Supplementary data for

Exposing the diversity of multiple infection patterns

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This appendix provides all the technical background and mathematical analyses that support the formal infection pattern definition and counting (section A), the investigated within-host model (sections B, C and D) and the identification of the infection patterns it generates (section E).

Appendix contents

As we consider two parasite types we label 1 and 2, we often have to deal with label-dependent quantities or objects for which the general form can be advantageously given using dummy indices. Thus, unless stated otherwise, i represents 1 and 2 while k respectively represents 2 and 1, and holds for their corresponding bold labels. j and ℓ are instead used for all couples of $\{1,2\}^2$. Hence, unless stated otherwise, the quantifications $\forall (i,k) \in \{1,2\}^2, i \neq k$ and $\forall (j,\ell) \in \{1,2\}^2$ are most often implied.

A Formal infection patterns

A.1 Host and inoculum classes

We define a host class as the set of parasite genotypes that steadily infect a host. With two parasite genotypes, there are four host classes: susceptible $\emptyset$ (uninfected host), singly infected by either genotype, $\{1\}$ and $\{2\}$, and doubly infected $\{1,2\}$, which we denote by $\mathbf{0}, \mathbf{1}, \mathbf{2}$ and $\mathbf{3}$ respectively.

We define an inoculum class as a set of parasite genotypes an infected host can simultaneously transmit. The inoculum classes associated to each infected host class are given in Table S1. Note that contrary to most studies on multiple infections we allow hosts to transmit any non-empty subset of the set of genotypes they are infected with, namely the doubly infected host can transmit genotype 1 alone, genotype 2 alone and both genotypes at the same time (which is inoculum class **3**).

infected host class	**1**	**2**	**3**
potential inoculum classes	**1**	**2**	**1**, **2**, **3**

Table S1: Infected host classes and subsequent inoculum classes.

Note that for further formal completeness, we also consider the empty inoculum class **0** that denotes the absence of inoculum.

A.2 Mapping

Formally, an infection pattern is a discrete map that associates inoculation outcomes to all the couples of host and inoculum classes. Importantly, for the following mapping framework to apply, we need to assume that the inoculation outcome is unique (an inoculation can only result in one host class). We denote by $\mathfrak{n}_2$ the number of infection patterns for 2 genotypes. Let ϕ be a map from the domain $\mathcal{D}_\phi$ that contains all possible couples of host and inoculum classes to the codomain of all possible host classes $\mathcal{H}_\phi$ ($\phi : \mathcal{D}_\phi \to \mathcal{H}_\phi$). The domain $\mathcal{D}_\phi$ can be seen as the product set of a host class set $\mathcal{H}_\phi$ and an inoculum class set I_ϕ, that is $\mathcal{D}_\phi = \mathcal{H}_\phi \times I_\phi$ where $\times$ denotes the Cartesian product. The biological meaning of a map ϕ is such that $\forall (\boldsymbol{h}, \boldsymbol{p}) \in \mathcal{D}_\phi, \phi(\boldsymbol{h}, \boldsymbol{p})$ is the outcome host class of the inoculation of a host of class $\boldsymbol{h}$ by an inoculum of class $\boldsymbol{p}$. Importantly, ϕ may not be surjective.

If the domain and the codomain of each map are assumed to be as large as possible, then an upper bound for $\mathfrak{n}_2$ can easily be found. Indeed, the set of all classes $\mathcal{A} = \{0,1,2,3\}$ contains all host and inoculum classes so that for any map ϕ, $\mathcal{H}_\phi \subset \mathcal{A}$, $I_\phi \subset \mathcal{A}$ and $\mathcal{C}_\phi \subset \mathcal{A}$. Using classical combinatorial formula, we have

$$\mathfrak{n}_2 \leq \mathrm{Card}\left\{\phi : \mathcal{A} \times \mathcal{A} \to \mathcal{A}\right\} = (\mathrm{Card}\mathcal{A})^{\mathrm{Card}\mathcal{A} \cdot \mathrm{Card}\mathcal{A}} = 4^{16} = 4,294,967,296.$$

This calculation is certainly very rough but it nevertheless shows that listing all possible maps and checking their biological relevance as an infection pattern is not an option. Therefore, we need to define necessary conditions for a map $\phi : \mathcal{D}_\phi \to \mathcal{C}_\phi$ to be an infection pattern.

Before proceeding, we need to mention the infection pattern where no parasite genotype ever reaches a stable within-host steady state. As chronic infection then never occurs, this map ϕ_0 is degenerate (with $= \mathcal{H}_{\phi_0} = \{\mathbf{0}\}$, $I_{\phi_0} = \emptyset, \phi_0(\mathbf{0},\mathbf{0}) = \boldsymbol{h}$). Because one can see this case as the trivial *no* infection pattern, it should be counted as one, but it will be ignored in the rules and counting shown hereafter and only added in the final sum.

A.3 Infection pattern requirements

The following rules stem from commonplace biological conceptions of inoculation and infection processes.

Rule 1 (type coherence). The inoculation of a host cannot result in an outcome class containing genotypes that belong neither to the inoculated host class nor to the inoculum class. Formally, $\forall (\boldsymbol{h},\boldsymbol{p}) \in \mathcal{D}_\phi, \phi(\boldsymbol{h},\boldsymbol{p}) \subset \boldsymbol{h} \cup \boldsymbol{p}$. This may seem trivial (genotypes do not come out of nowhere) but note that it implies that we do not allow for within host mutation alone to modify the class a host belongs to.

Rule 2 (host class stability). The inoculation of a host with parasite genotypes it is already infected with results in no change in the host class. Formally, $\forall \boldsymbol{h} \in \mathcal{H}_\phi, \forall \boldsymbol{p} \subset \boldsymbol{h}, \phi(\boldsymbol{h},\boldsymbol{p}) = \boldsymbol{h}$. This is justified by the assumptions that inoculum sizes are at least one order of magnitude below parasite loads and that the dynamics within the inoculated host are at stable equilibrium (otherwise the host class would not be an argument of ϕ). As $\forall \boldsymbol{h} \in \mathcal{H}_\phi, \mathbf{0} \subset \boldsymbol{h}$, a remarkable consequence of this rule is that $\forall \boldsymbol{h} \in \mathcal{H}_\phi, \phi(\boldsymbol{h},\mathbf{0}) = \boldsymbol{h}$.

Rule 3 (infecting type insensitivity). The outcomes of inoculations with or without genotypes that are already infecting the host must be identical. Formally, $\forall (\boldsymbol{h},\boldsymbol{p}) \in \mathcal{D}_\phi, \phi(\boldsymbol{h},\boldsymbol{p}) = \phi(\boldsymbol{h},\boldsymbol{p} \setminus \boldsymbol{h})$. As in rule 2, adding few individuals to an already-established parasite genotype does not qualitatively change the system, but the introduction of a previously absent genotype does.

Rule 4 (epidemiological connectivity). There has to be at least one sequence of inoculation and/or recovery events initiated from the susceptible host class that leads to each infected host class. The recovery process only matters here if singly infected hosts can be generated only through the recovery of doubly infected hosts and not by an inoculation event. We assume that a doubly infected host can always become singly infected through recovery if the corresponding singly infected class belongs to the host class set. It is straightforward that, due to the uniqueness of inoculation outcomes, any inoculation/recovery sequence starting from the susceptible class can lead to any infected host class in one, two or three steps. Therefore, by considering all sequences, one can easily show that this rule is formally equivalent to

$\forall (\boldsymbol{i},\boldsymbol{k}) \in \{\mathbf{1},\mathbf{2}\}^2, \boldsymbol{i} \neq \boldsymbol{k}$,

for singly infected hosts: $\boldsymbol{i} \in \mathcal{H}_\phi \iff \big(\phi(\mathbf{0},\boldsymbol{i}) = \boldsymbol{i}\big) \vee \big(\phi(\mathbf{0},\mathbf{3}) = \boldsymbol{i}\big) \vee \big(\phi(\mathbf{0},\mathbf{3}) = \mathbf{3}\big)$
$\vee \Big(\big(\big(\phi(\mathbf{0},\boldsymbol{k}) = \boldsymbol{k}\big) \vee \big(\phi(\mathbf{0},\mathbf{3}) = \boldsymbol{k}\big)\big) \wedge \big(\big(\phi(\boldsymbol{k},\boldsymbol{i}) = \boldsymbol{i}\big) \vee \big(\phi(\boldsymbol{k},\boldsymbol{i}) = \mathbf{3}\big)\big)\Big)$,

for doubly infected hosts: $\mathbf{3} \in \mathcal{H}_\phi \iff \big(\phi(\mathbf{0},\mathbf{3}) = \mathbf{3}\big)$
$\vee \Big(\big(\big(\phi(\mathbf{0},\boldsymbol{i}) = \boldsymbol{i}\big) \vee \big(\phi(\mathbf{0},\mathbf{3}) = \boldsymbol{i}\big)\big) \wedge \big(\big(\phi(\boldsymbol{i},\boldsymbol{k}) = \mathbf{3}\big) \vee \big(\big(\phi(\boldsymbol{i},\boldsymbol{k}) = \boldsymbol{k}\big) \wedge \big(\phi(\boldsymbol{k},\boldsymbol{i}) = \mathbf{3}\big)\big)\big)\Big)$,

where $\wedge$ and $\vee$ stand for logical conjunction (and) and logical disjunction (or) respectively. A remarkable consequence of this rule is that there has to be at least one inoculum that induces infection in susceptible hosts. Formally, $\exists \boldsymbol{p} \in I_\phi : \phi(\mathbf{0},\boldsymbol{p}) \neq \mathbf{0}$. This makes sense because parasites are not vertically transmitted.

