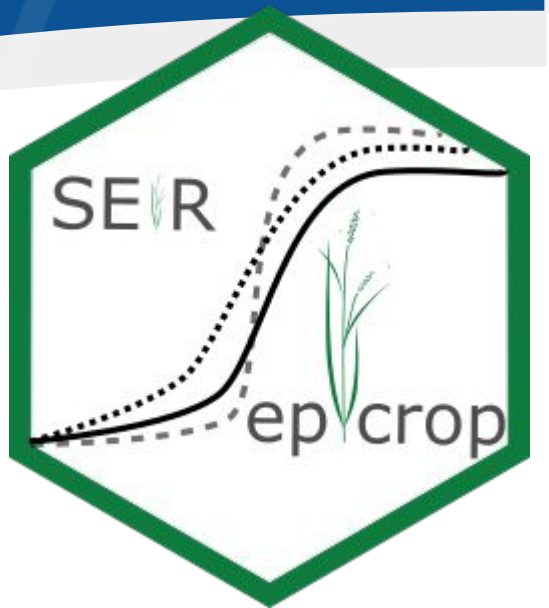
Simulation modelling crop diseases

Adam H. Sparks
Open Plant Pathology,
Department of Primary Industries and Regional Development Perth, Western Australia, AU, and
University of Southern Queensland Centre for Crop Health, Toowoomba, Queensland, AU



Equations, code and more!

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- *Equations, e.g.,* $\mathrm{d}S/\mathrm{d}t$

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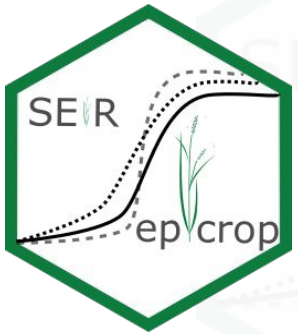
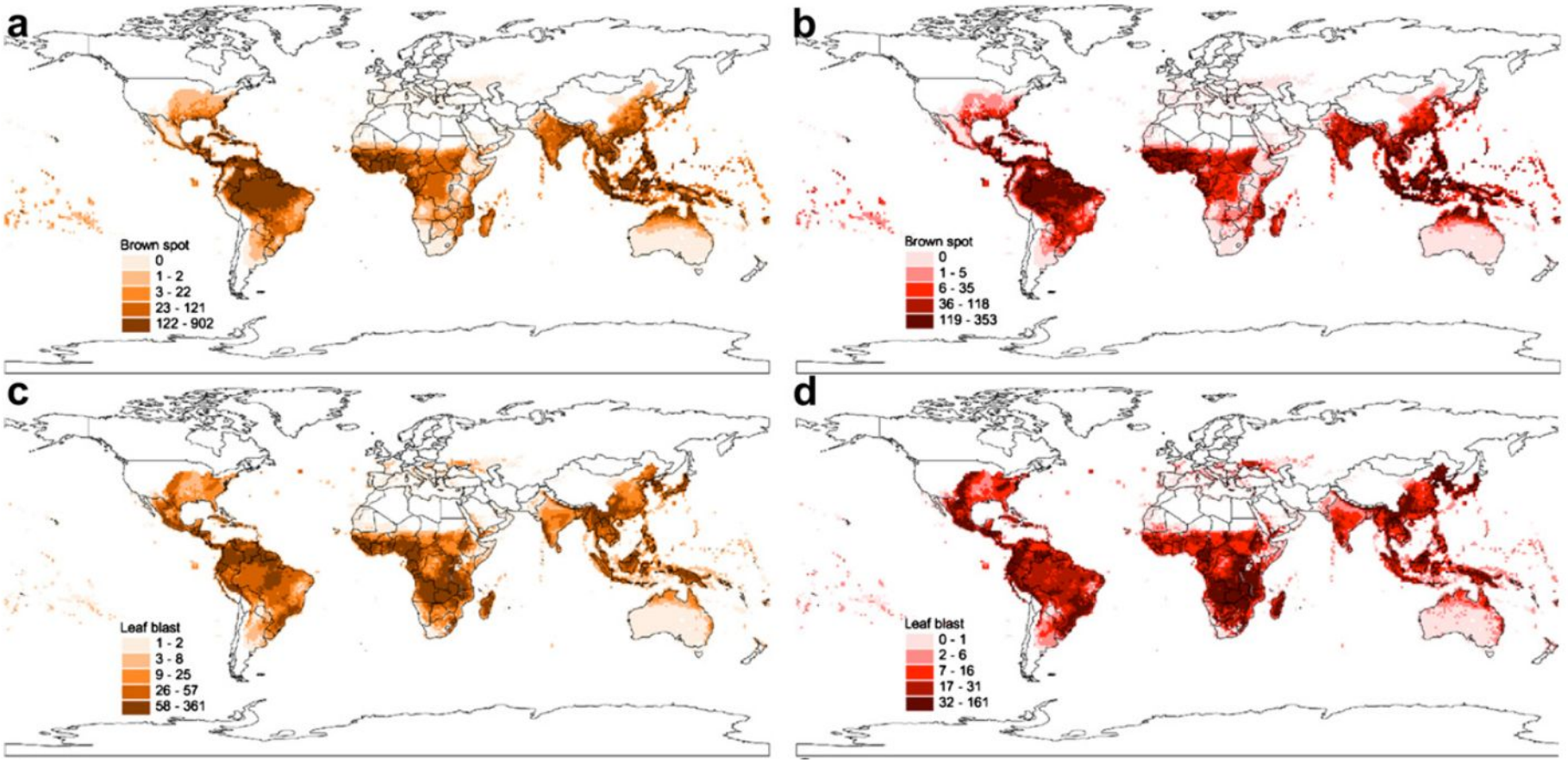
- This is regular text
- $\mathit{Equations,\ e.g.,}\ \mathrm{d}S/\mathrm{d}t$
- `Code, e.g., rhlim = 50`

