Epidemics, Demography and Migrations

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G. Schinaia - Epidemics and Immigration in a Local Community with Limited Resources and External Demographic Pressure

Applied Mathematical Sciences, Vol. 1, 2007, no. 35, 1737 - 1758

G. Schinaia - The Effects of Immigration Policies on the Diffusion of Infectious Diseases: Demographic Balance and Disease Control

Applied Mathematical Sciences, Vol. 2, 2008, no. 15, 701 - 718

G. Schinaia - Epidemics and Local Demographic Dynamics

MPRA No. 113062

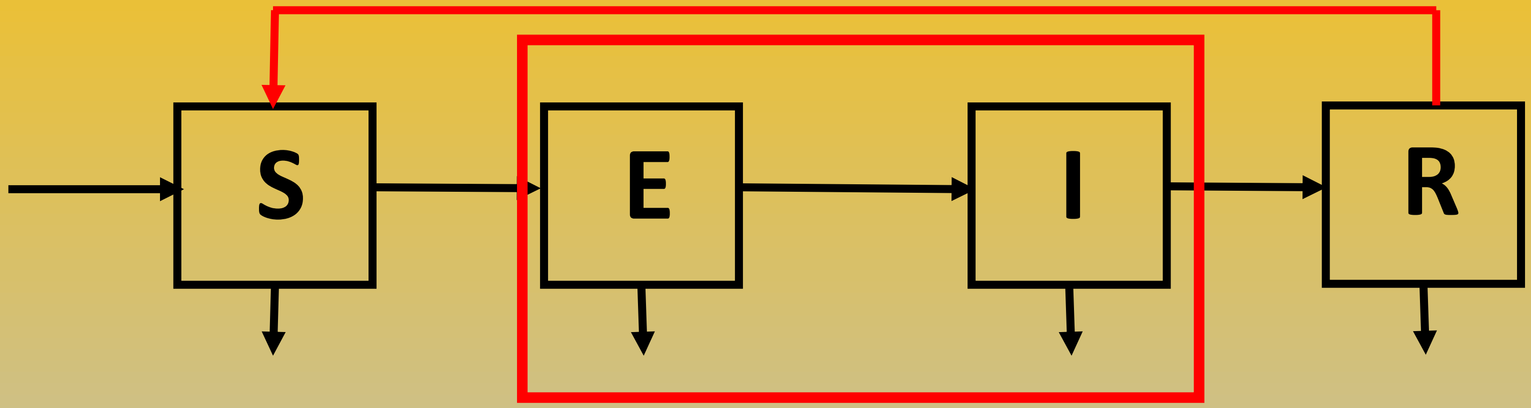
G. Schinaia - A Schematic Design of Epidemic Modelling with Variable Immigration Dynamics

arXiv pending

G. Schinaia - Optimal and Suboptimal Time Scheduling in the Estimation of Fractional Transfer Coefficients of Compartmental Systems

in progress

Subpopulation groups in the epidemic dynamics (Kermack-McKendrick Model, 1927)