We call the number of determining images of a map ϕ the lowest number of images $\phi(\boldsymbol{a},\boldsymbol{b})$ that completely determine a map that satisfies all infection pattern requirements. Combining these four rules allows us to reduce the number of determining images to five, namely $\phi(\mathbf{0},\mathbf{1}),\phi(\mathbf{0},\mathbf{2}),\phi(\mathbf{0},\mathbf{3}),\phi(\mathbf{1},\mathbf{2}),\phi(\mathbf{2},\mathbf{1})$. According to rule 1, $\phi(\mathbf{0},\mathbf{1}) \in \{\mathbf{0},\mathbf{1}\}$, $\phi(\mathbf{0},\mathbf{2}) \in \{\mathbf{0},\mathbf{2}\}$ and $\phi(\mathbf{0},\mathbf{3}),\phi(\mathbf{1},\mathbf{2}),\phi(\mathbf{2},\mathbf{1}) \in \mathcal{A}$. Therefore, there are "only" $2 \cdot 2 \cdot 4^3 = 256$ different maps left to consider (including the trivial infection pattern discussed above).

A.4 Redundancies

The count based on the maps that follow all 4 rules suffers from two kinds of redundancy. The first one is due to unnecessary distinction of maps according to their epidemiological meaning. The previous calculation indeed assumes that $\mathcal{H}_\phi = I_\phi = \mathcal{A}$, that is all hosts and inoculum classes are possible, which may not be true for all biological settings. For example, if genotype 1 requires the presence of genotype 2 to infect, then $\phi(\mathbf{1},\mathbf{2})$ is not defined. Therefore, maps that only differ from other maps because of this particular value which has no epidemiological relevance should be discounted (see Sofonea *et al.* (2015) for more details about "epidemiological classes"). The second kind of redundancy is induced by the symmetry between genotypes. We say that maps ϕ and ϕ' are twins if one can build ϕ' from ϕ by swapping 1 and 2 in both $\mathcal{H}$ and I, and conversely. More precisely, let us define the swapping function $\chi : \{\mathbf{0},\mathbf{1},\mathbf{2},\mathbf{3}\} \to \{\mathbf{0},\mathbf{1},\mathbf{2},\mathbf{3}\}$ such that $\chi(\mathbf{0}) = \mathbf{0}$, $\chi(\mathbf{3}) = \mathbf{3}$, $\chi(\mathbf{1}) = \mathbf{2}$ and $\chi(\mathbf{2}) = \mathbf{1}$. Then, ϕ and ϕ' are twins if and only if $\forall(\boldsymbol{h},\boldsymbol{p}) \in \mathcal{D}_\phi = \mathcal{D}_{\phi'}, \phi(\boldsymbol{h},\boldsymbol{p}) = \chi\left(\phi'\left(\chi(\boldsymbol{h}),\chi(\boldsymbol{p})\right)\right)$. A map ϕ that is its own twin is said label-symmetric. Note that if a map is not label-symmetric, then there always exists a distinct twin map $\phi' \neq \phi$ (one can simply build it using the χ function). If ϕ is an infection pattern, then it is not relevant to count ϕ' as well as an infection pattern since their difference only lies in the contingency of the genotype labelling.

A.5 Constrained counting

In the following, we introduce a way of counting all maps that satisfies the infection pattern requirements and takes care of these redundancies. The first kind of redundancy is managed through partitioning according to the possible domains $\mathcal{D}_\phi$, while the second kind is avoided through the use of $\boldsymbol{i}$ and $\boldsymbol{k}$ indices, with $(\boldsymbol{i},\boldsymbol{k}) \in \{\mathbf{1},\mathbf{2}\}^2, \boldsymbol{i} \neq \boldsymbol{k}$.

As defined above, the domain $\mathcal{D}_\phi$ of a map ϕ is the product set of the possible host class and the possible inoculum sets $\mathcal{H}_\phi$ and I_ϕ. Because the contents of $\mathcal{H}_\phi$ completely determine the contents of I_ϕ and consequently $\mathcal{D}_\phi$ (Table S1), a partition is given by the possible host class sets $\mathcal{H}_\phi$, as shown in Table S2. Note that for the sake of generality, we also considered simultaneous inoculations to occur which explains why the inoculum set in the case where $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$ is $I_\phi = \{\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$ and not just $\{\boldsymbol{i},\boldsymbol{k}\}$ (this is only the consequence of relaxing the assumption of non-overlapping inoculations). In Table S2, we list the determining images that are left in each case after eliminating those whose argument does not belong to $\mathcal{D}_\phi$ and those constrained by rule 4 to a single value.

host class set $\mathcal{H}_\phi$	$\{\mathbf{0},\boldsymbol{i}\}$	$\{\mathbf{0},\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$
inoculum class set I_ϕ	$\{\boldsymbol{i}\}$	$\{\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$			
$\phi(\mathbf{0},\boldsymbol{i})$ set	$\{\boldsymbol{i}\}$	$\{\mathbf{0}\}$	$\{\mathbf{0},\boldsymbol{i}\}$	$\{\mathbf{0},\boldsymbol{i}\}$	$\{\mathbf{0},\boldsymbol{i}\}$
$\phi(\mathbf{0},\boldsymbol{k})$ set	$\emptyset$	$\{\mathbf{0}\}$	$\{\mathbf{0}\}$	$\{\mathbf{0},\boldsymbol{k}\}$	$\{\mathbf{0},\boldsymbol{k}\}$
$\phi(\mathbf{0},\mathbf{3})$ set		$\{\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$
$\phi(\boldsymbol{i},\boldsymbol{k})$ set		$\emptyset$	$\{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$
$\phi(\boldsymbol{k},\boldsymbol{i})$ set			$\emptyset$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$

Table S2: Host class set partition and associated inoculum class set and determining image sets.

A.5.1 $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i}\}$ and $\mathcal{H}_\phi = \{\mathbf{0},\mathbf{3}\}$

If $\boldsymbol{i}$ or $\mathbf{3}$ is the only infected host class, their determining images are already determined so that there is only one infection pattern for each case.

A.5.2 $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$

If one single infection type (let us say $\boldsymbol{k}$) is impossible, then there are three free determining images, namely $\phi(\mathbf{0},\boldsymbol{i}) \in \{\mathbf{0},\boldsymbol{i}\}, \phi(\mathbf{0},\mathbf{3}) \in \{\mathbf{0},\boldsymbol{i},\mathbf{3}\}, \phi(\boldsymbol{i},\boldsymbol{k}) \in \{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$. Table S3 explores all combinations for these free images and checks the infection pattern requirements.

$\phi(\mathbf{0},\boldsymbol{i})$	$\phi(\mathbf{0},\mathbf{3})$	$\phi(\boldsymbol{i},\boldsymbol{k})$	is ϕ an infection pattern?
$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0},\boldsymbol{i},\mathbf{3}$	no (susceptible hosts never get infected)
	$\boldsymbol{i}$	$\mathbf{0},\boldsymbol{i}$	no (double infected hosts cannot be generated)
		$\mathbf{3}$	yes
	$\mathbf{3}$	$\mathbf{0},\boldsymbol{i},\mathbf{3}$	yes
$\boldsymbol{i}$	$\mathbf{0}$	$\mathbf{0},\boldsymbol{i}$	no (double infected hosts cannot be generated)
		$\mathbf{3}$	yes
	$\boldsymbol{i}$	$\mathbf{0},\boldsymbol{i}$	no (double infected hosts cannot be generated)
		$\mathbf{3}$	yes
	$\mathbf{3}$	$\mathbf{0},\boldsymbol{i},\mathbf{3}$	yes

Table S3: Free determining image combinations and satisfaction of the infection pattern requirements in the case of $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$.

It follows from Table S3 that there are 9 different infection patterns produced by this host class set.

A.5.3 $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$

If double infection is impossible, there are five free determining images, namely $\phi(\mathbf{0},\boldsymbol{i}) \in \{\mathbf{0},\boldsymbol{i}\}, \phi(\mathbf{0},\boldsymbol{k}) \in \{\mathbf{0},\boldsymbol{k}\}, \phi(\mathbf{0},\mathbf{3}) \in \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}, \phi(\boldsymbol{i},\boldsymbol{k}) \in \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}, \phi(\boldsymbol{k},\boldsymbol{i}) \in \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$.

Let us first count the number of label-symmetric infection patterns in this case. This implies that $\phi(\mathbf{0},\boldsymbol{i}) = \chi\left(\phi(\mathbf{0},\boldsymbol{k})\right), \phi(\boldsymbol{i},\boldsymbol{k}) = \chi\left(\phi(\boldsymbol{k},\boldsymbol{i})\right)$ and $\phi(\mathbf{0},\mathbf{3}) = \chi\left(\phi(\mathbf{0},\mathbf{3})\right)$. Moreover, from the last condition it comes that $\phi(\mathbf{0},\mathbf{3})$ has to be one of the two fixed points of the χ function which are $\mathbf{0}$ and $\mathbf{3}$, but since $\mathbf{3} \notin \mathcal{H}_\phi$, $\phi(\mathbf{0},\mathbf{3}) = \mathbf{0}$ necessarily. Table S4 explores all possible combinations for these free determining images and checks the infection pattern requirements.

$\phi(\mathbf{0},\boldsymbol{i})$	$\Leftrightarrow \phi(\mathbf{0},\boldsymbol{k})$	$\phi(\boldsymbol{i},\boldsymbol{k})$	$\Leftrightarrow \phi(\boldsymbol{k},\boldsymbol{i})$	is ϕ an infection pattern?
$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0},\boldsymbol{i},\boldsymbol{k}$	$\mathbf{0},\boldsymbol{k},\boldsymbol{i}$	no (susceptible hosts never get infected)
$\boldsymbol{i}$	$\boldsymbol{k}$	$\mathbf{0}$	$\mathbf{0}$	yes
		$\boldsymbol{i}$	$\boldsymbol{k}$	yes
		$\boldsymbol{k}$	$\boldsymbol{i}$	yes

Table S4: Free determining image combinations and satisfaction of the infection pattern requirements for label-symmetric maps in the case of $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$.

Thus, there are 3 label-symmetric infection patterns for $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$.

With computational help, we listed all non label-symmetric maps sharing this host class set and found that 60 of them satisfy rule 4 (data not shown). Hence, there are 30 distinct non label-symmetric infections patterns for $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$.

