

SUMMERFAIR combining data science and infection models for estimating transmission parameters

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Transmission in small populations



Context:

Transmission experiment with ESBL-producing E. coli.

Challenge at 8:00, swaps taken at 16:00 daily

Samples are cloaca swaps put on plate after standard dilution series

	Sample_time (days post challenge)										
Host_id	Challenge	0	1	2	3	4	5	6	7		
1	Yes	2	5	>6	4	3	4	-	-		
2	Yes	1	-	-	-	4	5	6	5		
3	Yes	<1	5	4	2	1	-	<1	-		
4	Νο	-	-	4	3	-	4	4	-		
5	Νο	-	<1	2	-	-	3	-	-		
6	No	-	-	4	3	-	-	-	<1		

- Biological / epidemiological factors:
 - Passage of inoculum
 - Intermittent shedding
 - Sensitivity and specificity of test

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2	Yes	1	-	-	-	4	5	6	5		
3	Yes	<1	5	4	2	1	-	<1	-		
4	No	-	-	4	3	-	4	4	-		
5	Νο	-	<1	2	-	-	3	-	-		
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- Which infection model:
 - Direct or indirect
 - Latency period
 - Recovery

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1	Yes	2	5	>6	4	3	4	-	-	
2	Yes	1	-	-	-	4	5	6	5	
3	Yes	<1	5	4	2	1	-	<1	-	
4	No	-	-	4	3	-	4	4	-	
5	No	-	<1	2	-	-	3	-	-	
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- Example:
 - S-I-S model
 - Low concentration after inoculation = passage

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4	Νο	-	-	4	3	-	4	4	-	
5	Νο	-	<1	2	-	-	3	-	-	
6	No	-	-	4	3	-	-	-	<1	

- Example:
 - S-L-I-S model
 - Assuming possibility of false negative if only once negative
 - Low concentration after inoculation = passage

	Sample_time (days post challenge)										
Host_id	Challenge	0	1	2	3	4	5	6	7		
1	Yes	2	5	>6	4	3	4	-	-		
2	Yes	1	-	-	-	4	5	6	5		
3	Yes	<1	5	4	2	1	-	<1	-		
4	Νο	-	-	4	3	-	4	4	-		
5	No	-	<1	2	-	-	3	-	-		
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Objective of SUMMERFAIR framework

• Facilitate application of different models and assumptions on transmission data in small populations

This requires **standardization of input data**

It allows for

- Data quality reports
- Visualisation
- Easy documentation and reproducibility of **data interpretation**



Data Mapping







- Biological / epidemiological factors:
 - Passage of inoculum
 - Intermittent shedding
 - Sensitivity and specificity of test

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Data interpretation rules

Generic structure:

##generic of a rule ####

rule.generic <-function(timeseries,var.id,...) {...}</pre>

- Returns a vector with 0,1,2 or 3 which codes for susceptible, latent, infectious and recovered.
- Preprogrammed *rules* are names rule.<interpretation>.<additional features>

Data interpretation rules

- Preprogrammed rules with one input vector
- asis, sincefirst, consecutive
- Preprogrammed rules with multiple input vectors
- any, sinceany, infectiousrecovered
- Additional features:
- recode, detectionLimit, cutoff

Interpretation rule asis.cutoff cutoff = 1

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Interpretation rule consecutive.cutoff cutoff = 1 2 consecutive days = positive / negative

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4	No	-	-	4	3	-	4	4	-	
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6	No	-	-	4	3	-	-	-	<1	



Data visualisation





Estimation

> localF\$estimation

```
Call: glm(formula = as.formula(paste("cbind(cases, s - cases) ~ ",
    paste(use.covars, collapse = "+"))), family = binomial(link = "cloglog"),
    data = data.filtered, offset = log((i1/n1) * dt))
```

Coefficients:

```
(Intercept) treatmentprobiotica I en S
-19.26 19.17
Degrees of Freedom: 27 Total (i.e. Null); 26 Residual
Null Deviance: 23.1
Residual Deviance: 17.9 AIC: 21.9
>
```

Work in progress



Discussion

- Data standardization
- Data interpretation
 - Automated
 - Documented
 - Reproducible
- Estimation
 - Reproducible
 - Reusable
- Adaptable code





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<u>https://github.com/UtrechtUniversity/autumn-</u> fair/blob/main/docs/SummerFAIR schema proposal V04.pdf

Data Mapping



Infection Transmission Ontology Slavco et al. 2022 https://doi.org/10.1109/eScience55777.2022.00021