epicrop, EPIRICE, EPIWHEAT, Epiwhat???

Who's who?

EPIRICE is a model developed and published by (Savary *et al.* 2012) for rice disease modelling. The ***cropsim*** package was written for this work (and other future work).



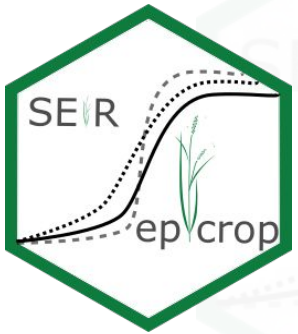


Subset of Figure 2 from Savary *et al.* 2012

epicrop, EPIRICE, EPIWHEAT, Epiwhat???

Who's who?

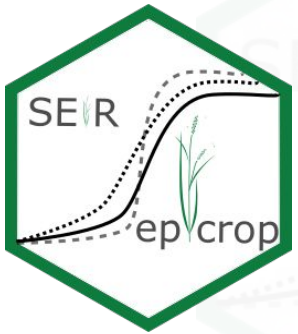
EPIWHEAT is a model developed and published by (Savary *et al.* 2015) for wheat disease modelling.



epicrop, EPIRICE, EPIWHEAT, Epiwhat???

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.

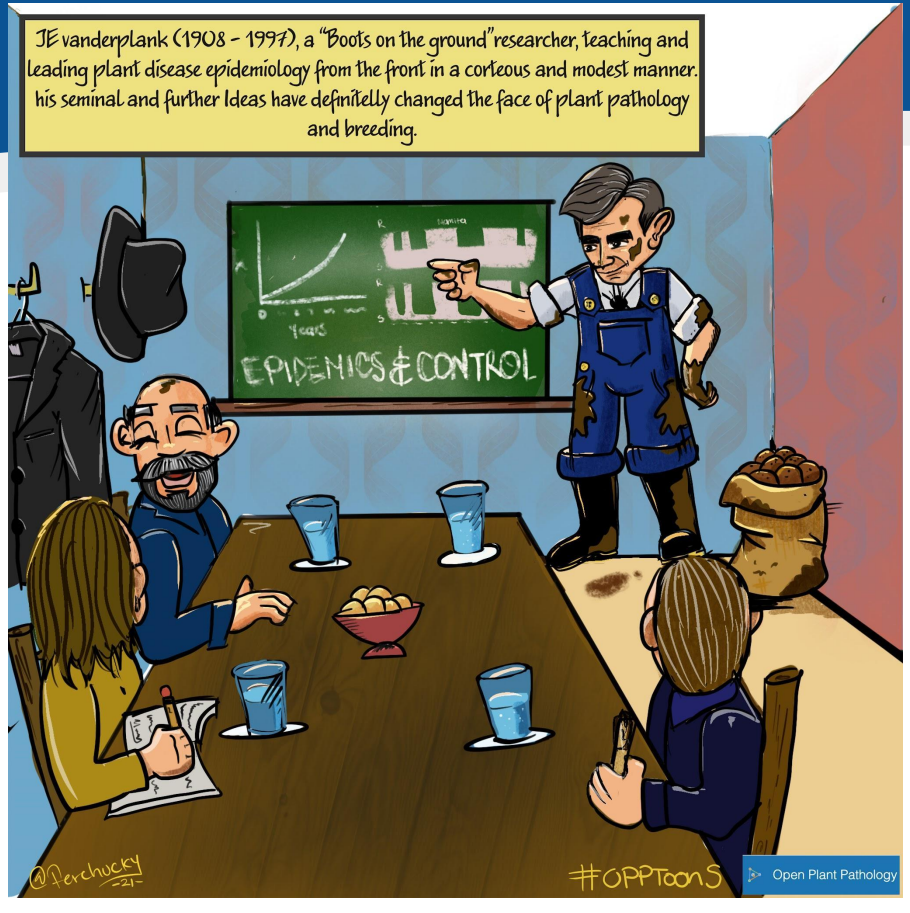


SEIR model

Susceptible-Exposed-Infectious-Removed

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

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

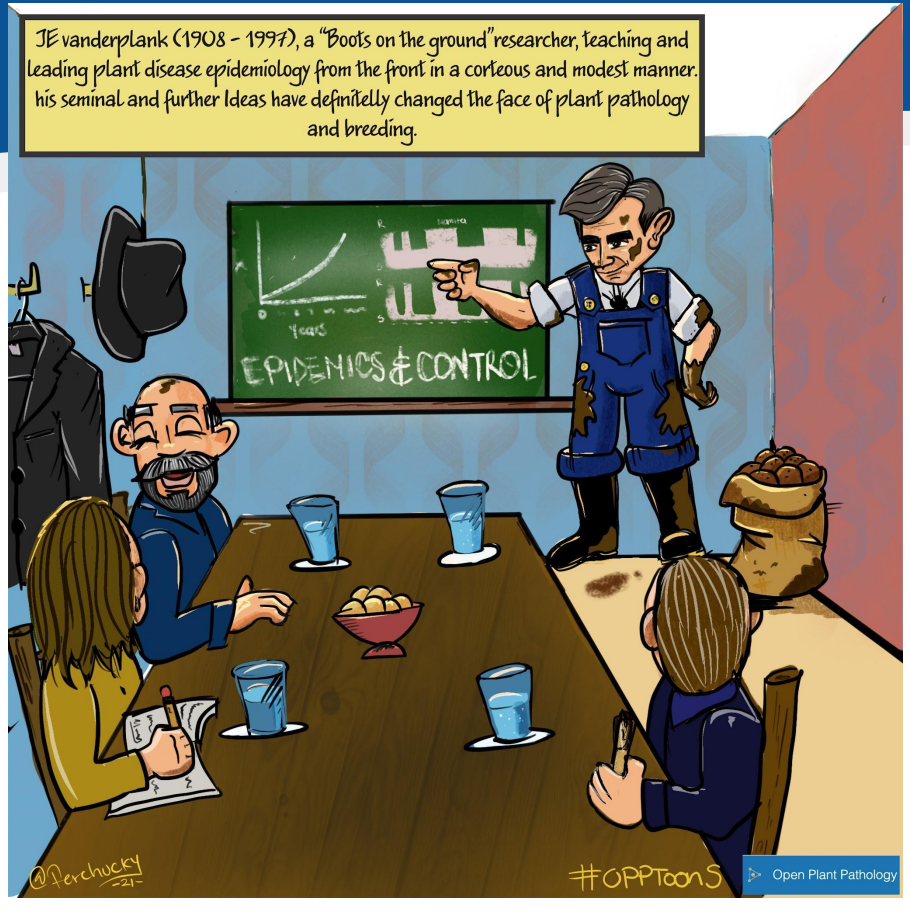


SEIR model

Susceptible-Exposed-Infectious-Removed

SEIR state variables in **EPIRICE**

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

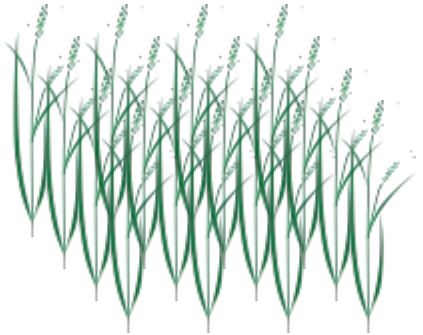