A.5.4 $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$

If all host classes are possible, there are five free determining images, namely $\phi(\mathbf{0},\boldsymbol{i}) \in \{\mathbf{0},\boldsymbol{i}\}, \phi(\mathbf{0},\boldsymbol{k}) \in \{\mathbf{0},\boldsymbol{k}\}, \phi(\mathbf{0},\mathbf{3}) \in \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}, \phi(\boldsymbol{i},\boldsymbol{k}) \in \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}, \phi(\boldsymbol{k},\boldsymbol{i}) \in \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$.

Let us first count the number of label-symmetric infection patterns in this case. This implies that $\phi(\mathbf{0},\boldsymbol{i}) = \chi\left(\phi(\mathbf{0},\boldsymbol{k})\right), \phi(\boldsymbol{i},\boldsymbol{k}) = \chi\left(\phi(\boldsymbol{k},\boldsymbol{i})\right)$ and $\phi(\mathbf{0},\mathbf{3}) = \chi\left(\phi(\mathbf{0},\mathbf{3})\right)$. Moreover, the last condition implies that $\phi(\mathbf{0},\mathbf{3})$ has to be one of the two fixed points of the χ function, which are $\mathbf{0}$ and $\mathbf{3}$.

Table S5 explores all possible combinations for these free determining images and checks the infection pattern requirements.

$\phi(\mathbf{0},\boldsymbol{i})$	$\Leftrightarrow \phi(\mathbf{0},\boldsymbol{k})$	$\phi(\mathbf{0},\mathbf{3})$	$\phi(\boldsymbol{i},\boldsymbol{k})$	$\Leftrightarrow \phi(\boldsymbol{k},\boldsymbol{i})$	is ϕ an infection pattern?
$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0}$	$\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}$	$\mathbf{0},\boldsymbol{k},\boldsymbol{i},\mathbf{3}$	no (susceptible hosts never get infected)
		$\mathbf{3}$	$\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}$	$\mathbf{0},\boldsymbol{k},\boldsymbol{i},\mathbf{3}$	yes
$\boldsymbol{i}$	$\boldsymbol{k}$	$\mathbf{0}$	$\mathbf{0},\boldsymbol{i},\boldsymbol{k}$	$\mathbf{0},\boldsymbol{k},\boldsymbol{i}$	no (double infected hosts cannot be generated)
			$\mathbf{3}$	$\mathbf{3}$	yes
		$\mathbf{3}$	$\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}$	$\mathbf{0},\boldsymbol{k},\boldsymbol{i},\mathbf{3}$	yes

Table S5: Free determining image combinations and satisfaction of the infection pattern requirements for label-symmetric maps in the case of $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$.

Thus, there are 9 label-symmetric infection patterns for $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$.

With computational help, we listed all non label-symmetric maps sharing this host class set and found that 120 of them satisfy rule 4 (data not shown). Hence, there are 60 distinct non label-symmetric infections patterns for $\mathcal{H}_\phi = \{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$.

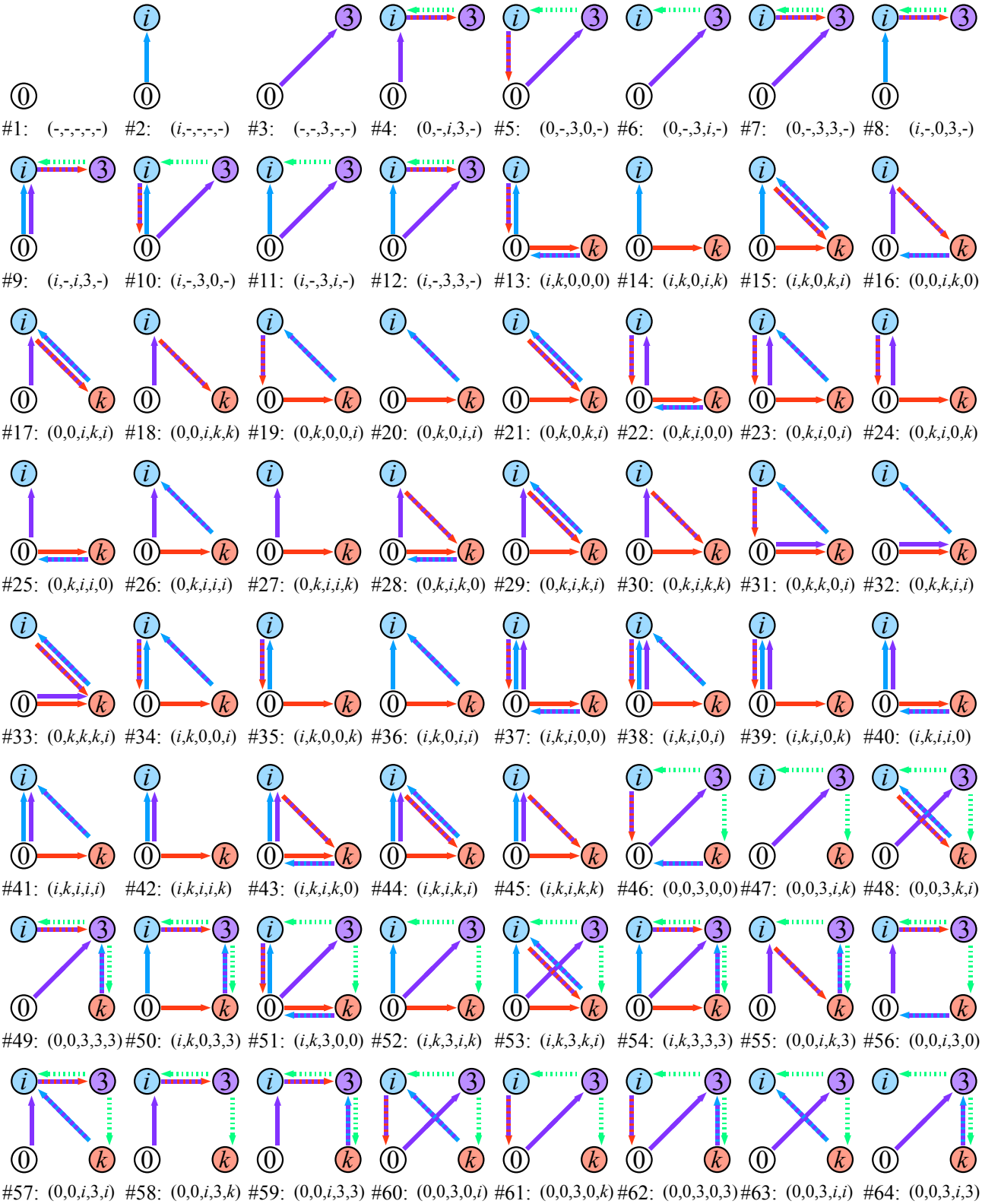
A.5.5 Counting summary and total

Table S6 sums up all the infection patterns we found for each host class set.

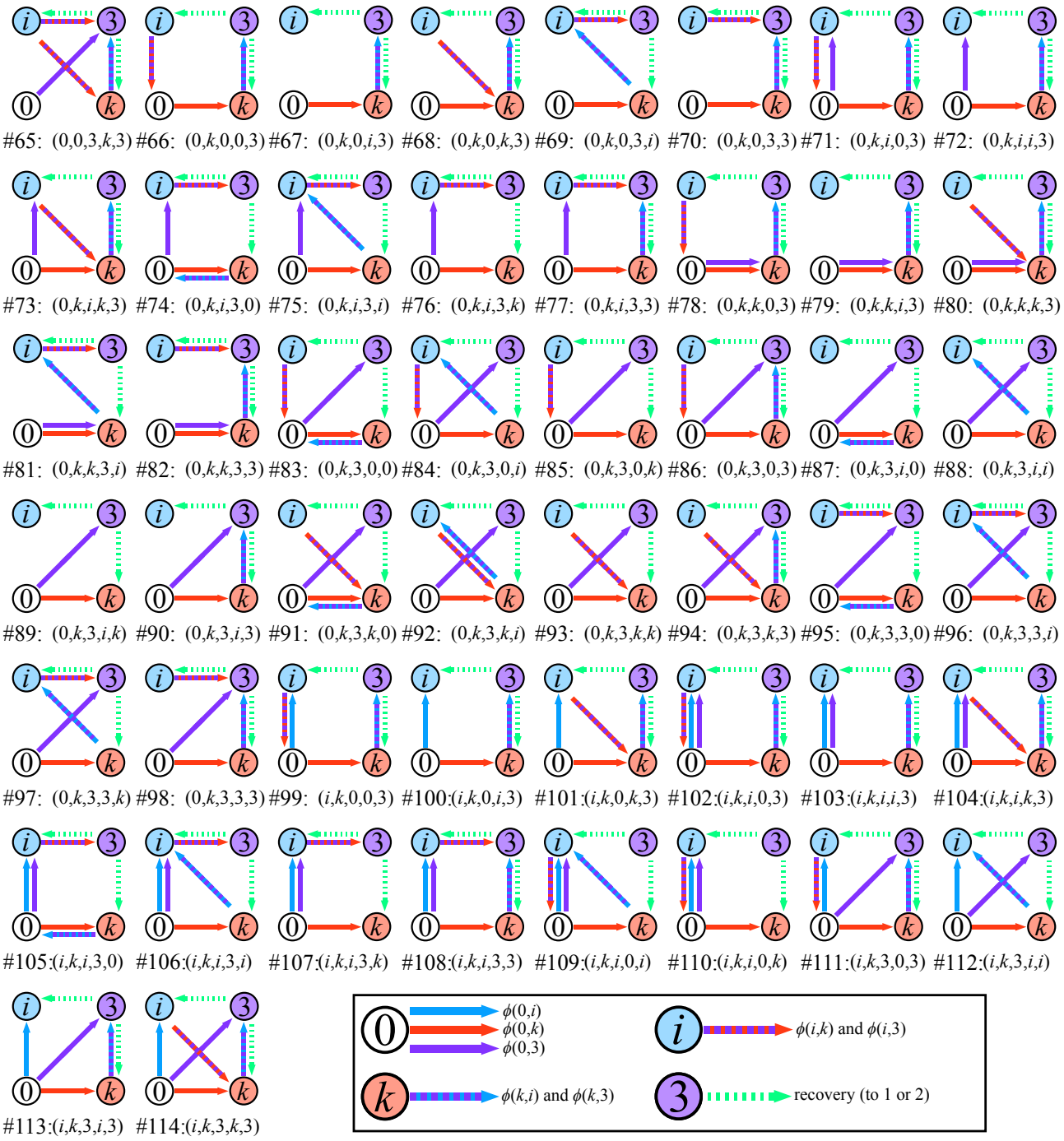
$\mathcal{H}_\phi$	$\{\mathbf{0}\}$	$\{\mathbf{0},\boldsymbol{i}\}$	$\{\mathbf{0},\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\mathbf{3}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k}\}$	$\{\mathbf{0},\boldsymbol{i},\boldsymbol{k},\mathbf{3}\}$
label-symmetric	1	0	1	0	3	9
non label-symmetric	0	1	0	9	30	60
total number of infection patterns	**114**					

Table S6: Summary of the infection pattern counting.

