

①

1. Given S species H habitats

Each species can be seen in 1, 2, ... M habitats
 $S_1, S_2, S_3, S_4, \dots$ etc represent # species found in exactly
i habitats.

$H_1, H_2, \dots, H_k, \dots, H_H$ represent # species seen in k^{th} habitat.

Given these constraints, determine the ~~maximum~~ distribution
of distinct combinations of habitats used by species.

Monte Carlo calculation

Assignments of habitats to species.

Problem: some species with more than one habitats may be
left, with ~~all~~ when only one habitat is remaining.

Algorithm: Given $S \times H$ matrix, whose elements are 1 or 0,
and given S row totals and H column totals, generate
the matrices satisfying these constraints.

Arrange Rows in descending order of row total, cols in ascending order
of col totals X

Start with species having maximum habitats.

Assign n randomly chosen habitats.

Decrement one from those habitat totals,

continue till end.

→ Proportional to habitats
→ all equals likely.

2. Use RDK technique to obtain # species in Ogriks @ zones

3. Zonation of Uttara Kannada based on bird similarity;

4. Minimum viable population analysis.

- a) single sex model, check with equal mortalities.
- b) Differences due to absence of age structure.
- c) Demographic stochasticity leading to ext. pop. size; unequal # ♂ & ♀
- d) " " ; age structure → cone of reproductive values.

5. Plot data

① General large map - 2 m x 1 m (1 km = 2 m ∴ 1 cm = 5 meters → 1 cm.

Each 20 x 20 grid = 4 cm x 4 cm.

Each hectare = 20 cm x 20 cm = one A4 size paper.

② Small map.

Since there are 50 x 25 quadrats each 20 x 20

tent mode can be used to represent

Ⓐ species density

Ⓑ strand density

Ⓒ Presence absence of any species etc.

Ⓓ species diversity etc.

③ Basic statistics

Ⓐ Distribution of # trees per species

Ⓑ " " for growth classes

Ⓒ Diversity indices, quadrat → hectare → plot

Ⓓ For some of the species, nearest neighbor analysis.

Ⓔ Make a 1250 x 50 table, quadrat x species, with # individuals in each.

④ more detailed analysis

Ⓐ Similarity between quadrats

Ⓑ species area curves

Ⓒ nearest neighbor analysis

Ⓓ tentations; area per tree

Ⓔ competition / association between species.

6. Optimal Harvesting.

- (i) 3D plot of $JH \times JP$, at each grid, av. yield.
- (ii) Fluctuations — uniform, normal, & correlated/unrelated.

7. RB model

- (i) consequences when inheritance is purely genetic.
- (ii) stability of pure ~~form~~ familial/random combination to invasion
- (iii) Alternative form of preference.

8. Mol. Dynamics & unwinding of chains.

~~Order~~ Separation time from freely rotating chains as a fⁿ of length; purely repulsive interaction.

9. Generation of 3/4 stranded DNA on tetrahedra

- (i) Circle & stick model, more than one concentric circle.
- (ii) Projections
- (iii) Space filling model with filled circles.
- (iv) Pinel operations

