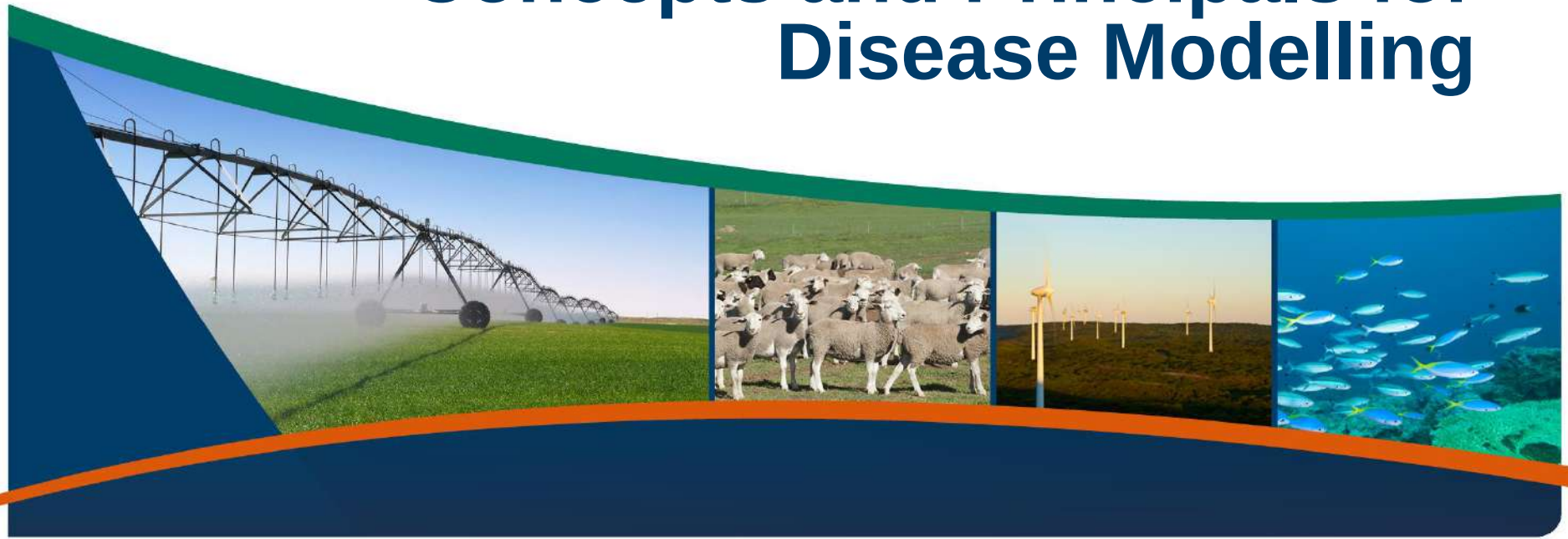
Department of
Primary Industries and Regional Development

GOVERNMENT OF WESTERN AUSTRALIA

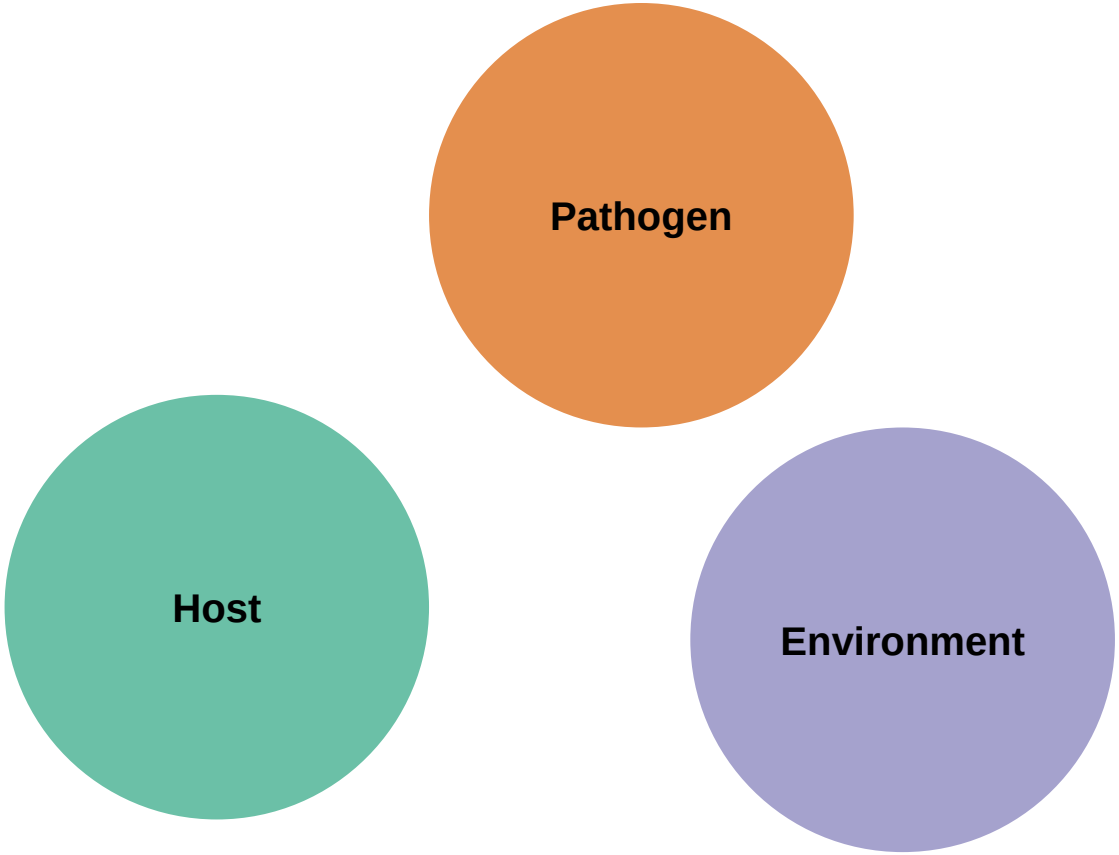
Concepts and Principals for Disease Modelling