To conclude, we find that, following our definition and related assumptions presented above, there are exactly 114 different infection patterns, all represented below (Figure S1).



(panel 1/2 ; see panel 2/2 and legend on next page)



(panel 2/2)

Figure S1: Exhaustive list of infection patterns for two parasite genotypes (according to requirements given in A.3).
The quintuple below each infection pattern graph gives the associated values of $\big(\phi(\mathbf{0},\boldsymbol{i}),\phi(\mathbf{0},\boldsymbol{k}),\phi(\mathbf{0},\mathbf{3}),\phi(\boldsymbol{i},\boldsymbol{k}),\phi(\boldsymbol{k},\boldsymbol{i})\big)$, and is denoted by – if undefined. Circled labels represent host classes and arrows transitions between host classes through inoculation or recovery. Full blue arrows represent inocula of genotype $\boldsymbol{i}$ alone, full red arrows represent inocula of genotype $\boldsymbol{k}$ alone, full purple arrows represent inocula of both genotypes, blue and purple dashed arrows represent inocula of genotype $\boldsymbol{i}$ and possibly genotype $\boldsymbol{k}$, and red and purple dashed arrows represent inocula of genotype $\boldsymbol{k}$ and possibly genotype $\boldsymbol{i}$. Green dashed arrows represent recovery from the doubly infected host class to singly infected host classes. For the sake of clarity, recovery arrows from infected host classes to the susceptible host class and looping inoculation arrows (when $\phi(\boldsymbol{h},\boldsymbol{p})=\boldsymbol{h}$) are not shown.

B The within-host dynamics

B.1 Vectorial formulation

We recall the equations of the within-host dynamics for the focal genotype i:

$$\begin{cases} \frac{\mathrm{d}X_i}{\mathrm{d}t} = \left(\varrho_i + \eta_{i,i}X_i + \eta_{i,k}X_k + \gamma_{i,i}Y_i + \gamma_{i,k}Y_k - \sigma_{i,i}Z_i - \sigma_{i,k}Z_k\right)X_i \\ \frac{\mathrm{d}Y_i}{\mathrm{d}t} = \upsilon(u_iX_i - Y_i), \\ \frac{\mathrm{d}Z_i}{\mathrm{d}t} = \upsilon(v_iX_i - Z_i). \end{cases} , \tag{1}$$

Let us denote by $\mathcal{W} \coloneqq \left\{\mathbf{w} \in \mathbb{R}^6\right\}$ the space where all possible variable vectors lie, hereafter referred to as the "double inoculation space" (DIS). Any variable vector in the DIS can also be seen as a concatenated vector $\mathbf{w} = \begin{bmatrix} \mathbf{w}_i & \mathbf{w}_k \end{bmatrix}$, where $\mathbf{w}_i$ is the genotype i restricted variable vector of the form $\mathbf{w}_i = \begin{bmatrix} X_i & Y_i & Z_i \end{bmatrix}$.

The single inoculation case is characterised by the absence of genotype k, that is $X_k = Y_k = Z_k = 0$ for all times $t \in \mathbb{R}_+$. Therefore the variable vector is restrained to the following subspace of the DIS, $\mathcal{W}_i \coloneqq \left\{\mathbf{w} \in \mathcal{W} : X_k = Y_k = Z_k = 0\right\}$, which we call the "single inoculation space i" (SIS_i), $\mathcal{W}_i \subsetneq \mathcal{W}$.

For the sake of concision, r_i hereafter denotes the instantaneous growth rate defined such that $f_{\mathrm{x},i}(\mathbf{w}) = r_i(\mathbf{w})X_i$, that is $r_i(\mathbf{w}) \coloneqq \varrho_i + \sum\limits_{j\in\{1,2\}} \left(\eta_{i,j}X_j + \gamma_{i,j}Y_j - \sigma_{i,j}Z_j\right)$. Moreover, defining concatenated functions as $\mathbf{f}_i \coloneqq \begin{bmatrix} f_{\mathrm{x},i} & f_{\mathrm{y},i} & f_{\mathrm{z},i} \end{bmatrix}^{\mathbf{T}}$ and $\mathbf{f} \coloneqq \begin{bmatrix} \mathbf{f}_i & \mathbf{f}_k \end{bmatrix}^{\mathbf{T}}$, system (1) can be written under the vectorial form as $\forall t \in \mathbb{R}_+$,

$$\frac{\mathrm{d}\mathbf{w}^{\mathbf{T}}}{\mathrm{d}t}(t) = \mathbf{f}(\mathbf{w}(t)). \tag{2}$$

We call solution of (1) the set of values taken by the variables $X_1, Y_1, Z_1, X_2, Y_2, Z_2$ through time, from $t = 0$ to a potentially infinite $T > 0$. Except on a set of measure zero, such a solution always exists and is unique for a given initial condition. Consequently, for any initial condition $\mathbf{a} \in \mathcal{W}$, $\mathbf{w}^{[\mathbf{a}]}$ denotes the solution of (1) that started in $\mathbf{a}$. Note that in most biologically relevant parameter sets, the solution is defined for all $T > 0$. Nonetheless, for the sake of completeness, we also address cases where parasite loads explode (see section D).

B.2 Jacobian matrices

The Jacobian matrix associated to (1) in single infection, denoted by $\mathbf{J}_i$, is only evaluated in $\mathcal{W}_i^*$ and is equal to

$$\begin{aligned}\forall \mathbf{w} \in \mathcal{W}_i^*, \mathbf{J}_i(\mathbf{w}) &= \frac{\partial \mathbf{f}_i}{\partial \mathbf{w}_i}(\mathbf{w}), \\ &= \begin{bmatrix} \varrho_i + \gamma_{i,i} Y_i - \sigma_{i,i} Z_i + 2\eta_{i,i} X_i & \gamma_{i,i} X_i & -\sigma_i X_i \\ v u_i & -v & 0 \\ v v_i & 0 & -v \end{bmatrix}, \end{aligned} \tag{3}$$

while its double infection counterpart, denoted by $\mathbf{J}_3$, is evaluated in $\mathcal{W}$ and is equal to

$$\begin{aligned}\forall \mathbf{w} \in \mathcal{W}, \mathbf{J}_3(\mathbf{w}) &= \frac{\partial \mathbf{f}}{\partial \mathbf{w}}(\mathbf{w}), \\ &= \begin{bmatrix} r_i(\mathbf{w}) + \eta_{i,i} X_i & \gamma_{i,i} X_i & -\sigma_{i,i} X_i & \eta_{i,k} X_i & \gamma_{i,k} X_i & -\sigma_{i,k} X_i \\ v u_i & -v & 0 & 0 & 0 & 0 \\ v v_i & 0 & -v & 0 & 0 & 0 \\ \eta_{k,i} X_k & \gamma_{k,i} X_k & -\sigma_{k,i} X_k & r_k(\mathbf{w}) + \eta_{k,k} X_k & \gamma_{k,k} X_k & -\sigma_{k,k} X_k \\ 0 & 0 & 0 & v u_k & -v & 0 \\ 0 & 0 & 0 & v v_k & 0 & -v \end{bmatrix}. \end{aligned} \tag{4}$$

All the notations related to the within-host dynamics and their vectorial formalism are given in Table S7.