10. Antigen antibody interaction.

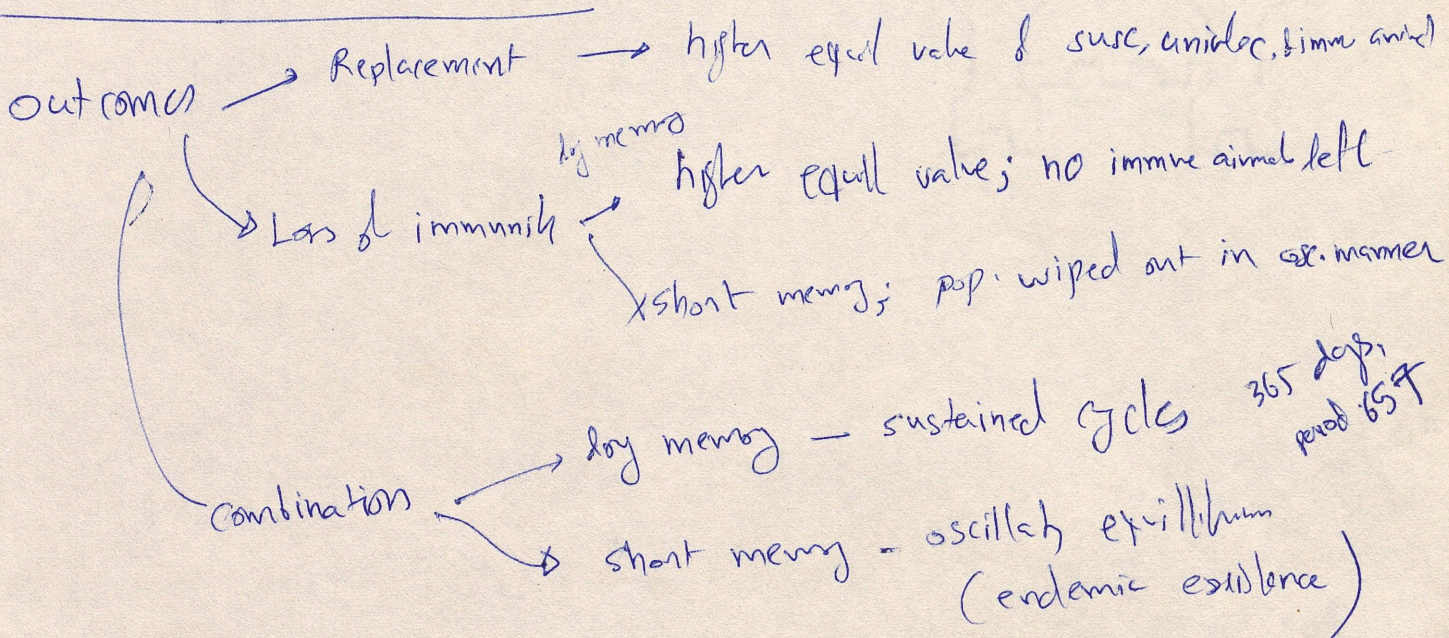
- i) Search for specific sequences
- ii) Characterize ϕ/ψ d. plot as maps
- iii) Take coords from Protein structure bank & plot.

rep02d.out

59	10	0.00100	0.05000	0.10000	0.90000	0.99880	0.00120	0.00013	0.00120
59	10	0.00100	0.05000	0.50000	0.50000	0.99933	0.00067	0.00067	0.00120
59	10	0.00100	0.05000	0.90000	0.10000	0.99987	0.00013	0.00120	0.00120
104	10	0.00100	0.10000	0.10000	0.90000	0.99820	0.00180	0.00020	0.00140
104	10	0.00100	0.10000	0.50000	0.50000	0.99900	0.00100	0.00100	0.00140
104	10	0.00100	0.10000	0.90000	0.10000	0.99980	0.00020	0.00180	0.00140
5001	10	0.00100	0.15000	0.10000	0.90000	0.99614	0.00383	0.00043	0.00160
5001	10	0.00100	0.15000	0.50000	0.50000	0.99772	0.00213	0.00213	0.00160
5001	10	0.00100	0.15000	0.90000	0.10000	0.99960	0.00043	0.00384	0.00160
5001	10	0.00100	0.20000	0.10000	0.90000	0.95612	0.04376	0.00486	0.00180
5001	10	0.00100	0.20000	0.50000	0.50000	0.96761	0.03226	0.03226	0.00180
5001	10	0.00100	0.20000	0.90000	0.10000	0.98631	0.01363	0.12265	0.00180
5001	164	0.00100	0.25000	0.10000	0.90000	0.62938	0.37061	0.04118	0.03022
5001	184	0.00100	0.25000	0.50000	0.50000	0.65513	0.34500	0.34500	0.04644
5001	233	0.00100	0.25000	0.90000	0.10000	0.74201	0.25809	2.32273	0.10837
5001	113	0.00100	0.30000	0.10000	0.90000	0.42516	0.57470	0.06386	0.08534
5001	123	0.00100	0.30000	0.50000	0.50000	0.48124	0.51862	0.51862	0.12185
5001	147	0.00100	0.30000	0.90000	0.10000	0.61513	0.38476	3.46270	0.22526
5001	91	0.00100	0.35000	0.10000	0.90000	0.30061	0.69925	0.07769	0.14500
5001	97	0.00100	0.35000	0.50000	0.50000	0.38008	0.61979	0.61979	0.19601
5001	113	0.00100	0.35000	0.90000	0.10000	0.52730	0.47280	4.25426	0.31837
245	78	0.00100	0.40000	0.10000	0.90000	0.22069	0.77931	0.08659	0.20215
5001	83	0.00100	0.40000	0.50000	0.50000	0.31566	0.68420	0.68420	0.26254
5001	94	0.00100	0.40000	0.90000	0.10000	0.46128	0.53861	4.84752	0.39224
214	69	0.00100	0.45000	0.10000	0.90000	0.16710	0.83290	0.09254	0.25465
5001	73	0.00100	0.45000	0.50000	0.50000	0.27168	0.72818	0.72818	0.32127
5001	82	0.00100	0.45000	0.90000	0.10000	0.41001	0.58988	5.30890	0.45199
194	63	0.00100	0.50000	0.10000	0.90000	0.13010	0.86990	0.09666	0.30302
5001	66	0.00100	0.50000	0.50000	0.50000	0.23992	0.76001	0.76001	0.37214
1348	73	0.00100	0.50000	0.90000	0.10000	0.36911	0.63089	5.67801	0.50127