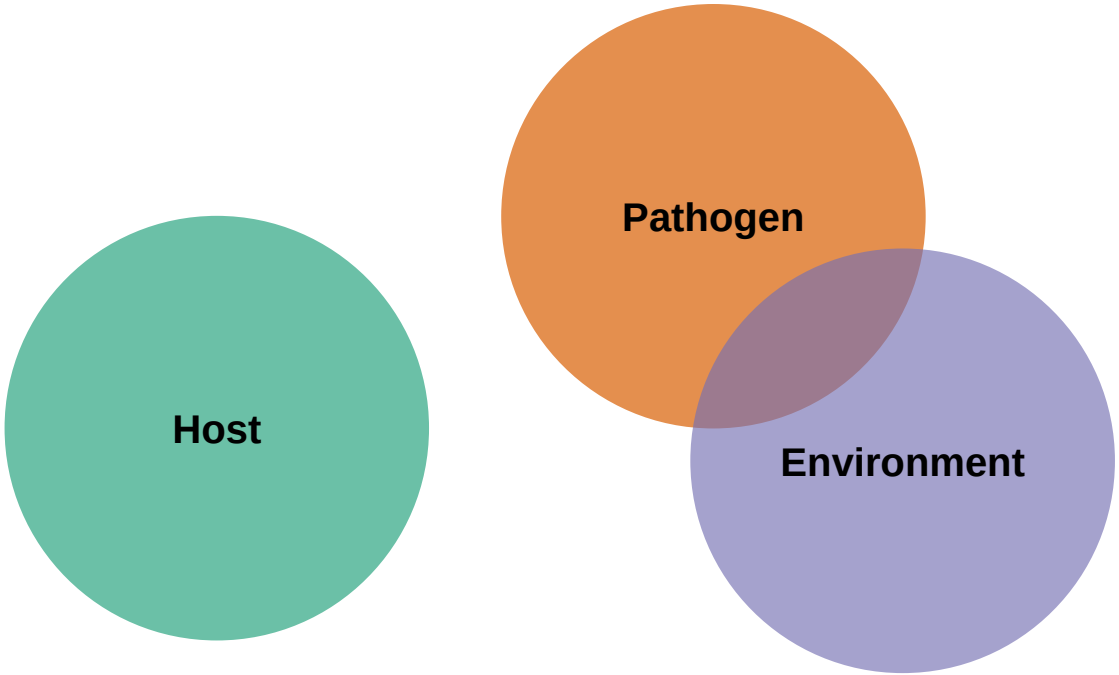
“Essentially, all models are wrong, but some are useful.”