B.3 Notation table

symbol	set or value	meaning
	time-dependent variables	
X_i	$\in \mathcal{F}(\mathbb{R}_+, \mathbb{R})$	parasite load
Y_i	$\in \mathcal{F}(\mathbb{R}_+, \mathbb{R})$	public goods concentration
Z_i	$\in \mathcal{F}(\mathbb{R}_+, \mathbb{R})$	spite concentration
	constant parameters	
ϱ_i	$\in \mathbb{R}^\star$	basic growth rate
u_i	$\in \mathbb{R}_+^\star$	public goods production rate
v_i	$\in \mathbb{R}_+^\star$	spite production rate
$\eta_{j,\ell}$	$\in \mathbb{R}^\star$	parasite-load dependent effect
$\gamma_{j,\ell}$	$\in \mathbb{R}_+^\star$	public goods effect
$\sigma_{j,\ell}$	$\in \mathbb{R}_+^\star$	spite effect
υ	$\in \mathbb{R}_+^\star$	public production standard clearing rate
	vectorial notations	
$\mathbf{w}_i$	$= \begin{bmatrix} X_i & Y_i & Z_i \end{bmatrix}$	genotype restricted variable vector
$\mathbf{w}$	$= \begin{bmatrix} X_1 & Y_1 & Z_1 & X_2 & Y_2 & Z_2 \end{bmatrix}$	variable vector
$\mathcal{W}_i$	$= \{\mathbf{w} \in \mathcal{W} : \mathbf{w}_k = \mathbf{0}_3\}$	single inoculation space i (SIS_i)
$\mathcal{W}$	$= \{\mathbf{w} \in \mathbb{R}^6\}$	double inoculation space (DIS)
	system dynamics notations	
$\mathbf{w}^{[\mathbf{a}]}$	$\in \mathcal{F}(\mathbb{R}_+, \mathcal{W}) : \mathbf{w}(0) = \mathbf{a}$	within-host dynamics solution for initial condition $\mathbf{a}$
$f_{\text{x},i}, f_{\text{y},i}, f_{\text{z},i}$	$\in \mathcal{F}(\mathcal{W}, \mathbb{R})$	within-host dynamics functions
r_i	$= \varrho_i + \sum_{j \in \{1,2\}} \eta_{i,j} X_j + \gamma_{i,j} Y_j - \sigma_{i,j} Z_j$	instantaneous growth rate
$\mathbf{f}_i$	$= \begin{bmatrix} f_{\text{x},i} & f_{\text{y},i} & f_{\text{z},i} \end{bmatrix}^{\mathbf{T}} \in \mathcal{F}(\mathcal{W}, \mathbb{R}^3)$	genotype restricted within-host dynamics function vector
$\mathbf{f}$	$= \begin{bmatrix} \mathbf{f}_i & \mathbf{f}_k \end{bmatrix}^{\mathbf{T}} \in \mathcal{F}(\mathcal{W}, \mathbb{R}^6)$	within-host dynamics function vector
$\mathbf{J}_i$	$= \frac{\partial \mathbf{f}_i}{\partial \mathbf{w}_i} \in \mathcal{F}(\mathcal{W}, \mathfrak{M}_3(\mathbb{R}))$	single infection Jacobian matrix
$\mathbf{J}_3$	$= \frac{\partial \mathbf{f}}{\partial \mathbf{w}} \in \mathcal{F}(\mathcal{W}, \mathfrak{M}_6(\mathbb{R}))$	double infection Jacobian matrix

Table S7: Within-host dynamics notations.
$\mathbb{R}$ denotes the set of real numbers $(-\infty, +\infty)$ while $._+$, $._-$ and $.^\star$ and their combination denote restriction to non-negative, non-positive and non-zero numbers respectively. Note that $\mathcal{F}$ denotes the set of functions over the argument sets.

C Fixed point analysis

Although we could not prove it analytically for all parameter sets, the within-host dynamics of our model seems not to generate behaviours such as sustained oscillations or chaos. All simulations done so far show either asymptotic convergence to fixed point or finite time explosions (see next section). Because they govern the long-term behaviour of the system, the analysis of these fixed points is thus the unavoidable step to investigate the within-host outcomes.

C.1 Determination

The set of fixed points of (1) is the intersection set of the nullclines, or zero-growth isoclines, that is the parts of the space over which a variable is stationary (Simonyi and Kaszás, 1968). In our within-host model, respectively these are

$$\begin{cases} \mathcal{X}_i & := \{\mathbf{w} \in \mathcal{W} : f_{\mathrm{x},i}(\mathbf{w}) = 0\}, \\ \mathcal{Y}_i & := \{\mathbf{w} \in \mathcal{W} : f_{\mathrm{y},i}(\mathbf{w}) = 0\}, \\ \mathcal{Z}_i & := \{\mathbf{w} \in \mathcal{W} : f_{\mathrm{z},i}(\mathbf{w}) = 0\}. \end{cases} \tag{5}$$

It is straightforward that the public production nullclines can be expressed as

$$\begin{cases} \mathcal{Y}_i : & (Y_i = u_i X_i), \\ \mathcal{Z}_i : & (Z_i = v_i X_i). \end{cases} \tag{6}$$

Then,

$$\mathbf{w}_i \in \mathcal{Y}_i \cap \mathcal{Z}_i \Longleftrightarrow \mathbf{w}_i = X_i \mathbf{c}_i, \tag{7}$$

where $\mathbf{c}_i := \begin{bmatrix} 1 & u_i & v_i \end{bmatrix}$ is the direction vector of the the $\mathcal{Y}_i \cap \mathcal{Z}_i$ space.

Since $f_{\mathrm{x},i}(\mathbf{w}) = r_i(\mathbf{w}) X_i$, the parasite load nullcline $\mathcal{X}_i$ can be partitioned into two subsets: $\mathcal{X}_i = \mathcal{X}_i^\circ \cup \mathcal{X}_i^\star$, with $\mathcal{X}_i^\circ \cap \mathcal{X}_i^\star = \emptyset$, where they respectively correspond to the absence, $\mathcal{X}_i^\circ : (X_i = 0)$, and presence,

$$\mathcal{X}_i^\star : \left(X_i = \frac{-1}{\eta_{i,i}} \left(\varrho_i + \gamma_{i,i} Y_i + \gamma_{i,k} Y_k - \sigma_{i,i} Z_i - \sigma_{i,k} Z_k + \eta_{i,k} X_k \right) \neq 0 \right), \tag{8}$$

of genotype i. Note that $\mathcal{W}_i^\prime = \mathcal{X}_k^\circ \cap \mathcal{Y}_k \cap \mathcal{Z}_k$.

Because of (7), the stationary parasite loads constrain the stationary values of public productions. Owing to the partition of the parasite load nullcline, the set of all fixed points is thus

$$\begin{aligned} \widehat{\mathcal{W}} &:= \mathcal{X}_i \cap \mathcal{Y}_i \cap \mathcal{Z}_i \cap \mathcal{X}_k \cap \mathcal{Y}_k \cap \mathcal{Z}_k, \\ &= \left(\mathcal{X}_i^\circ \cup \mathcal{X}_i^\star\right) \cap \left(\mathcal{X}_k^\circ \cup \mathcal{X}_k^\star\right) \cap (\mathcal{Y}_i \cap \mathcal{Z}_i \cap \mathcal{Y}_k \cap \mathcal{Z}_k), \\ &= \left(\left(\mathcal{X}_i^\circ \cap \mathcal{X}_k^\circ\right) \cup \left(\mathcal{X}_i^\star \cap \mathcal{X}_k^\circ\right) \cup \left(\mathcal{X}_i^\circ \cap \mathcal{X}_k^\star\right) \cup \left(\mathcal{X}_i^\star \cap \mathcal{X}_k^\star\right)\right) \cap (\mathcal{Y}_i \cap \mathcal{Z}_i \cap \mathcal{Y}_k \cap \mathcal{Z}_k). \end{aligned}$$

It is straightforward that there are exactly four different fixed points.

The first one is simply the origin of $\mathbb{R}^6$ and corresponds to the absence of infection. We denote it by $\widehat{\mathbf{w}}_0$ and call it the "uninfected fixed point" (UFP),

$$\widehat{\mathbf{w}}_0 = \mathbf{0}_6.$$

The next two correspond to the case where only one genotype persists, while the other vanishes. The "singly infected fixed point i" (SIFP$_i$), denoted by $\widehat{\mathbf{w}}_i$, is thus the fixed point for which genotype i infects alone. It is easy to show that

$$\widehat{\mathbf{w}}_i = \left[x_i^\circ \mathbf{c}_i \quad \mathbf{0}_3 \right], x_i^\circ := \frac{-\varrho_i}{\eta_{i,i} + \gamma_{i,i} u_i - \sigma_{i,i} v_i} \in \mathbb{R}^\star, \tag{9}$$

where x_i° denotes the non-zero stationary parasite load of the SIFP$_i$.

The last fixed point corresponds to the stationary coexistence of both parasite genotypes within the host, so we call it the "doubly infected fixed point" (DIFP). Let us denote by x_i the parasite load of genotype i associated to this fixed point. Finding a non-zero solution $(x_i, x_k) \neq (0,0)$ comes down to solving the following linear system

$$\begin{cases} r_1(\widehat{\mathbf{w}}) = 0, \\ r_2(\widehat{\mathbf{w}}) = 0, \end{cases} \overset{(6)}{\iff} \begin{cases} \varrho_1 + \gamma_{1,1} u_1 x_1 + \gamma_{1,2} u_2 x_2 - \sigma_{1,1} v_1 x_1 - \sigma_{1,2} v_2 x_2 + \eta_{1,1} x_1 + \eta_{1,2} x_2 = 0, \\ \varrho_2 + \gamma_{2,1} u_1 x_1 + \gamma_{2,2} u_2 x_2 - \sigma_{2,1} v_1 x_1 - \sigma_{2,2} v_2 x_2 + \eta_{2,1} x_1 + \eta_{2,2} x_2 = 0, \end{cases}$$

$$\iff \mathbf{M} \begin{bmatrix} x_1 \\ x_2 \end{bmatrix} = - \begin{bmatrix} \varrho_1 \\ \varrho_2 \end{bmatrix}, \tag{10}$$

where $\mathbf{M} = \left(m_{j,\ell} \right)_{(j,\ell) \in \{1,2\}^2}$. We call $\mathbf{M}$ the stationary interaction matrix. Its elements, the stationary interaction effects, are defined as

$$m_{j,\ell} := \eta_{j,\ell} + \gamma_{j,\ell} u_\ell - \sigma_{j,\ell} v_\ell. \tag{11}$$

More precisely, $m_{j,\ell}$ is the sum of the interaction effects over genotype j from genotype ℓ, where the parasite loads of genotypes j and ℓ (j might be equal to ℓ) are at their non-zero stationary values.

The linear system (10) has a unique solution almost everywhere over the parameter space and it is given by

$$\begin{bmatrix} x_1 \\ x_2 \end{bmatrix} = -\mathbf{M}^{-1} . \begin{bmatrix} \varrho_1 \\ \varrho_2 \end{bmatrix} = \frac{1}{m_{1,1} m_{2,2} - m_{1,2} m_{2,1}} \begin{bmatrix} m_{1,2} \varrho_2 - m_{2,2} \varrho_1 \\ m_{2,1} \varrho_1 - m_{1,1} \varrho_2 \end{bmatrix}.$$

The DIFP is therefore the following vector

$$\widehat{\mathbf{w}}_3 = \begin{bmatrix} x_i \mathbf{c}_i & x_k \mathbf{c}_k \end{bmatrix}, x_i = \frac{m_{i,k} \varrho_k - m_{k,k} \varrho_i}{m_{i,i} m_{k,k} - m_{i,k} m_{k,i}} \in \mathbb{R}^\star. \tag{12}$$

Finally, note that the $\widehat{\mathbf{w}}_0$ and $\widehat{\mathbf{w}}_i$ belong to $\mathcal{W}_i'$ while $\widehat{\mathbf{w}}_j$ and $\widehat{\mathbf{w}}_3$ do not.

