ECOLOGICAL DETERMINANTS OF PLAGUE IN MADAGASCAR

Modelling for better understanding – E2M2

RAKOTOARIMANANA Feno M. Jacob-MD-MPH
Epidemiological and Clinical Research Unit
Institut Pasteur de Madagascar

Background

More than 200 reported cases /years in Madagascar + high and unpredictable risk of epidemic

Table 3 Risk factors of human plague: RR (95% CI)

Risk factor	Unit of comparison	RR (95% CI)	*P*-value
Flea index	>1 vs ⩽1	1.93 (1.61, 2.33)	<0.0001
Rodent density	Per 3% increase	1.23 (1.15, 1.32)	<0.0001
Rainfall	<10 vs ⩾10 mm	1.44 (1.17, 1.77)	<0.0001
Months[a]	Dry vs wet months	2.07 (1.64, 2.62)	<0.0001

[a]Dry season was from December through April.

Hau V Pham et al. , 2009-Vietnam

Research questions

➔What are the main environnemental factors influencing incidence of human plague in Madagascar ? *(retrospective analysis)*

➔How pneumonic plague will spread out in cities of Madagascar? (*outbreak scenario modelling*)

Thanks to Vero, Angelo, Anthonio

STATISTICAL MODEL :

1-What are the main environnemental factors influencing incidence of human plague in Madagascar ? *(retrospective analysis)*

Dependant variable (*source CLP-IPM database*):

- **All reported cases**
  - Bubonic plague
  - Pneumonic plague

Potential predictors :

- Flea index (sentinel site) *source Entomology&Plague-Unit IPM*
- Rodent density (*sentinel site*) *source Entomology&Plague Unit IPM*
- Temperature
- Rainfall
- Normalized Difference Vegetation Index (NDVI)
- Altitude

➔ **Poisson/negative binomial regression** (link log) – mixed effet

➔ **Hypothesis** : The number of cases is associated with ecological factors

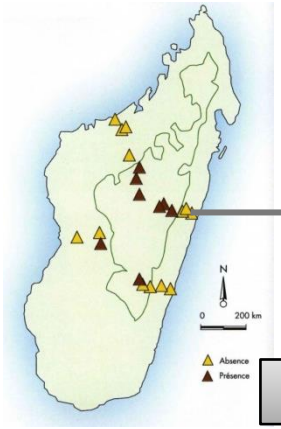
m1=glmer(cases~temp+rainfall+NDVI *#as factor#* +altitude + rodent + flea + (1| boundaries.limits), family ='poisson ', data=plague.data)

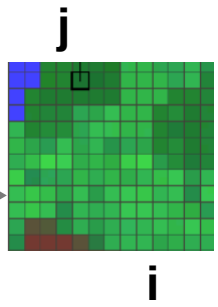
MECHANISTIC MODEL

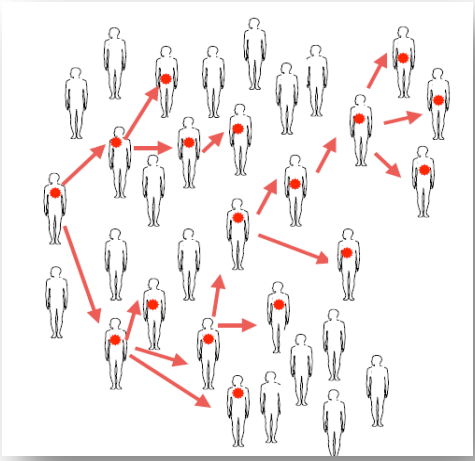
How pneumonic plague will spread out in cities of Madagascar? (*outbreak scenario)*

Approaches : a SEIR model mixed to a spatial analysis

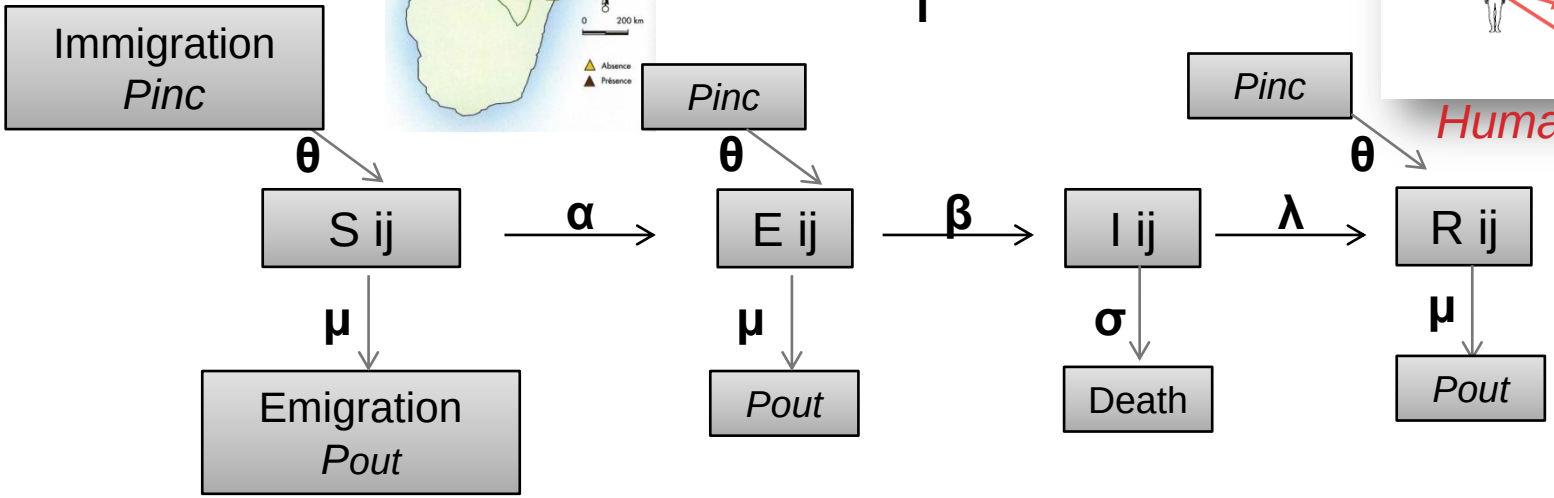
Hypothesis : Pneumonic plague spreading depends on population mobility/time/transmission rate-death rate







Human to Human



Assumptions : SEIR analysis by cell + no return from Recovery to Susceptible

Geography unit (district/commune boundaries) = shapefiles (vector data)➔ divided to cell (raster)

Time <-seq(0,365 , by=1)

NEXT STEPS

1-Mechanistic model of retrospective data outbreak

2-How do interactions between human, rodent and flea hosts maintain bubonic plague endemically in Madagascar?

3-Molecular epidemiology of resistant strains of *Yersinia pestis*

THANKS TO E2M2 STAFF (INSTRUCTORS-MENTORS)& ALL STUDENTS