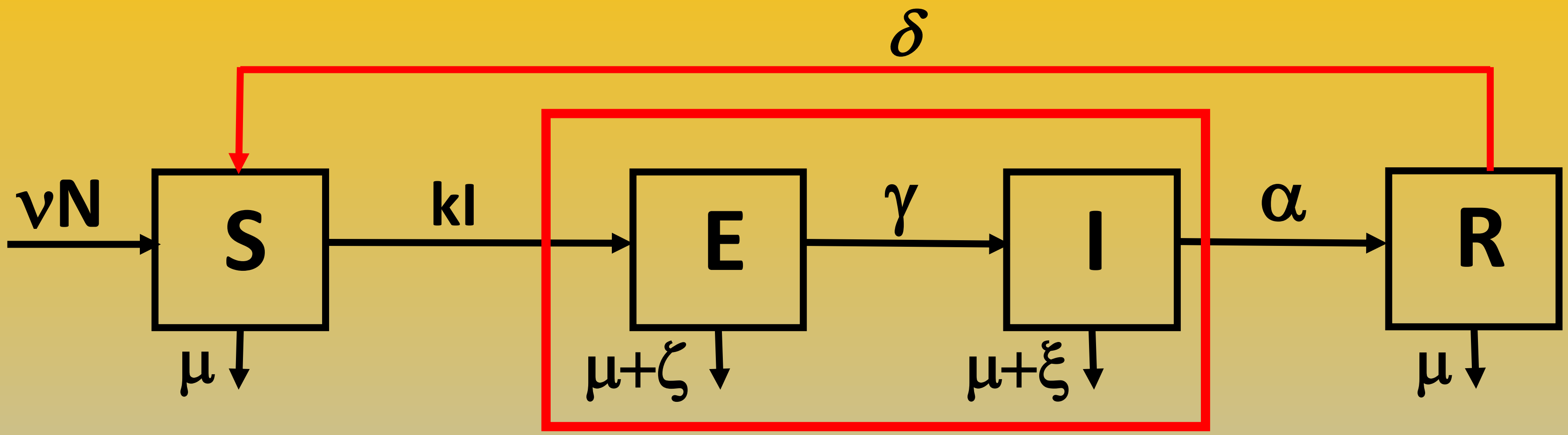
S – susceptible individuals

(E – individuals exposed to the infection: infected but not infectious)

I – infected and infectious individuals

R – individuals removed from the infection process

PARAMETERS controlling the epidemic dynamics (closed population: N=S+E+I+R)



ν, μ – birth and death rates

α – removal/recovery rate

k – force of infection

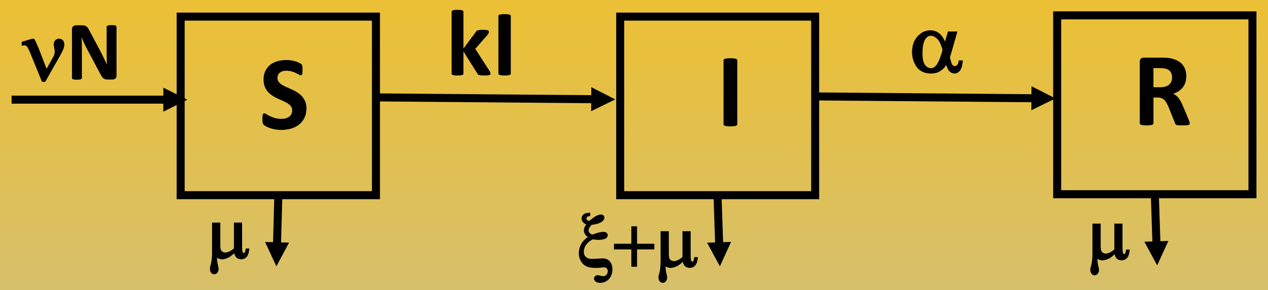
γ – rate of infectiousness for infected individuals