EPIRICE

Additional components to a SEIR model

Additional components in **EPIRICE**

- Spatial aggregation of disease, (a)
- Crop growth, (RRG)
- Crop senescence, (RRS)



Rate of Infection

$$\mathrm{d}L/\mathrm{d}t = \mathrm{RI} = R_{\mathrm{c}} I C^{\mathrm{a}}$$

Crop development

$$\mathrm{d}H/\mathrm{d}t = \mathrm{RG} = \mathrm{RRG}H(1 - (\mathrm{TS}/Sx))$$

Crop development

$$\mathrm{d}S/\mathrm{d}t = \mathrm{RS} = \mathrm{RRS}H$$

Crop development

$$\mathrm{d}S/\mathrm{d}t = \mathrm{RS} = \mathrm{RP} = \mathrm{RRS}H$$

Canopy moisture effects

RcW, modifier for R_c (the basic infection rate corrected for removals) for moisture in canopy (values are bound 0 - 1)

Temperature effects

RcT, modifier for R_c (the basic infection rate corrected for removals) for air temperature (values are bound 0 - 1)

Age effects

RcA, modifier for R_c (the basic infection rate corrected for removals) for crop age (values are bound 0 - 1)

R_c

Basic infection rate corrected for removals

$$R_c = \mathrm{RcOpt}\ \ \mathrm{RcA}\ \ \mathrm{RcT}\ \ \mathrm{RcW}$$ (See lines 268-269 SEIR.R)

R_c

Basic infection rate corrected for removals

$$r_l = \ln(x_2/x_1)/(t_2-t_1)$$

$$R_c = r_l/\{\exp(-r_l p) - \exp(-r_l[p + i])\}$$

R_c

Basic infection rate corrected for removals

$$r_l = \ln(x_2/x_1)/(t_2-t_1)$$

$$R_c = r_l/\{\exp(-r_l p) - \exp(-r_l[p + i])\}$$

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_l	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*

A note on Tungro epidemics

$$PRI_t = (PRI_{t-1} + R_t)e^{-k}$$

(Chevallier, 1983)

Installing *epicrop*

It's all there!

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

Installing epicrop

It's all here!

```
if (!require("remotes"))
  install.packages("remotes")
remotes::install_github("adamhsparks/epicrop",
                        build_vignettes = TRUE)
```

Using epicrop

It’s all here!

```
library(“epicrop”)
vignette("epicrop")
```

https://adamhsparks.com/

adamhsparks@gmail.com

@adamhsparks

openplantpathology.slack.com

github.com/adamhsparks