–G. E. P. Box

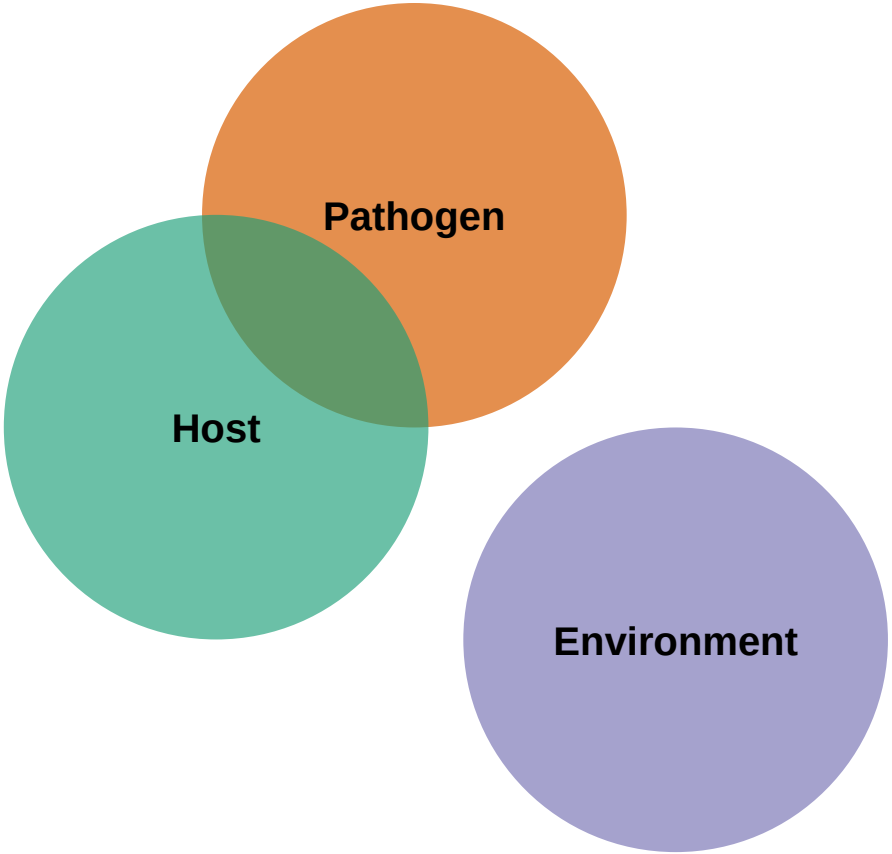
Plant Disease Triangle



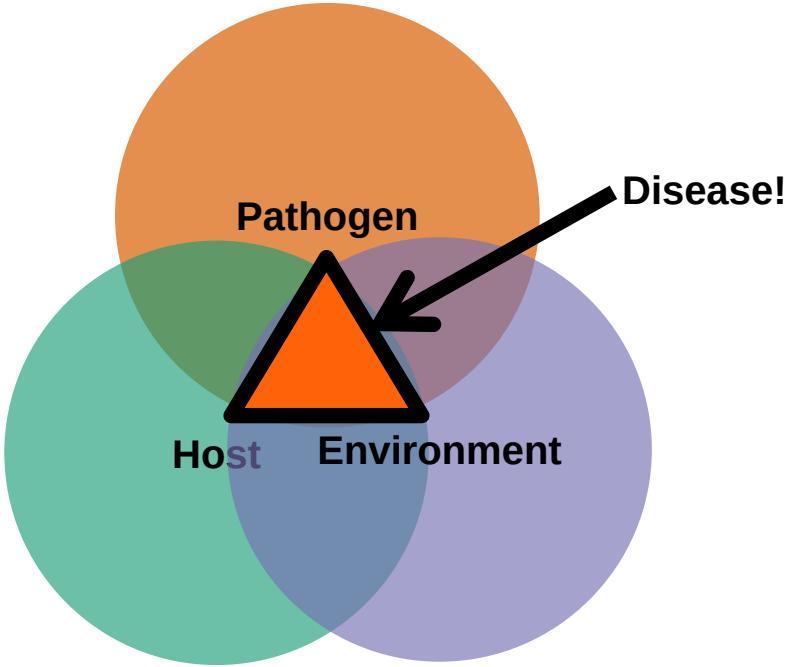
Plant Disease Triangle



Plant Disease Triangle



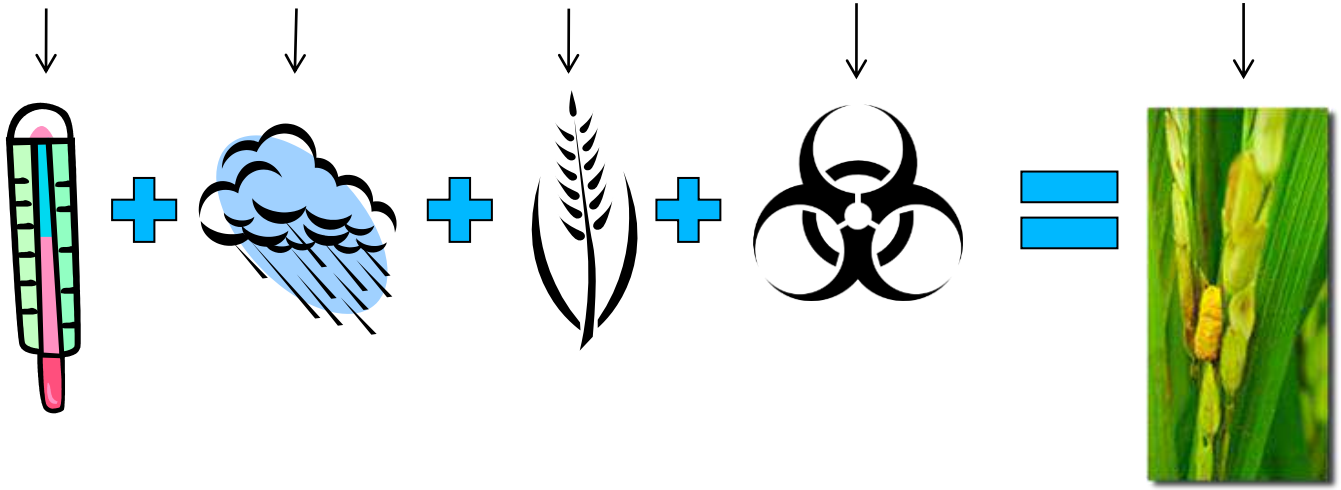
Plant Disease Triangle



Reality. Simplified.