δ – rate of loss of immunity

ξ, ζ – extra mortality rates

S.I.R. model

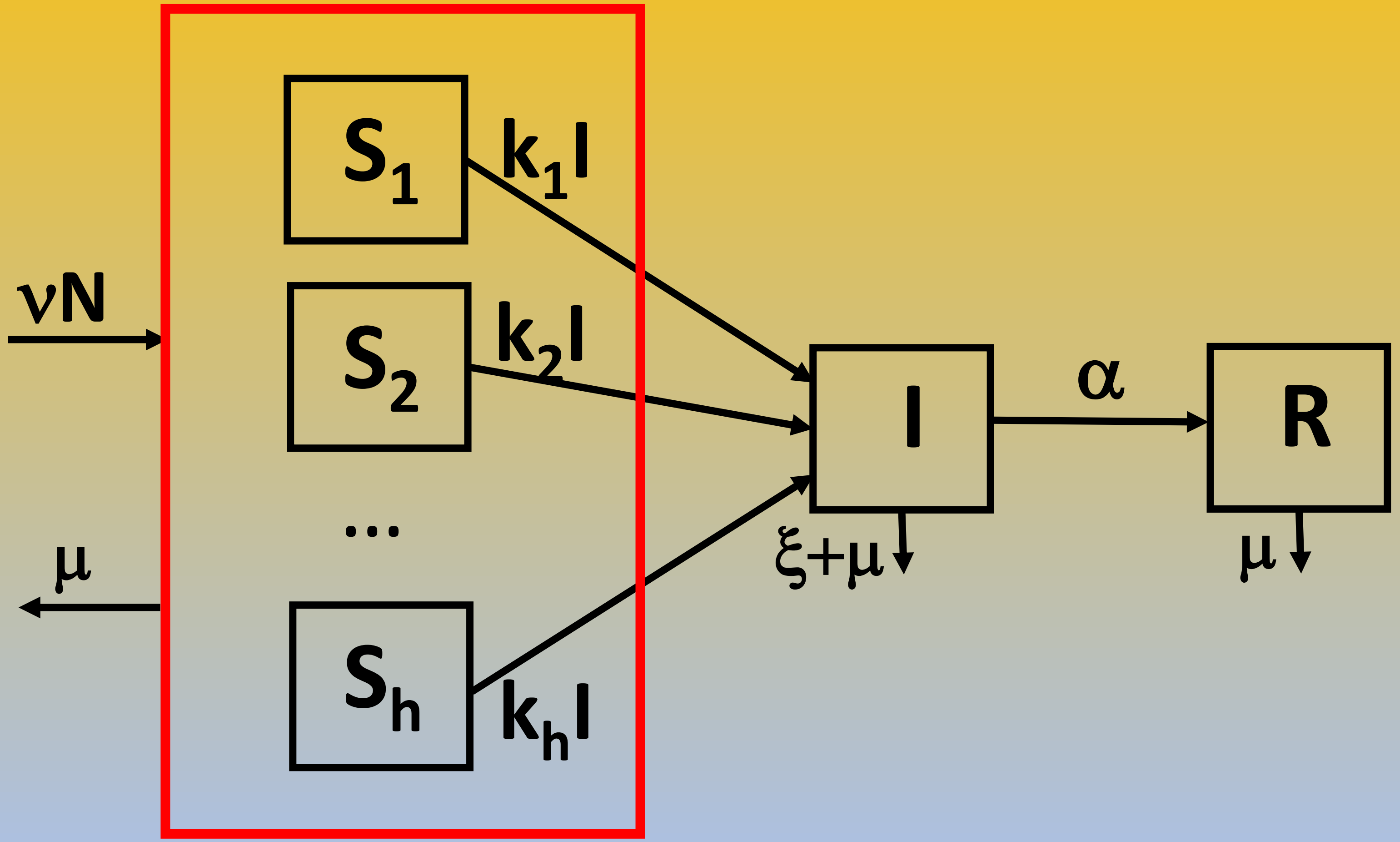
an infection that generates a partially fatal infection with recovery/immunity