As a conclusion, the stationary values of the parasite loads in single infection, x_i°, and in double infection, x_i, are governed by the elements of the stationary interaction matrix $\mathbf{M} = \left(m_{j,\ell} \right)_{(j,\ell) \in \{1,2\}^2}$.

C.2 Feasibility

Hereafter, the comparison symbols $\succeq$ and $\succ$ are the element-wise versions of $\geq$ and $>$, that is for instance $\mathbf{A} = \left(a_{j,\ell}\right) \succeq b \iff \forall\,(j,\ell), a_{j,\ell} \geq b$. Due to the biological meaning of its components, a variable vector $\mathbf{w}$ is said to be "feasible" if none of its elements is negative, that is $\mathbf{w} \succeq 0$. The subset of feasible variable vectors is denoted by $\mathcal{W}_+ = \left\{\mathbf{w} \in \mathcal{W} : \mathbf{w} \succeq 0\right\}$.

Let us show that $\mathcal{W}_+$ is positively invariant, that is $\mathbf{a} \in \mathcal{W}_+ \Longrightarrow \forall t \in \mathbb{R}_+, \mathbf{w}^{[\mathbf{a}]}(t) \in \mathcal{W}_+$. From $\frac{\mathrm{d}X_i}{\mathrm{d}t} = r_i X_i$, it comes that

$$X_i(t) = X_i(0)\, e^{\int_0^t r_i X_i(\tau)\mathrm{d}\tau},$$

so $X_i(0) \geq 0 \Longrightarrow \forall t \in \mathbb{R}_+, X_i(t) \geq 0$.

Applying this result to $\frac{\mathrm{d}Y_i}{\mathrm{d}t} = v(u_i X_i - Y_i)$, we get the following inequality

$$\frac{\mathrm{d}Y_i}{\mathrm{d}t} \geq -vY_i.$$

Let $\underline{Y_i}$ be the solution of $\begin{cases} \frac{\mathrm{d}\underline{Y_i}}{\mathrm{d}t} = -v\underline{Y_i} \\ \underline{Y_i}(0) = Y_i(0) \geq 0 \end{cases}$, that is $\underline{Y_i}(t) = Y_i(0)e^{-vt} \geq 0$. Thus, $\frac{\mathrm{d}Y_i}{\mathrm{d}t} \geq \frac{\mathrm{d}\underline{Y_i}}{\mathrm{d}t}$ implies $Y_i(t) \geq \underline{Y_i}(t) \geq 0, \forall t \in \mathbb{R}_+$. The same holds for Z_i. By symmetry with j, we conclude that $\mathcal{W}_+$ is positively invariant.

Using the same reasoning, it is straightforward that $\mathcal{W}_+ \cap \mathcal{W}_i'$ is positively invariant as well. As a consequence, the within-host variables always have feasible values if they start from a feasible value and we ignore solutions that do not lie in $\mathcal{W}_+$.

For the sake of simplicity and biological relevance, we do not consider subsets of the parameter space with measure zero, meaning that x_i° and x_i cannot be equal to 0. Since v represents a clearing rate and u_i and v_i production rates, these parameters are positive. We therefore have the following feasibility condition on the non trivial fixed points owing to the fact that $\mathbf{c}_i > 0$,

$$\begin{aligned} (\widehat{\mathbf{w}}_i \succeq 0) &\iff x_i^\circ > 0, \\ &\iff \mathrm{sgn}\left(\varrho_i\right) \neq \mathrm{sgn}\left(m_{i,i}\right), \end{aligned} \tag{13}$$

and

$$\begin{aligned} \widehat{\mathbf{w}}_3 \succeq 0 &\iff (x_i > 0) \wedge (x_k > 0), \\ &\iff \mathrm{sgn}\left(m_{i,i}m_{k,k} - m_{i,k}m_{k,i}\right) = \mathrm{sgn}\left(m_{i,k}\varrho_k - m_{k,k}\varrho_i\right) = \mathrm{sgn}\left(m_{k,i}\varrho_i - m_{i,i}\varrho_k\right), \end{aligned} \tag{14}$$

where sgn is the sign function ($\mathrm{sgn}(x) := \frac{x}{|x|}, \forall x \neq 0$ and $\mathrm{sgn}(0) := 0$) and $\wedge$ is the logical conjunction (and). Condition (13) states that in order for one genotype to show a feasible stationary parasite load in single infection, either reproduction can be achieved without any public good ($\varrho_i > 0$) and is restrained by some density-dependence effects ($m_{i,i} < 0$), or reproduction is public-good dependent ($\varrho_i < 0, m_{i,i} > 0$). Condition (14) has no straightforward interpretation.

C.3 Local asymptotic stability

A fixed point $\widehat{\mathbf{w}}$ is said to be locally asymptotically stable (LAS, but simply 'stable' in the main text) in a given space Ω if any trajectory $\mathbf{w}^{[\mathbf{a}]}(t)$ on Ω, with $\mathbf{a}$ close enough to $\widehat{\mathbf{w}}$, remains close to $\widehat{\mathbf{w}}$ for all later times and $\mathbf{w}^{[\mathbf{a}]}(\infty) := \lim_{t\to\infty} \mathbf{w}^{[\mathbf{a}]}(t) = \widehat{\mathbf{w}}$ (see Wiggins (2003) for a more formal definition). A necessary and sufficient condition for a fixed point to be LAS in a given space Ω is that all the eigenvalues of its associated Jacobian matrix evaluated in Ω have a negative real part (Wiggins, 2003). Otherwise, the fixed point is unstable in Ω.

Local asymptotic stability is a useful property to predict the behaviour of the system in a close neighbourhood of one of its fixed points. After a small perturbation, the system returns to the fixed point if stable and moves away from it if unstable.

Local asymptotic stability of a fixed point may be effective in one space but not in another. An interesting biological consequence of this is that the inoculation by genotype j of a host already singly infected by genotype i can result in the persistence of genotype j and in the elimination of genotype i from the host. Recall that the UFP and the SIFP belong to $\mathcal{W}_i' \subsetneq \mathcal{W}$; we thus have to distinguish between being LAS in $\mathcal{W}_i'$ and being LAS in $\mathcal{W}$.

C.3.1 Necessary and sufficient condition for UFP to be LAS in $\mathcal{W}$ and $\mathcal{W}_i'$

Let us study the the stability of the UFP $\widehat{\mathbf{w}}_0$ in $\mathcal{W}$. The Jacobian matrix evaluated in this point is

$$\mathbf{J}_3(\widehat{\mathbf{w}}_0) = \begin{bmatrix} \varrho_i & 0 & 0 & 0 & 0 & 0 \\ \upsilon u_i & -\upsilon & 0 & 0 & 0 & 0 \\ \upsilon v_i & 0 & -\upsilon & 0 & 0 & 0 \\ 0 & 0 & 0 & \varrho_k & 0 & 0 \\ 0 & 0 & 0 & \upsilon u_k & -\upsilon & 0 \\ 0 & 0 & 0 & \upsilon v_k & 0 & -\upsilon \end{bmatrix},$$

the eigenvalues of which are simply $\mathrm{Sp}(\mathbf{J}_3(\widehat{\mathbf{w}}_0)) = \{\varrho_i, \varrho_k, -\upsilon\}$, because it is a lower triangular matrix. Therefore, we have

$$\widehat{\mathbf{w}}_0 \text{ is LAS in } \mathcal{W} \Longleftrightarrow \big(\varrho_1 < 0\big) \wedge \big(\varrho_2 < 0\big). \tag{15}$$

Obviously, $\mathbf{J}_i(\widehat{\mathbf{w}}_0)$ is equal to the upper left 3×3 block of $\mathbf{J}_3(\widehat{\mathbf{w}}_0)$ and is also a lower triangular matrix, so

$$\widehat{\mathbf{w}}_0 \text{ is LAS in } \mathcal{W}_i' \Longleftrightarrow \varrho_i < 0. \tag{16}$$

C.3.2 Necessary and sufficient condition for SIFP$_i$ to be LAS in $\mathcal{W}_i'$

Let us study the stability of the SIFP$_i$ $\widehat{\mathbf{w}}_i$ in $\mathcal{W}_i'$, that is when there is only one genotype in the system. The Jacobian matrix evaluated at this point is

$$\mathbf{J}_i(\widehat{\mathbf{w}}_i) = \begin{bmatrix} \eta_{i,i} x_i^\circ & \gamma_{i,i} x_i^\circ & -\sigma_i x_i^\circ \\ \upsilon u_i & -\upsilon & 0 \\ \upsilon v_i & 0 & -\upsilon \end{bmatrix},$$

the eigenvalues of which are the roots of the following polynomial

$$
\begin{aligned}
|\mathbf{J}_i(\widehat{\mathbf{w}}_i) - \lambda I_3| &= \begin{vmatrix} \eta_{i,i}x_i^\circ - \lambda & \gamma_{i,i}x_i^\circ & -\sigma_{i,i}x_i^\circ \\ \upsilon u_i & -\upsilon - \lambda & 0 \\ \upsilon v_i & 0 & -\upsilon - \lambda \end{vmatrix}, \\
&= (-\upsilon-\lambda)^2\left(\eta_{i,i}x_i^\circ - \lambda\right) - \left(-\sigma_{i,i}x_i^\circ\right)(-\upsilon-\lambda)\upsilon v_i - (-\upsilon-\lambda)\gamma_{i,i}x_i^\circ \upsilon u_i, \\
&= -(\upsilon+\lambda)\left((\lambda+\upsilon)\left(\lambda - \eta_{i,i}x_i^\circ\right) + \upsilon\sigma_{i,i}v_i x_i^\circ - \upsilon\gamma_{i,i}u_i x_i^\circ\right).
\end{aligned}
$$