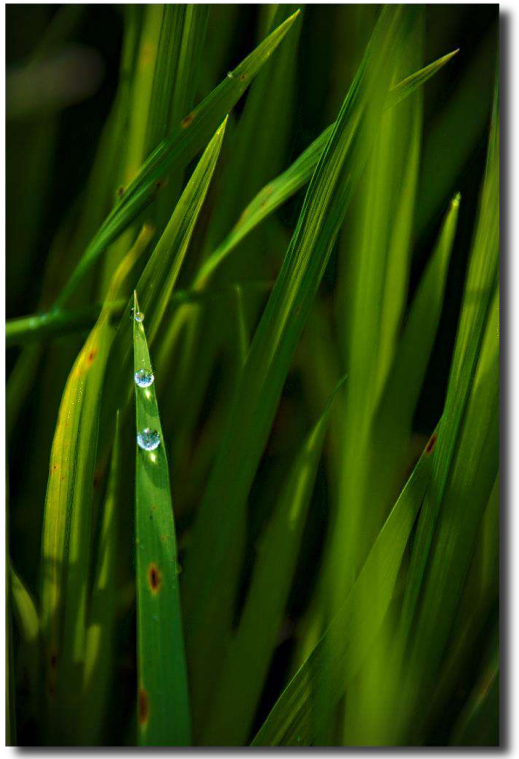
Crop Health Models

Environment + Host + Pathogen = **Disease**



Why use models?

- Decision support tools
- Simplification
- Faster



Tactical models

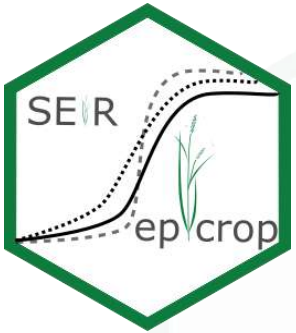
Simulation modelling

EPIRICE

A simple model of rice diseases

epicrop and EPIRICE, who's who?

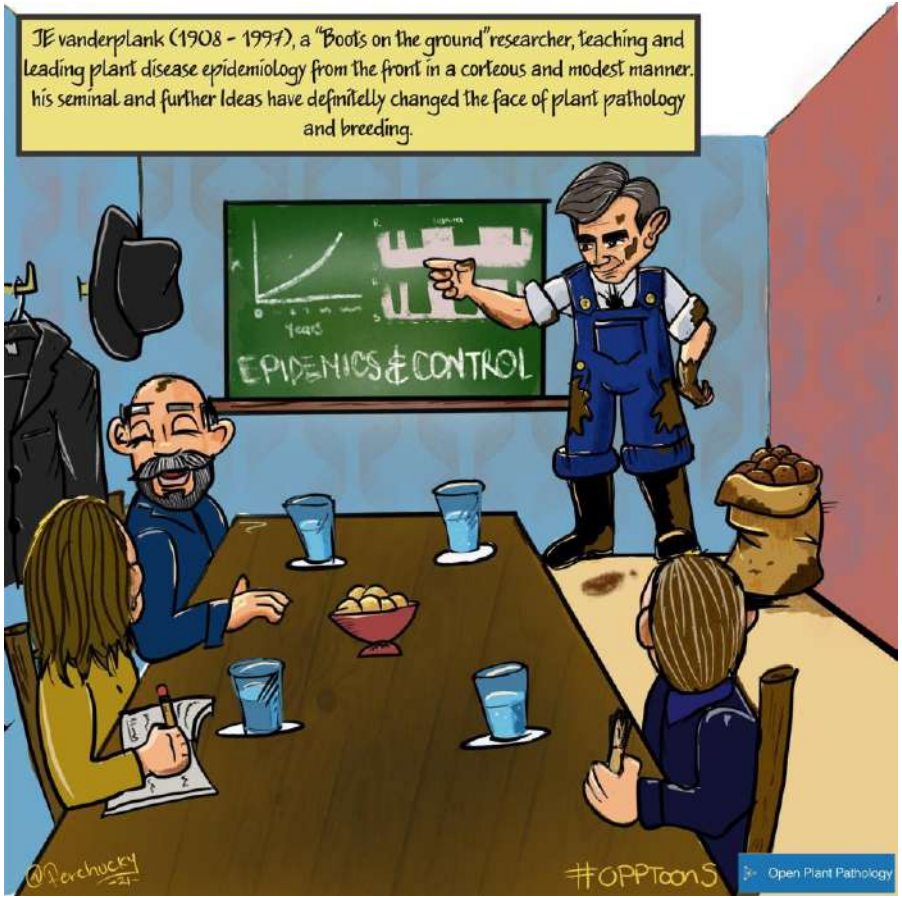
epicrop (Sparks 2021) is a fork of the ***cropsim*** R package (Hijmans *et al.* 2017) and was designed to make using the **EPIRICE** model (Savary *et al.* 2012) easier to use for rice disease modelling using freely available weather data from NASA and CHC UC Santa Barbara.