$$\begin{cases} \frac{dS(t)}{dt} = \nu N - kI(t)S(t) - \mu S(t) \\ \frac{dI(t)}{dt} = kI(t)S(t) - (\mu + \xi + \alpha)I(t) \\ \frac{dR(t)}{dt} = \alpha I(t) - \mu R(t) \end{cases}$$

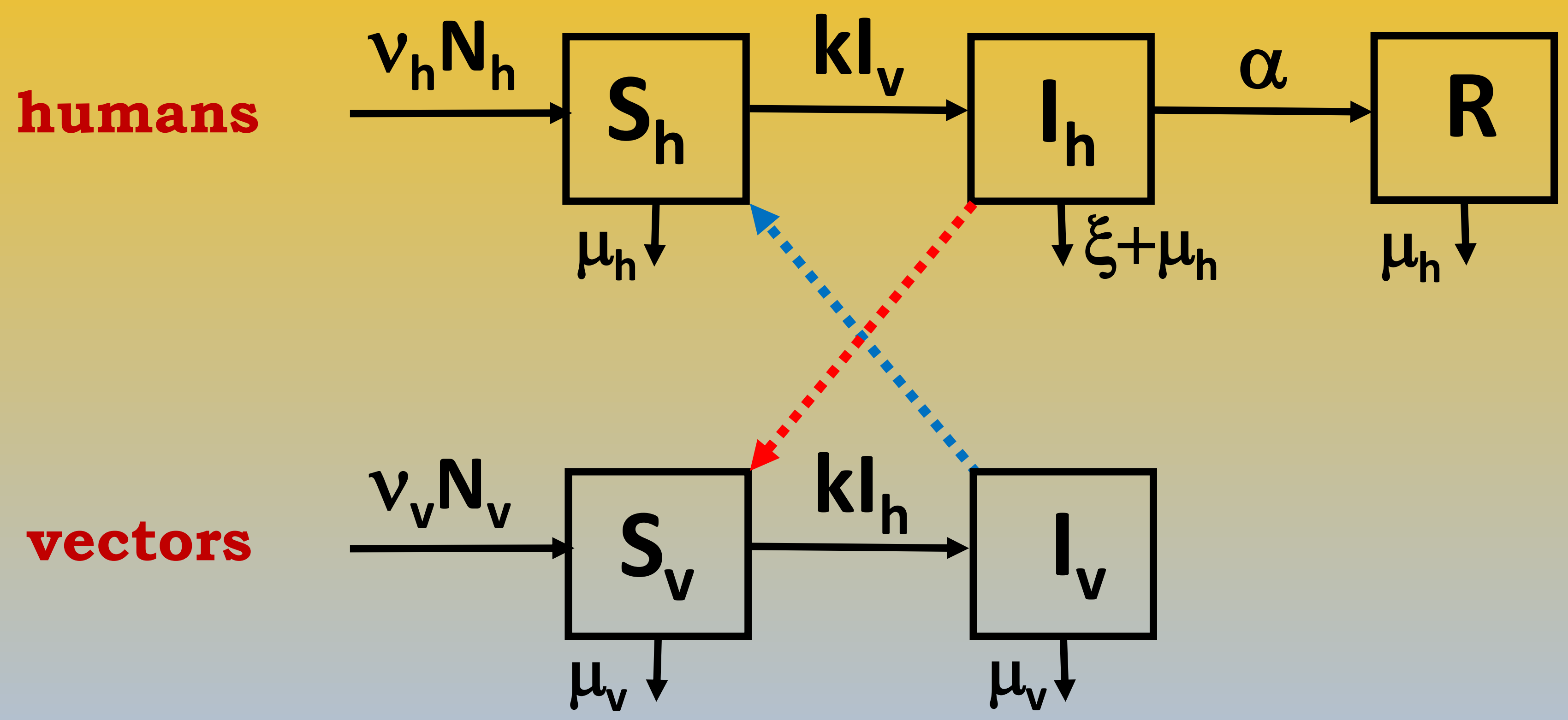
COMPOUND MODELS (1)