A first obvious eigenvalue is $\lambda_0 = -\upsilon < 0$. The remaining eigenvalues are the roots of the polynomial

$$
\lambda^2 + \left(\upsilon - \eta_{i,i}x_i^\circ\right)\lambda - \upsilon x_i^\circ\left(\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i\right) \overset{(9)}{=} \lambda^2 + \left(\upsilon + \frac{\varrho_i\eta_{i,i}}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i}\right)\lambda + \upsilon\varrho_i,
$$

the discriminant of which is

$$
\begin{aligned}
\Delta &= \left(\upsilon + \frac{\varrho_i\eta_{i,i}}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i}\right)^2 - 4\upsilon\varrho_i, \\
&= \upsilon^2 + \frac{2\upsilon\varrho_i\eta_{i,i}}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i} + \left(\frac{\varrho_i\eta_{i,i}}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i}\right)^2 - 4\upsilon\varrho_i, \\
&= \upsilon^2 - \frac{-2\upsilon\varrho_i\eta_{i,i}}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i} + \left(\frac{\varrho_i\eta_{i,i}}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i}\right)^2 - \frac{4\upsilon\varrho_i\left(\gamma_{i,i}u_i - \sigma_{i,i}v_i\right)}{\eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i}, \\
&= \left(\upsilon - \frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - \frac{4\upsilon\varrho_i\left(\gamma_{i,i}u_i - \sigma_{i,i}v_i\right)}{m_{i,i}}.
\end{aligned}
$$

In order to simplify the calculus, we make two assumptions without significant loss of biological relevance. First, we assume that the public goods production rate (u_i) has the same order of magnitude than the spite production rate (v_i). Note that otherwise the slowest public production dynamics could be assumed constant. Second, we assume that a parasite genotype benefits much more from its own public good than it is affected by its own spite, in absolute value ($\gamma_{i,i} \gg \sigma_{i,i}$). By formally combining these two assumptions, we assume from now on that

$$
\gamma_{i,i}u_i > \sigma_{i,i}v_i. \tag{17}
$$

If we use this inequality and (13) (we are only interested in the stability of feasible fixed points), it is straightforward that $\Delta > 0$. The remaining two eigenvalues are then the following real numbers

$$
\lambda_{1,2} = -\frac{1}{2}\left(\upsilon + \frac{\varrho_i\eta_{i,i}}{m_{i,i}} \pm \sqrt{\left(\upsilon + \frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4\upsilon\varrho_i}\right).
$$

Two cases must be considered according to (13) because either $\varrho_i < 0 \wedge m_{i,i} > 0$ or $\varrho_i > 0 \wedge m_{i,i} < 0$.

In the first case,

$$\begin{aligned}
\varrho_i < 0 &\iff -4v\varrho_i > 0,\\
&\iff \left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i > \left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 > 0,\\
&\iff \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i} > \left|v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right| > 0,\\
&\iff -\left|v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right| + \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i} > 0,\\
&\implies -\frac{1}{2}\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}} - \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i}\right) > 0,
\end{aligned}$$

so one of the eigenvalues is positive, meaning that $\widehat{\mathbf{w}}_i$ is unstable in $\mathcal{W}_i^{\prime}$.

In the second case,

$$\begin{aligned}
m_{i,i} < 0 &\iff \eta_{i,i} + \gamma_{i,i}u_i - \sigma_{i,i}v_i < 0,\\
&\overset{(17)}{\implies} \eta_{i,i} < 0,
\end{aligned} \tag{18}$$

and

$$\begin{aligned}
\varrho_i > 0 &\iff -4v\varrho_i < 0,\\
&\iff 0 < \left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i < \left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2,\\
&\iff 0 < \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i} < \left|v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right|,\\
&\iff \left|v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right| - \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i} > 0,\\
&\iff -\left|v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right| - \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i} < -\left|v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right| + \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i} < 0,\\
&\overset{(18)}{\iff} -\frac{1}{2}\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}} + \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i}\right) < -\frac{1}{2}\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}} - \sqrt{\left(v+\frac{\varrho_i\eta_{i,i}}{m_{i,i}}\right)^2 - 4v\varrho_i}\right) < 0,
\end{aligned}$$

that is both eigenvalues are negative.

To conclude on the local asymptotic stability in $\mathcal{W}_i^{\prime}$ of the SIFP$_i$,

$$\widehat{\mathbf{w}}_i \text{ is LAS in } \mathcal{W}_i^{\prime} \iff \big(\varrho_i > 0\big) \wedge \big(m_{i,i} < 0\big). \tag{19}$$

C.3.3 Necessary and sufficient condition for SIFP$_i$ to be LAS in $\mathcal{W}$

Let us study the local stability of the SIFP$_i$ $\widehat{\mathbf{w}}_i$ in $\mathcal{W}$, that is when there are two parasite genotypes in the system.

The Jacobian matrix evaluated at this point is

$$\mathbf{J}_3(\widehat{\mathbf{w}}_i) = \begin{bmatrix} \eta_{i,i}x_i^\circ & \gamma_{i,i}x_i^\circ & -\sigma_{i,i}x_i^\circ & \eta_{i,k}x_i^\circ & \gamma_{i,k}x_i^\circ & -\sigma_{i,k}x_i^\circ \\ \upsilon u_i & -\upsilon & 0 & 0 & 0 & 0 \\ \upsilon v_i & 0 & -\upsilon & 0 & 0 & 0 \\ 0 & 0 & 0 & r_k(\widehat{\mathbf{w}}_i) & 0 & 0 \\ 0 & 0 & 0 & \upsilon u_k & -\upsilon & 0 \\ 0 & 0 & 0 & \upsilon v_k & 0 & -\upsilon \end{bmatrix}.$$

It appears that this matrix can be written as a block matrix using the single infection Jacobian matrices the definition of which can be extended to $\mathcal{W}$ as follows:

$$\mathbf{J}_3(\widehat{\mathbf{w}}_i) = \begin{bmatrix} \mathbf{J}_i(\widehat{\mathbf{w}}_i) & \mathbf{A} \\ \mathbf{0} & \mathbf{J}_k(\widehat{\mathbf{w}}_i) \end{bmatrix}.$$

Thus, the eigenvalues λ of this matrix cancel

$$\det(\mathbf{J}_3(\widehat{\mathbf{w}}_i) - \lambda\mathbf{I}_6) = \det(\mathbf{J}_i(\widehat{\mathbf{w}}_i) - \lambda\mathbf{I}_3)\det(\mathbf{J}_k(\widehat{\mathbf{w}}_i) - \lambda\mathbf{I}_3).$$

By definition, the roots of $\det(\mathbf{J}_i(\widehat{\mathbf{w}}_i) - \lambda\mathbf{I}_3)$ are the eigenvalues of $\mathbf{J}_i(\widehat{\mathbf{w}}_i)$. From the previous results, we know that these roots are all negative iff $\varrho_i > 0 \wedge m_{i,i} < 0$. Put differently, the stability of $\widehat{\mathbf{w}}_i$ in $\mathcal{W}_i'$ is a necessary condition of the stability of $\widehat{\mathbf{w}}_i$ in $\mathcal{W}$.

By definition, the roots of $\det(\mathbf{J}_k(\widehat{\mathbf{w}}_i) - \lambda\mathbf{I}_3)$ are the eigenvalues of $\mathbf{J}_k(\widehat{\mathbf{w}}_i) = \begin{bmatrix} r_k(\widehat{\mathbf{w}}_i) & 0 & 0 \\ \upsilon u_k & -\upsilon & 0 \\ \upsilon v_k & 0 & -\upsilon \end{bmatrix}$. This matrix is a lower triangular matrix so its spectrum is straightforwardly $\mathrm{Sp}(\mathbf{J}_k(\widehat{\mathbf{w}}_i)) = \{-\upsilon, r_k(\widehat{\mathbf{w}}_i)\}$. Expliciting the instantaneous growth rate, we find that

$$\begin{aligned} r_k(\widehat{\mathbf{w}}_i) &= \varrho_k + \gamma_{k,i}u_i x_i^\circ - \sigma_{k,i}v_i x_i^\circ + \eta_{k,i}x_i^\circ, \\ &= \varrho_k + m_{k,i}x_i^\circ, \\ &= \varrho_k - \frac{m_{k,i}}{m_{i,i}}\varrho_i, \end{aligned}$$

which is negative iff $m_{i,i}\varrho_k > m_{k,i}\varrho_i$.

In conclusion, and owing to symmetry, the necessary and sufficient condition for the EFPs to be LAS is the following

$$\widehat{\mathbf{w}}_i \text{ is LAS in } \mathcal{W} \iff \big(\varrho_i > 0\big) \wedge \big(m_{i,i} < 0\big) \wedge \big(m_{i,i}\varrho_k > m_{k,i}\varrho_i\big). \tag{20}$$

Note that $\big(\varrho_i > 0\big) \wedge \big(m_{i,i} < 0\big) \wedge \big(m_{i,i}\varrho_k > m_{k,i}\varrho_i\big) \Longrightarrow \big(\varrho_k < 0\big) \vee \big(m_{k,i} < 0\big)$. A consequence of this result, which proves to be useful later on, is that

$$\widehat{\mathbf{w}}_i \text{ LAS in } \mathcal{W} \Longrightarrow r_k(\widehat{\mathbf{w}}_i) < 0. \tag{21}$$

C.3.4 Necessary and sufficient condition for DIFP to be LAS in $\mathcal{W}$

The double infection Jacobian matrix evaluated in $\widehat{\mathbf{w}}_3$ is

$$\mathbf{J}_3(\widehat{\mathbf{w}}_3) = \begin{bmatrix} \eta_{i,i}x_i & \gamma_{i,i}x_i & -\sigma_{i,i}x_i & \eta_{i,k}x_i & \gamma_{i,k}x_i & -\sigma_{i,k}x_i \\ \upsilon u_i & -\upsilon & 0 & 0 & 0 & 0 \\ \upsilon v_i & 0 & -\upsilon & 0 & 0 & 0 \\ \eta_{k,i}x_k & \gamma_{k,i}x_k & -\sigma_{k,i}x_k & \eta_{k,k}x_k & \gamma_{k,k}x_k & -\sigma_{k,k}x_k \\ 0 & 0 & 0 & \upsilon u_k & -\upsilon & 0 \\ 0 & 0 & 0 & \upsilon v_k & 0 & -\upsilon \end{bmatrix},$$

the eigenvalues of which are too large to be shown and no parametric condition for local asymptotic stability can easily be extracted from them. Therefore, stability of the DIFP has to be addressed either numerically, either through a more restrictive condition that provides its global stability.