What's a SEIR Model?

SEIR (Susceptible-> Exposed-> Infectious->Removed) model

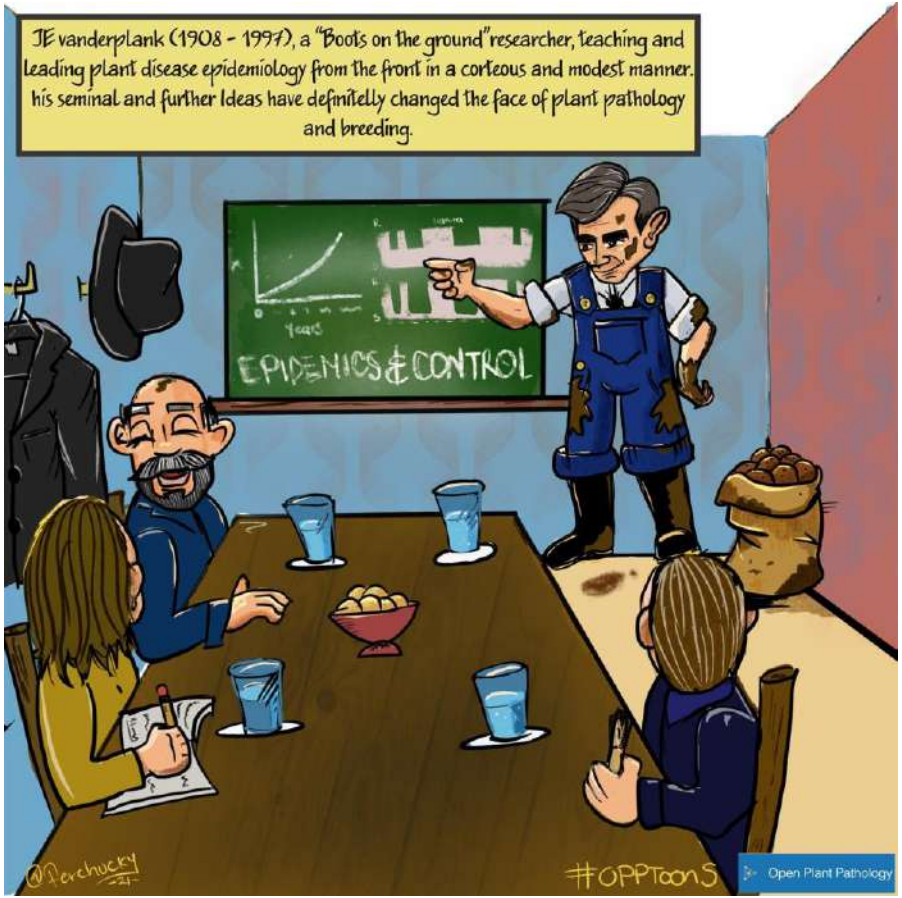
- Van der Plank (1963)
- Zadoks (1971)
- Madden (2006)