Final time Peak Init freq c death Rate Surv. Rate suc. imm. dead num # infect in epidemic

Higher death rate, bigger, later peak, but higher eqval succ. population
 Higher c, lower eqval rate, bigger peak, earlier

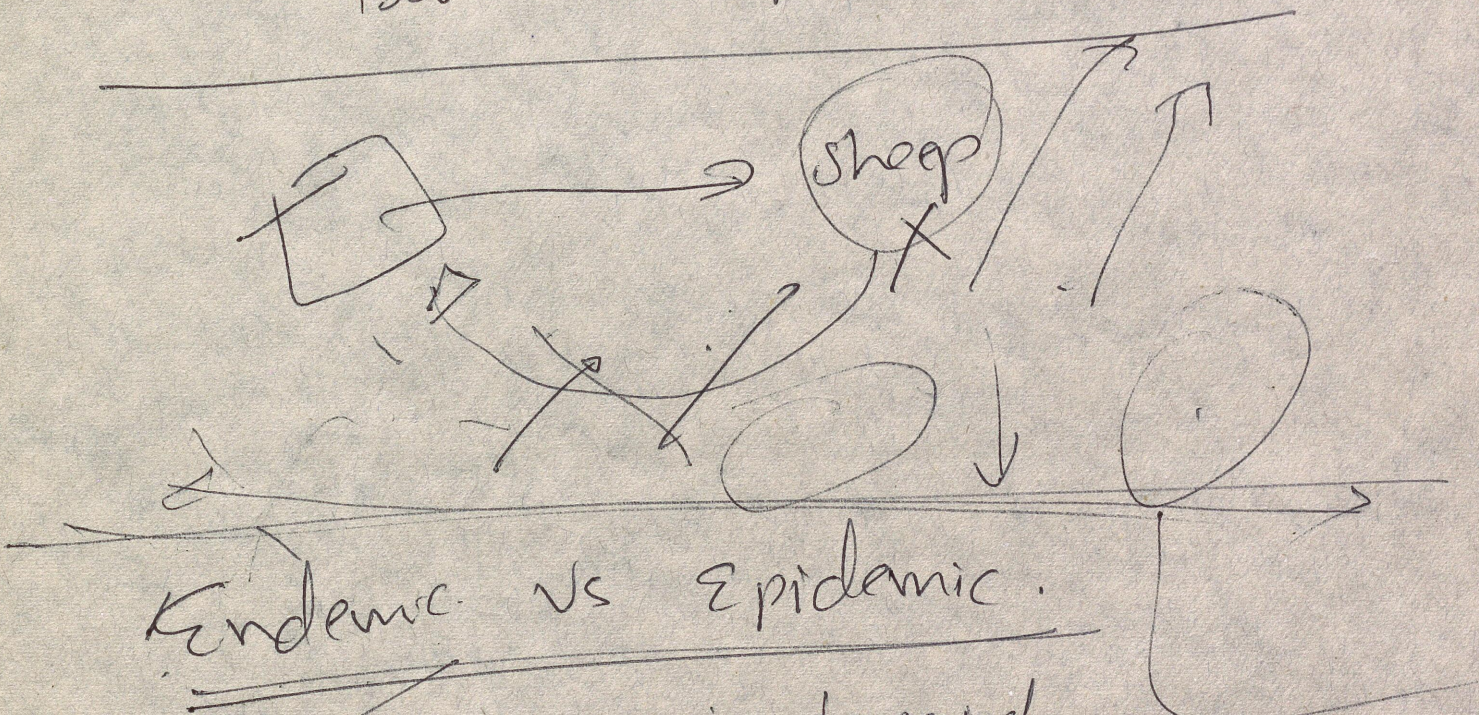


1. Init, Surv, 2. obj, 3. h, 4. Meth, 5. Res, 6. Disc. (7. Tall chart, 8. Reco, 9. Plot, 10. Deg.)