Heterogeneity (e.g.: phenotype-related susceptibility)



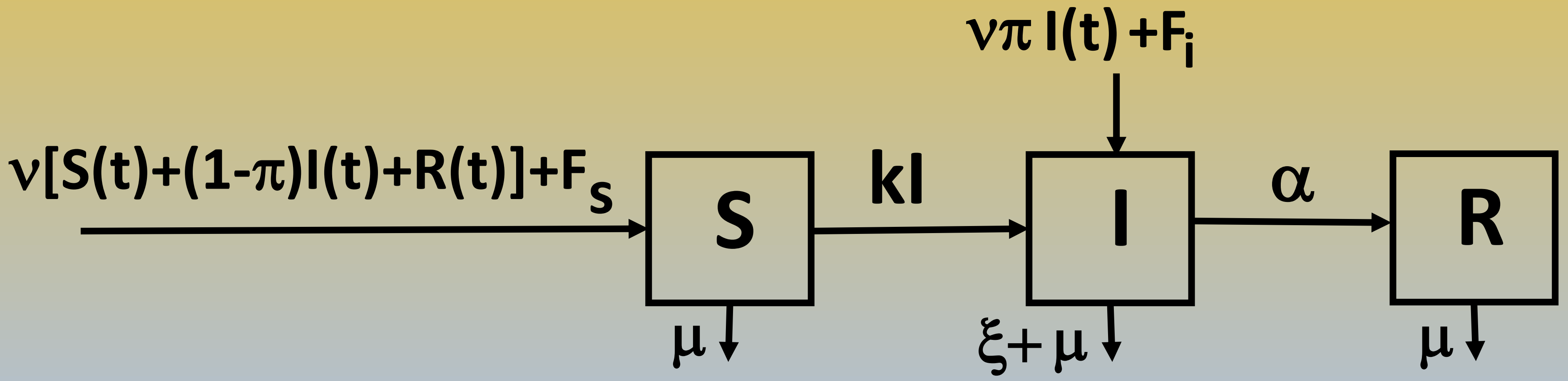
COMPOUND MODELS (2)

Vector borne infection (e.g.: malaria, yellow fever, dengue, west Nile …)



S.I.R. model with variable demographic dynamics

vertical transmission
partially fatal disease
immigration



Population/Immigration models
(autonomous systems)

1. **variable population, constant immigration**
   (prisons, migratory areas, new development areas)

   Brauer, Van der Driessche *Models for transmission of disease with immigration of infectives* MathBiosci *2001, 171(2)*

2. **constant population, variable immigration**
   (unsaturated demography, imbalanced resources)