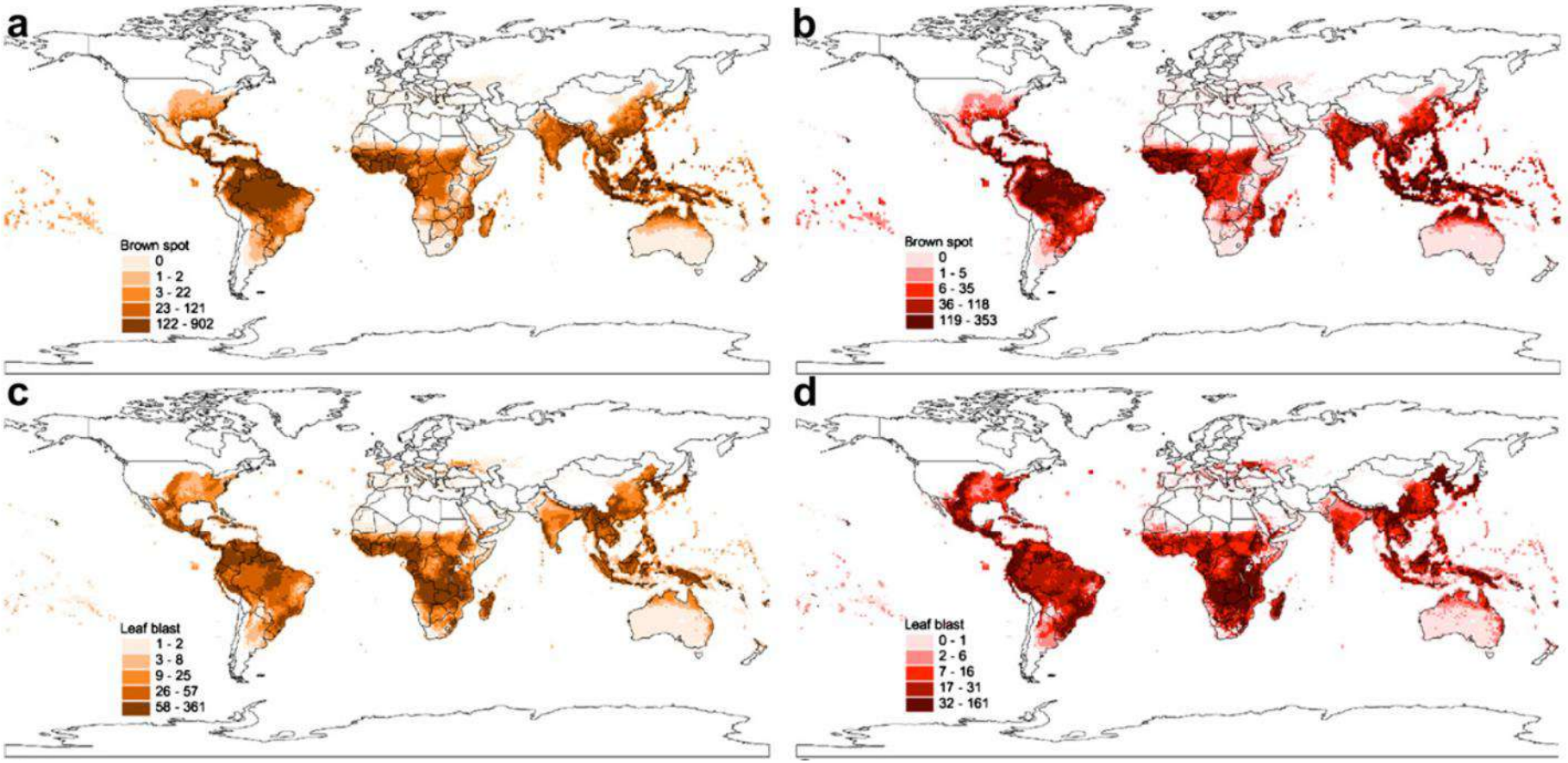


What's a SEIR Model?

SEIR state variables in **EPIRICE**

- Healthy (*H*)
- Latent (*L*)
- Infectious (*I*)
- Post-infectious (*P*)





Subset of Figure 2 from Savary *et al.* 2012

Acronym	Variable type	Variable meaning	Dimension
H	State variable	Number of healthy sites	[NSites]
L	State variable	Number of latent sites	[NSites]
I	State variable	Number of infectious sites	[NSites]
P	State variable	Number of post-infectious (removed) sites	[NSites]
a	Parameter	Aggregation coefficient	[−]
i	Parameter	Duration of infectious period	[day]
p	Parameter	Duration of latent period	[day]
RcOpt	Parameter	Potential basic infection rate corrected for removals	[NSites NSites^{-1}day^{-1}]
RcA	Parameter	Modifier for R_c for crop age	[−]
RcT	Parameter	Modifier for R_c for temperature	[−]
RcW	Parameter	Modifier for R_c for wetness	[−]
RRG	Parameter	Relative rate of growth	[NSites NSites^{-1}day^{-1}]
RRS	Parameter	Relative rate of senescence	[NSites NSites^{-1}day^{-1}]
RP	Parameter	Rate of senescence induced by disease	[NSites day^{-1}]
Sx	Parameter	Maximum number of sites	[NSites]
R_c	Variable	Basic infection rate corrected for removals	[NSites NSites^{-1}day^{-1}]
TS	Variable	Total number of sites	[NSites]

Table 1 from Savary *et al. 2012*

System's attribute	Parameter[a]	Disease				
		Leaf blast	Brown spot	Bacterial blight	Sheath blight	Tungro
Sites	Site size	45 mm^2 of a leaf	10 mm^2 of a leaf	1 leaf	1 tiller	1 plant
	Sx	30,000	100,000	3200	800	100
	References[b]	(1)	(2)	(3,4)	(3,4)	(5)
Crop growth	RRG	0.1	0.1	0.1	0.2	0
	RRS	0.01	0.01	0.01	0.005	0
	References[b]	(3,4,6)	(3,4,6)	(3,4,6)	(3,4)	(7)
Epidemic onset	Date	15 DACE	20 DACE	20 DACE	30 DACE	25 DACE
	References[b]	(8)	(9)	(10)	(3)	(7)
Residence times	p	5	6	5	3	6
	i	20	19	30	120	120
	References[b]	(11,12)	(13,14)	(15)	(16)	(17)
Infection rate	r_I	0.28	0.19	0.25	0.23	0.10
	R_c (calculated)	1.14	0.61	0.87	0.46	0.18
	References[b]	(8)	(18)	(19)	(20)	(21)
Age effect	RcA	(Strong) decrease with plant age	(Strong) increase with plant age	Decrease with plant age	(Slight) increase over age	(Strong) decrease with plant age
	References[b]	(22)	(23)	(24)	(25)	(26)
Temperature effect	RcT	Optimum: 25 °C	Optimum: 20 °C	Optimum: 28 °C	Optimum: 28 °C	Optimum: 31 °C
	References[b]	(27)	(13)	(28)	(29)	(30)
Wetness effect	RcW	1 if canopy wet, 0 otherwise	1 if canopy wet, 0 otherwise	1 if canopy wet, 0 otherwise	1 if canopy wet, 0 otherwise	Unaffected
	References[b]	(31)	(31)	(32)	(33)	
Aggregation	a	1	1	1	2.8	1
	References[b]				(34)	