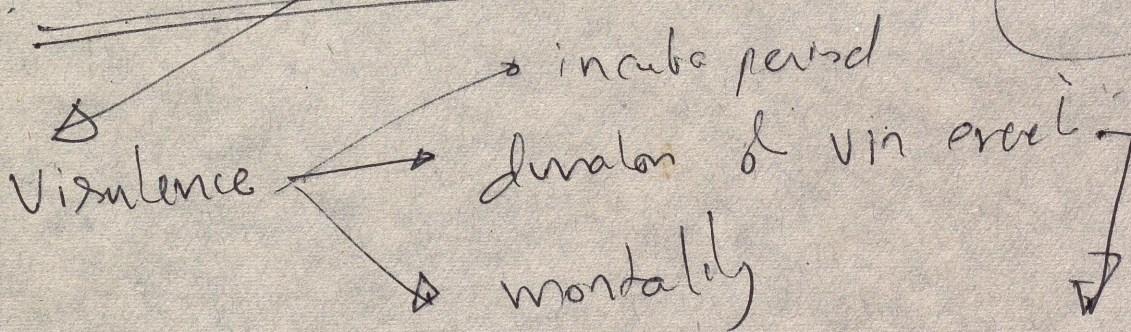
①

Combination of parameters
which will make endemic vs epidemic
with regard to occurrence & variety degrees
& virulence.

Bovine sinderper

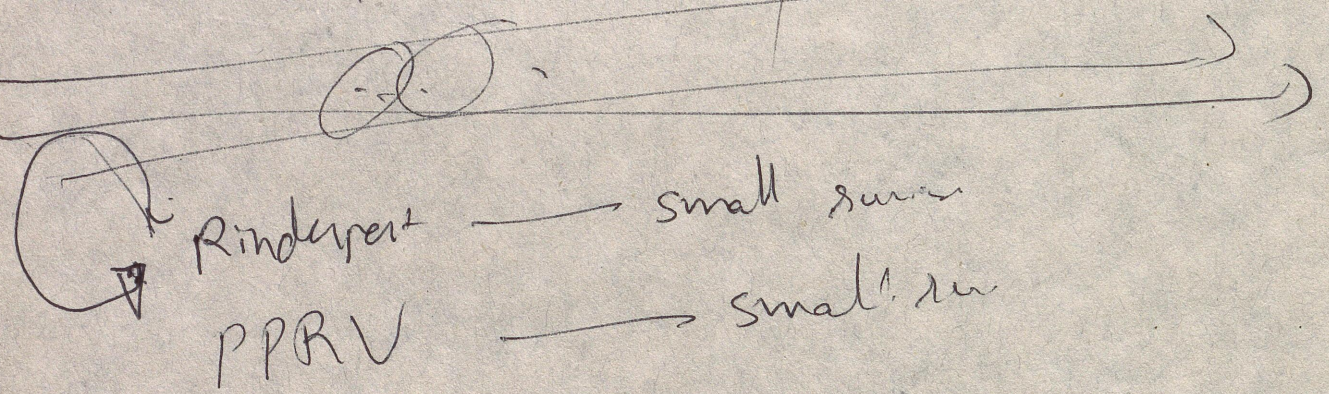
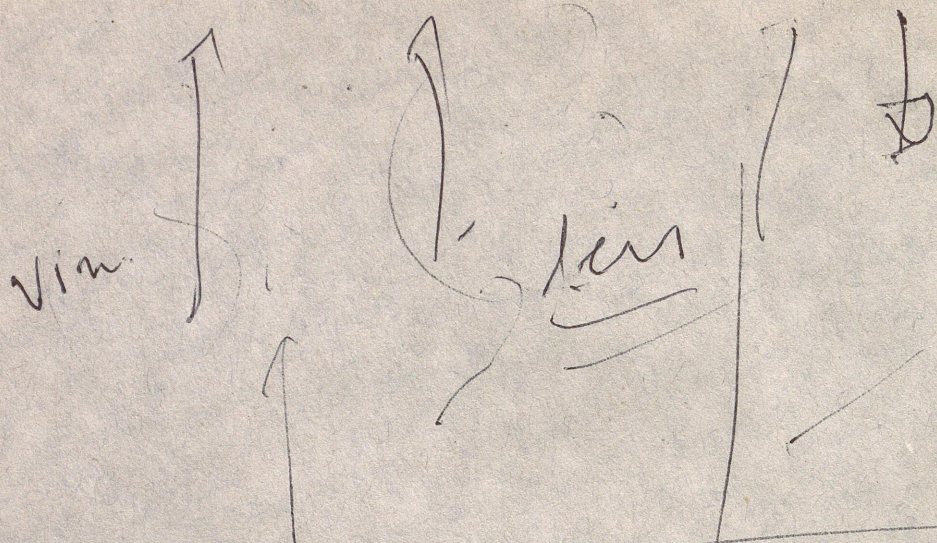