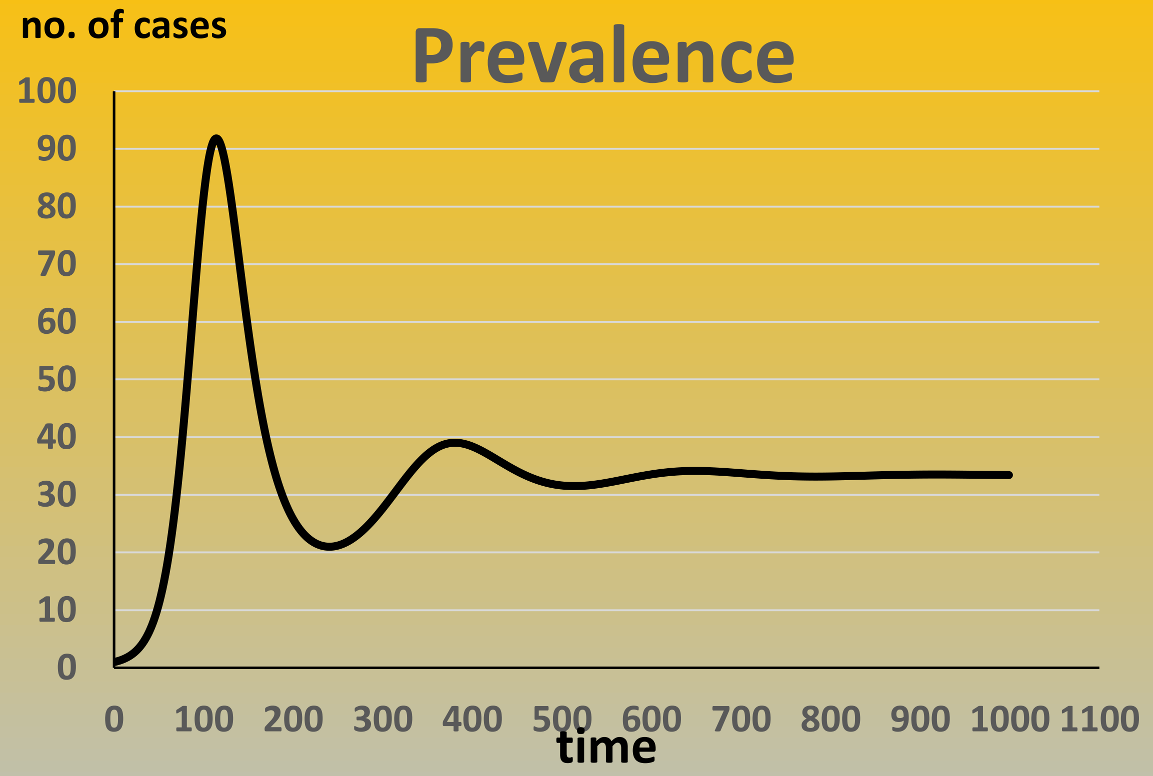
$$\frac{dN(t)}{dt} = \frac{dS(t)}{dt} + \frac{dI(t)}{dt} + \frac{dR(t)}{dt} = 0$$