Table 2 from Savary *et al. 2012*

epicrop

Modelling rice diseases. Simplified.

Installing *epicrop*

https://github.com/adamhsparks/epicrop **(code)**
http://adamhsparks.github.io/epicrop/ **(docs)**

Installing *epicrop*

```
if (!require("remotes"))
  install.packages("remotes")

remotes::install_github("adamhsparks/epicrop”
                        build_vignettes =
                        TRUE)
```

Using *epicrop*

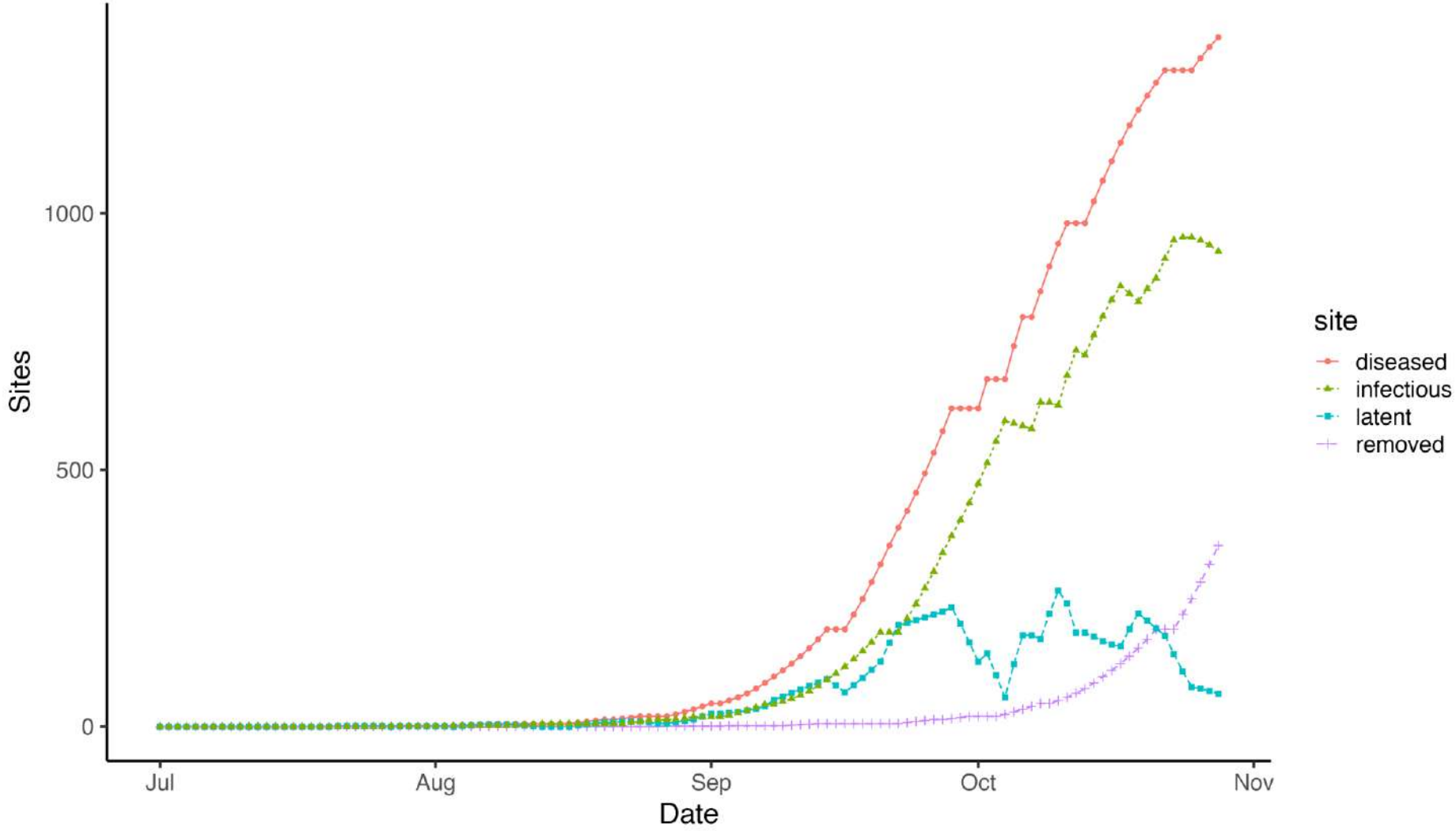
```
library("epicrop")

vignette("epicrop")
```

