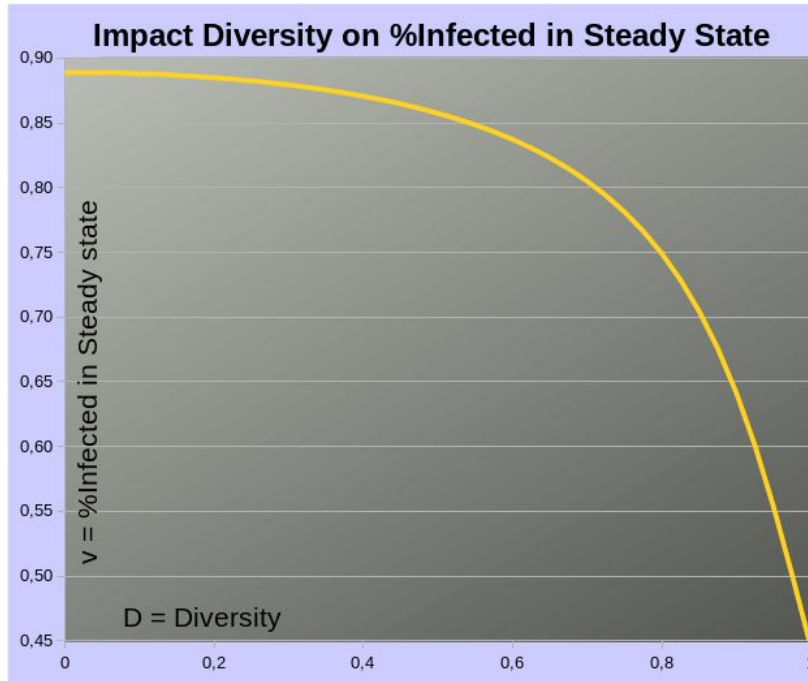
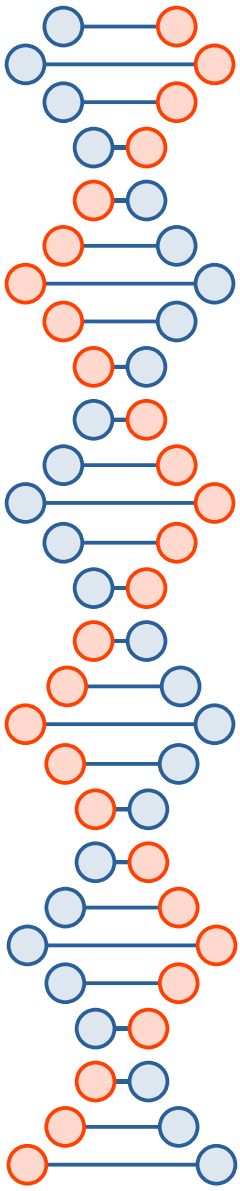
Impact Diversity on Steady State (v) – $R_0 = 2$



Impact Diversity on Steady State (v) – $R_0 = 5$



Impact Diversity on Steady State (v) – $R_0 = 9$



Conclusions

- MacArthur – Wilson theory of Island Bio Geography: smaller populations are more likely to become extinct.
- Contagious diseases = fast mutating predators. Multi-cell organisms cannot adapt to prevent epidemics.
- Mono-cultures have no diversity within the population, the distance to the HIT is at maximum.
- The more dominant and genetically uniform a species becomes, the more it is impacted by epidemics.
- When more pathogens can meet the criterion ($R_0 > 1$), epidemics become more frequent and more severe.
- For the size of populations an equilibrium is likely.

- The heterogeneous SIS model ($m=2$) can be used to determine the effect of diversity, when comparing any two groups of species that differ in their shared susceptibility for a contagious disease.
- The more genetically different those two groups become, the lower the impact of epidemics gets and the better the chances are for survival of the population as a whole.
- Thus, contagious diseases stimulate genetic diversity.

Open Questions:

- Eliminate SIS model restrictions, e.g. populations not perfectly mixed, multiple Predator – Prey relations, mutating diseases.
- Investigate: contagious diseases + MacArthur-Wilson theory of Island Bio-geography → optimal size of populations.