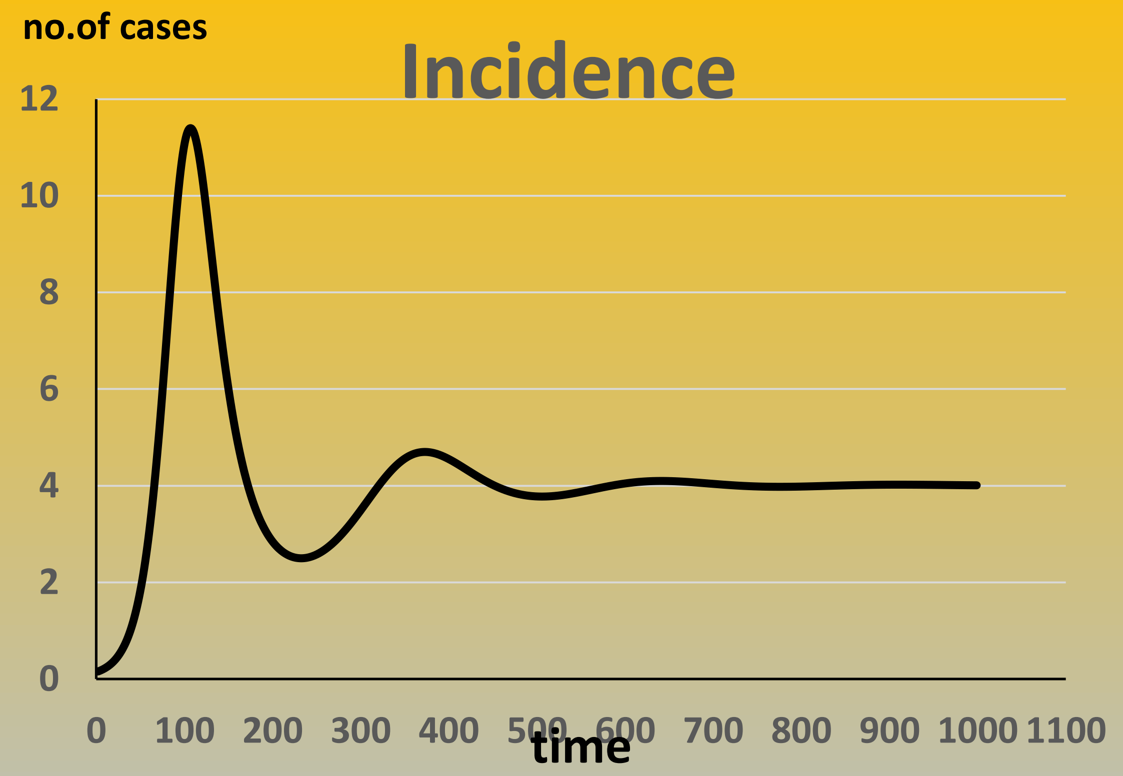
$$\begin{cases} F_S(t) = (1-p)\{(\mu-\nu)[S(t)+I(t)+R(t)] + \xi I(t)\} \\ F_I(t) = p\{(\mu-\nu)[S(t)+I(t)+R(t)] + \xi I(t)\} \end{cases}$$

$$\begin{cases} \frac{dS(t)}{dt} = \nu[S(t) + (1-\pi)I(t) + R(t)] - \big(\mu + kI(t)\big)S(t) + (1-p)\{(\mu-\nu)[S(t)+I(t)+R(t)] + \xi I(t)\} \\ \frac{dI(t)}{dt} = kI(t)S(t) + \nu\pi S(t) - \mu S(t) + p\{(\mu-\nu)[S(t)+I(t)+R(t)] + \xi I(t)\} \\ \frac{dR(t)}{dt} = \alpha S(t) - \mu R(t) \end{cases}$$

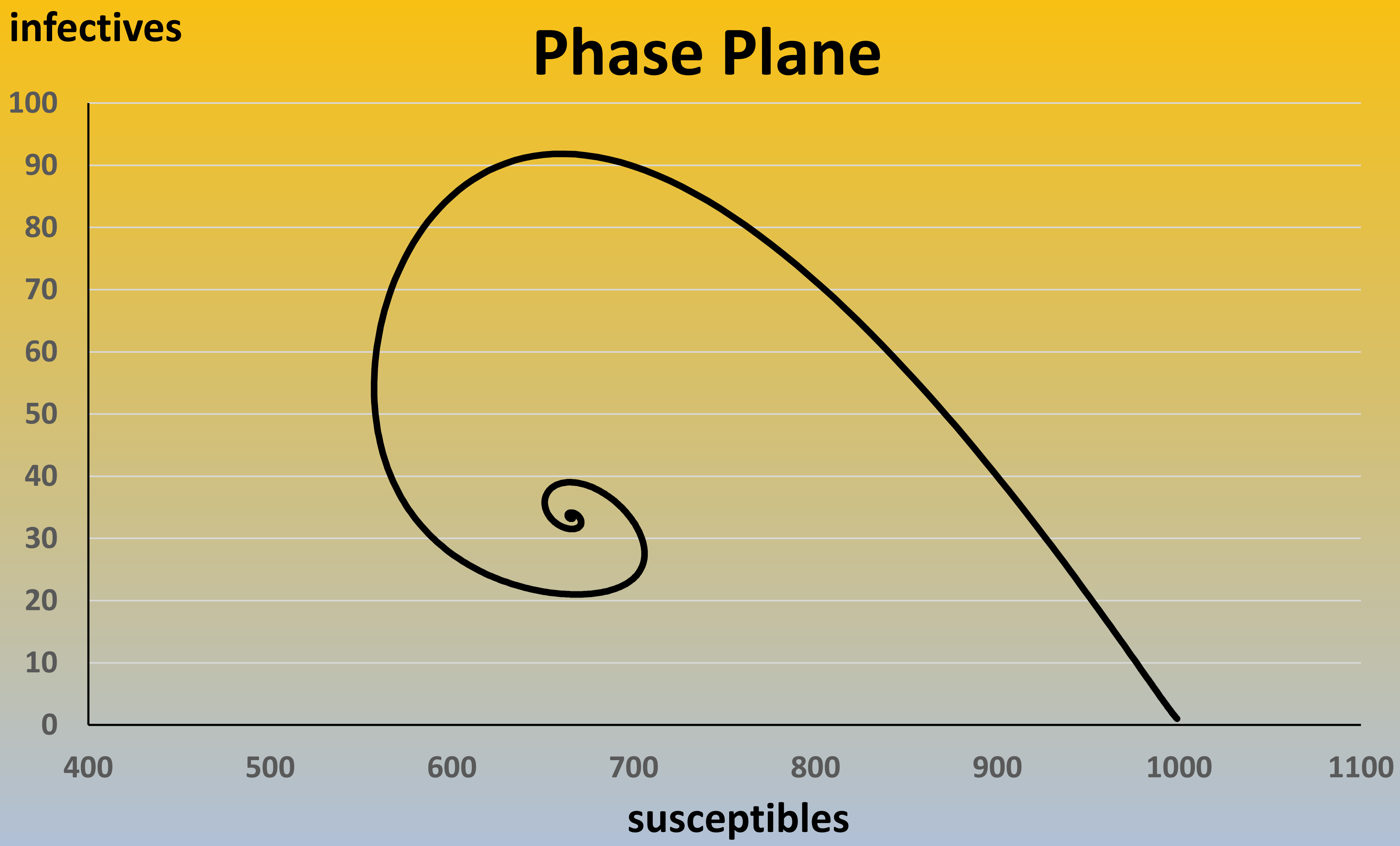
$$R_0 = \frac{kN}{\mu + (1-p)(\xi-\pi) - p\nu + \alpha}$$