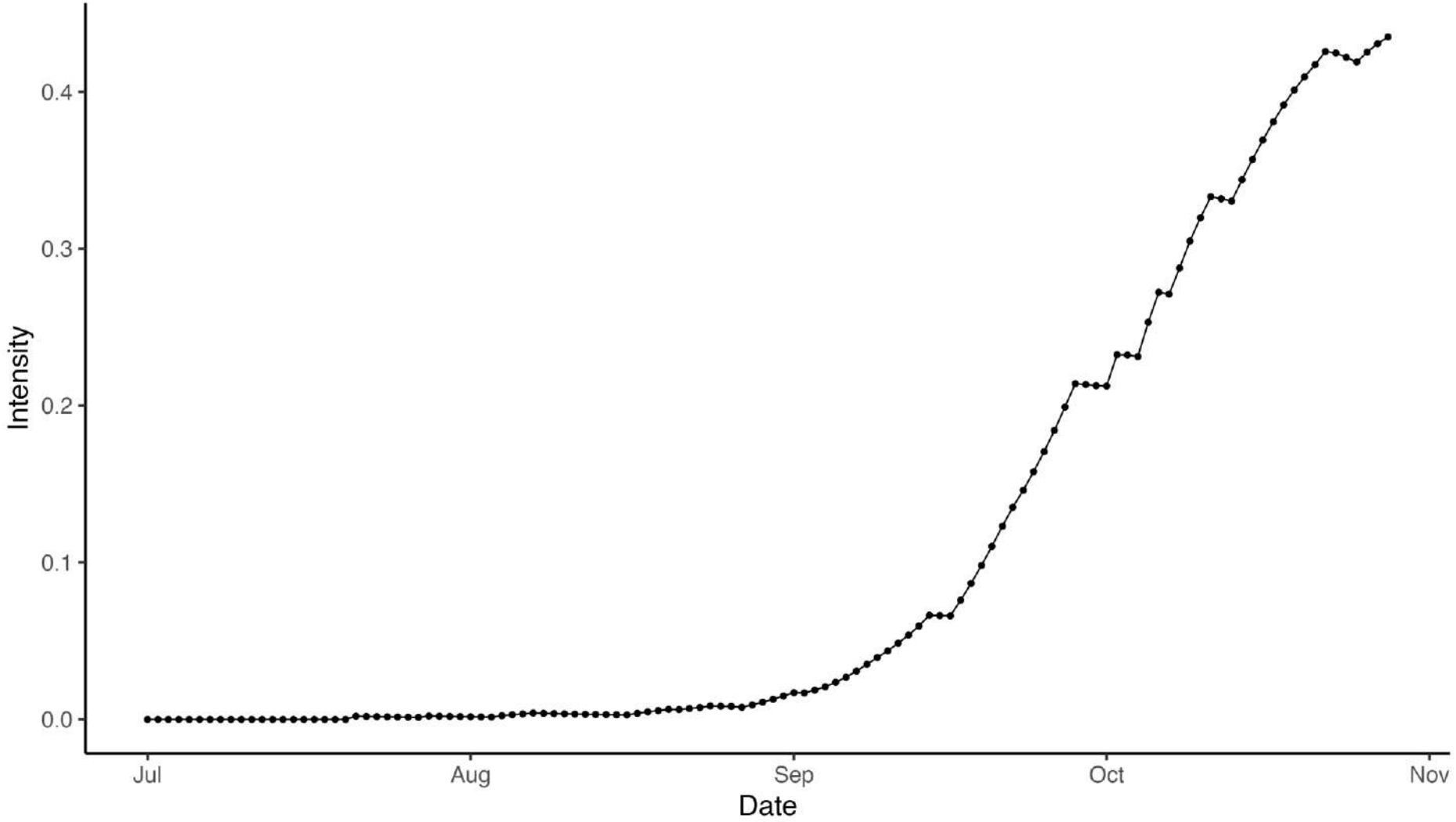
Using *epicrop*

```
# Fetch weather for year 2000 season at the
# IRRI Zeigler Experiment Station
wth <- get_wth(
  lonlat = c(121.25562, 14.6774),
  dates = c("2000-01-01", "2000-12-31")
)
```

Using *epicrop*

```
# Predict bacterial blight intensity for the
# year 2000 wet season at IRRI
bb <- predict_bacterial_blight(wth = wth,
                               emergence = "2000-07-01")
```


Sites
1000
500
0
Jul
Aug
Sep
Oct
Nov
Date
site
diseased
infectious
latent
removed


0.4
0.3
0.2
0.1
0.0
Intensity
Jul
Aug
Sep
Oct
Nov
Date

Using *epicrop*

https://github.com/adamhsparks/epicrop **(code)**
http://adamhsparks.github.io/epicrop/ **(docs)**

Thank you

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