Endemic vs Epidemic.



②

one virus \xrightarrow{um} ~~one~~ sheep
cattle.



Rinderep → small sur
 PPRV → small sur

2.5 VNT 3-8 PPRV
 VNT mul fiber →
 1-1 / RV

1. ~~PPRV~~ Rinde in small & large survents
2. PPRV / Rinderep comp. →
3. Evol. & virulenc

Mathematical models of PPRV outbreaks: Epidemiological and evolutionary consequences.

The ~~pestis~~ pestes-des-petit-ruminant virus (PPRV) is closely related to the Rinderpest virus (RPV), but differs from it in its narrower ~~host~~ host range; while the ~~rinderpest~~ ^{PPRV} infects cattle, sheep and goats, ~~RPV~~ PPRV is specific to sheep and goats. The ~~rinderpest~~ ^{RPV} RN has in southern Indian regions, while ~~rinderpest~~ ^{RPV} RN epidemics have been known since the last century, PPRV outbreaks are of a much more recent origin.

~~The~~ The presentation would describe deterministic and stochastic models of the spread of PPRV and RPV in metapopulation of ~~cattle~~ ^{cattle} and ~~heads several~~ ^{heads} of a population of small ruminants, which normally separated into ~~a~~ many distinct, isolated herds, but with occasional intermingling composed of many isolated herds of small ruminants, which occasionally intermingle. — a situation normally present in south Indian villages.

(2)

~~Based Use of the~~ The models would be used to the use of the models to answer questions such as dependence & understand phenomena's factors

The probabilities & ^{of occurrence of epidemics and extent of the magnitude} ~~buildup~~ of epidemics, ^{as influenced} factors such as ~~typical~~ herd size, mixing rates, ~~cross-protection~~ extent of cross-protection for the two viruses etc., as obtained from the models would be presented. ~~while the~~ Possible application of the model to plan effective vaccination strategies would be described. Inquiries of possible evolutionary outcomes & competition between the competing viruses would be described.

COMVET03

all cloven hooved animal? Rv 19 Nov
sheep & goats only? PPRV
Rv known Report of PPRV
Whereas that same for PPRV

(1) deterministic model

(2) long term —

running simulations over & over again

(3) Mixing

(4) wild life

* (5) Population Genetic models

to explore the evolⁿ of

diff. levels of violence

* (6) Dynamics of Co-infection

of Small ruminants with

RVA PPRV

~~the~~ Co-evolution of the

two viruses having different
infection cycles.

{ RVA → small ruminant
 ↔ large "
PPRV → small ruminant only