double bifurcation threshold: $R_0 = 1$; $p(\mu-\nu) = 0$





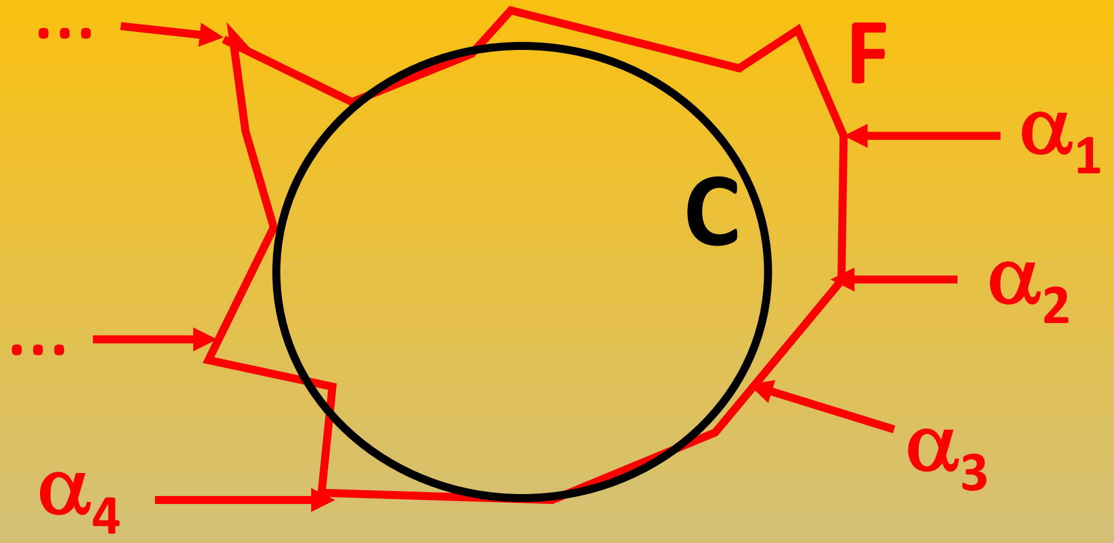
$R_0 = 1.78$ $p(\mu - \nu) = 0.000022$

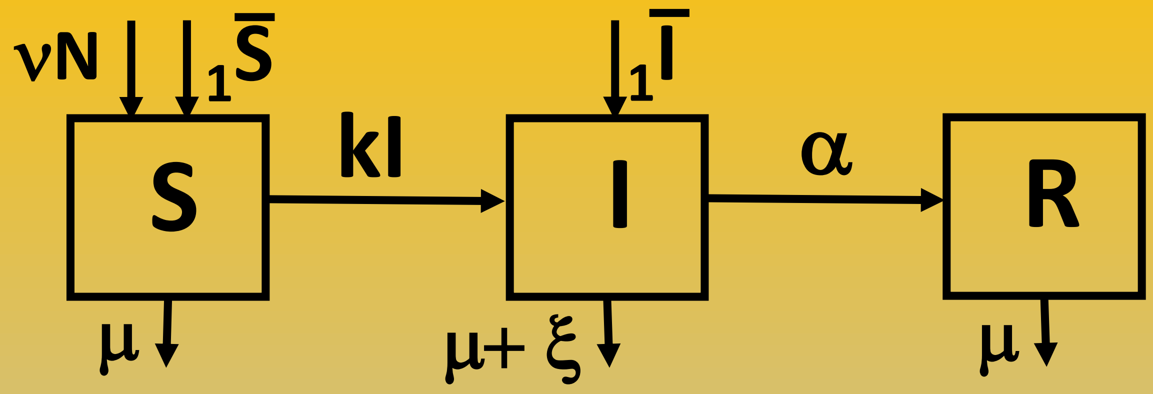

infectives
Phase Plane
100
90
80
70
60
50
40
30
20
10
0
400
500
600
700
800
900
1000
1100
susceptibles

COMPOUND MODELS (3)

Space/intensity variable immigration

$$Y(t) = \oint_F \mathbf{Y}(t;\boldsymbol{\alpha})d\boldsymbol{\alpha} = \oint_F q(\boldsymbol{\alpha})\mathbf{Y}(t;\boldsymbol{\alpha})d\boldsymbol{\alpha} + \oint_F \big(1 - q(\boldsymbol{\alpha})\big)\mathbf{Y}(t;\boldsymbol{\alpha})d\boldsymbol{\alpha} = \oint_F {}_1\mathbf{I}(t;\boldsymbol{\alpha})d\boldsymbol{\alpha} + \oint_F {}_1\mathbf{S}(t;\boldsymbol{\alpha})d\boldsymbol{\alpha}$$





$$Y(t) = \int_C {}_1\mathbf{I}\big(t; \boldsymbol{\alpha}(\theta)\big)\boldsymbol{\alpha}'(\theta)d\theta + \int_C {}_1\mathbf{S}\big(t; \boldsymbol{\alpha}(\theta)\big)\boldsymbol{\alpha}'(\theta)d\theta = {}_1\bar{\mathbf{I}} + {}_1\bar{\mathbf{S}}$$

By separating the two sources of variability we have:

$$S(t, \theta) = {}_0S(t)\ {}_1\mathbf{S}(t; \theta)\boldsymbol{\alpha}'(\theta)d\theta$$

$$I(t, \theta) = {}_0I(t)\ {}_1\mathbf{I}(t; \theta)\boldsymbol{\alpha}'(\theta)d\theta$$

Time-constant immigration flows

$$S(t;\theta) = {}_{(0)}S(t) + {}_{(1)}\mathbf{S}(\theta)\boldsymbol{\alpha}'(\theta) \quad I(t;\theta) = {}_{(0)}I(t) + {}_{(1)}\mathbf{I}(\theta)\boldsymbol{\alpha}'(\theta)$$

Constant proportion of infectives in the immigration flow

$$S(t;\theta) = {}_{(0)}S(t) + (1-q)\mathbf{Y}(t;\theta)\boldsymbol{\alpha}'(\theta) \quad I(t;\theta) = {}_{(0)}I(t) + q\mathbf{Y}(t;\theta)\boldsymbol{\alpha}'(\theta)$$

Time-constant immigration flows with a constant proportion of infectives

$$S(t;\theta) = {}_{(0)}S(t) + (1-q)\mathbf{Y}(\theta)\boldsymbol{\alpha}'(\theta) \quad I(t;\theta) = {}_{(0)}I(t) + q\mathbf{Y}(\theta)\boldsymbol{\alpha}'(\theta)$$

Space-independent, non-infective immigration

$$S(t;\theta) = S(t) = {}_{(0)}S(t) + {}_{(1)}S(t) \quad I(t;\theta) = {}_{(0)}I(t) + {}_{(1)}\mathbf{I}(t;\theta)\boldsymbol{\alpha}'(\theta)$$


That's all Folks!
SUPERB wallpapers

containment vs no containment