C.4 Summary

Table S8 sum ups the notations and results related to fixed points analysis.

symbol	**value**	**meaning**
$\mathbf{c}_i$	$= \begin{bmatrix} 1 & u_i & v_i \end{bmatrix}$	public productions nullcline direction vector i
$m_{j,\ell}$	$= \eta_{j,\ell} + \gamma_{j,\ell}u_\ell - \sigma_{j,\ell}v_\ell,$	stationary interaction effect of ℓ over j
x_i°	$= -\frac{\varrho_i}{m_{i,i}}$	stationary parasite load in single infection
x_i	$= \frac{m_{i,k}\varrho_k - m_{k,k}\varrho_i}{m_{i,i}m_{k,k} - m_{i,k}m_{k,i}}$	stationary parasite load in double infection
$\widehat{\mathbf{w}}_0$	$= \mathbf{0}_6$	uninfected fixed point (UFP)
$\widehat{\mathbf{w}}_i$	$= \begin{bmatrix} x_i^\circ\mathbf{c}_i & \mathbf{0}_3 \end{bmatrix}$	singly infected fixed point i (SIFP$_i$)
$\widehat{\mathbf{w}}_3$	$= \begin{bmatrix} x_i\mathbf{c}_i & x_k\mathbf{c}_k \end{bmatrix}$	doubly infected fixed point (DIFP)
$\widehat{\mathcal{W}}$	$= \{\widehat{\mathbf{w}}_0, \widehat{\mathbf{w}}_1, \widehat{\mathbf{w}}_2, \widehat{\mathbf{w}}_3\}$	fixed point set

Table S8: Fixed points analysis notations and result summary.

The results of the local stability analysis in both spaces are given in Table S9 along with the feasibility conditions.

fixed point	**feasibility condition**	**local asymptotic stability condition if feasible**	
		in $\mathcal{W}_i'$	**in** $\mathcal{W}$
$\widehat{\mathbf{w}}_0$ (UFP)	always	$\varrho_i < 0$	$(\varrho_1 < 0) \wedge (\varrho_2 < 0)$
$\widehat{\mathbf{w}}_i$ (SIFP$_i$)	$\operatorname{sgn}(\varrho_i) \neq \operatorname{sgn}(m_{i,i})$	$(\varrho_i > 0) \wedge (m_{i,i} < 0)$	$(\varrho_i > 0) \wedge (m_{i,i} < 0)$ $\wedge\, (m_{k,i}\varrho_i < m_{i,i}\varrho_k)$
$\widehat{\mathbf{w}}_3$ (DIFP)	$\operatorname{sgn}(m_{i,i}m_{k,k} - m_{i,k}m_{k,i})$ $= \operatorname{sgn}(m_{i,k}\varrho_k - m_{k,k}\varrho_i)$ $= \operatorname{sgn}(m_{k,i}\varrho_i - m_{i,i}\varrho_k)$	none ($\widehat{\mathbf{w}}_3 \notin \mathcal{W}_i'$)	not shown

Table S9: Fixed points analysis notations and result summary.

D Finite time explosion solutions

D.1 Preliminary result

Let us define the following quantity $P_i := v_i Y_i - u_i Z_i$, the time derivative of which is

$$\begin{aligned}\frac{\mathrm{d}P_i}{\mathrm{d}t} &= v_i \frac{\mathrm{d}Y_i}{\mathrm{d}t} - u_i \frac{\mathrm{d}Z_i}{\mathrm{d}t},\\ &= vv_i(u_i X_i - Y_i) - vu_i(v_i X_i - Z_i),\\ &= -vY_i - vZ_i,\\ &= -vP_i.\end{aligned}$$

It follows from this that $\forall t \in \mathbb{R}_+, P_i(t) = P_i(0)e^{-vt}$. Two cases are then to be distinguished. Either genotype i is newly inoculated in the host, which means no public production of its kind is already present, that is $Y_i(0) = Z_i(0) = 0$, yielding $P_i(0) = 0$. Or genotype i is already present in the host when the dynamics are followed up and it is usually at some fixed point, where $Y_i = u_i X_i$ and $Z_i = v_i X_i$, also yielding $P_i(0) = v_i u_i X_i - u_i v_i X_i = 0$. In both cases, $P_i(t) = 0$ yielding a time independent correlation between public production concentrations,

$$\forall t \in \mathbb{R}_+, v_i Y_i = u_i Z_i. \tag{22}$$

Note that even if different initial conditions than the above are taken, this correlation is reached exponentially (all the more fast as the standard clearing rate v is high).

D.2 In singly inoculated hosts

Here we show that when there is no feasible and LAS fixed point in the SIS_i, formulated as $\varpi_i = \emptyset$ (see definition in next section), genotype i parasite load explodes in finite time in a singly inoculated host.

From Table S9, assuming the emptiness of ϖ_i implies that $\varrho_i > 0$ and $m_{i,i} > 0$, that is $\eta_{i,i} + \gamma_{i,i}u_i > \sigma_{i,i}v_i$ hence $\eta_{i,i} > 0$. Considering a newly singly inoculated host, we have $X_i(0) = \varepsilon > 0$, all other variables being 0 at $t = 0$. Using (22), it follows that

$$\begin{aligned}\frac{\mathrm{d}X_i}{\mathrm{d}t} &= \left(\varrho_i + \eta_{i,i}X_i + \gamma_{i,i}Y_i - \sigma_{i,i}Z_i\right)X_i,\\ &= \left(\varrho_i + \eta_{i,i}X_i + \left(\gamma_{i,i} - \sigma_{i,i}\frac{v_i}{u_i}\right)Y_i\right)X_i,\end{aligned}$$

yet $\gamma_{i,i} - \sigma_{i,i}\frac{v_i}{u_i} > 0$ because of assumption (17), the following inequality holds

$$\frac{\mathrm{d}X_i}{\mathrm{d}t} \geq \left(\varrho_i + \eta_{i,i}X_i\right)X_i > 0.$$

Let $\underline{X_i}$ satisfy $\frac{\mathrm{d}\underline{X_i}}{\mathrm{d}t} = \left(\varrho_i + \eta_{i,i}\underline{X_i}\right)\underline{X_i}$, $\underline{X_i}(0) = X_i(0) = \varepsilon$. Defining $f := \frac{1}{\underline{X_i}}$, f satisfies the following ODE,

$$\frac{\mathrm{d}f}{\mathrm{d}t} = -\varrho_i f - \eta_{i,i},$$

the solution of which is

$$\begin{aligned} f(t) &= \left(f(0)+\frac{\eta_{i,i}}{\varrho_i}\right)e^{-\varrho_i t}-\frac{\eta_{i,i}}{\varrho_i}, \\ i.e.\ \frac{1}{\underline{X_i}(t)} &= \left(\frac{1}{\varepsilon}+\frac{\eta_{i,i}}{\varrho_i}\right)e^{-\varrho_i t}-\frac{\eta_{i,i}}{\varrho_i}, \end{aligned}$$

yielding

$$\underline{X_i}(t)=\frac{\varrho_i\varepsilon}{\left(\varrho_i+\eta_{i,i}\varepsilon\right)e^{-\varrho_i t}-\eta_{i,i}\varepsilon}.$$

But $\underline{X_i}(t)$ is not defined for t^* such that

$$\left(\varrho_i+\eta_{i,i}\varepsilon\right)e^{-\varrho_i t^*}-\eta_{i,i}\varepsilon = 0,$$

i. e.

$$t^*=\frac{1}{\varrho_i}\log\left(1+\frac{\varrho_i}{\eta_{i,i}\varepsilon}\right)\in\mathbb{R}_+^\star.$$

Therefore $\lim\limits_{t\to t^*}\underline{X_i}(t)=+\infty$.

Because $\frac{\mathrm{d}X_i}{\mathrm{d}t}\geq\frac{\mathrm{d}\underline{X_i}}{\mathrm{d}t}$ and $\underline{X_i}(0)=X_i(0)=\varepsilon>0$, it follows that $\lim\limits_{t\to t^*}X_i(t)=+\infty$ as well. To conclude, if the parasite traits are such that neither the UFP nor the SIFP$_i$ are feasible and LAS in the SIS$_i$, then the parasite load of genotype i explodes in finite time.

D.3 In doubly inoculated hosts

Here we show the existence of scenarios when both parasite genotypes reach their SIFP in singly inoculated hosts but their parasite load explodes in finite time when they occur together in doubly inoculated hosts.

First, this requires that the two SIFPs are feasible and LAS in their respective SIS, $\varpi_1=\{\widehat{\mathbf{w}}_1\},\varpi_2=\widehat{\mathbf{w}}_2\}$ and that there is no feasible and LAS fixed point in the DIS, that is $\varpi=\emptyset$ (see notations in next section). From Table S9, it follows that $\forall(j,\ell)\in\{1,2\}^2, j\neq\ell, \varrho_j>0, m_{j,j}<0, m_{\ell,j}\varrho_j>m_{j,j}\varrho_\ell$.

Let us follow the total parasite load in the host ($X:=X_1+X_2$), starting from the moment when both parasite genotypes are present (either due to a co-inoculation or to a secondary inoculation). We have

$$\frac{\mathrm{d}X}{\mathrm{d}t} = \frac{\mathrm{d}X_1}{\mathrm{d}t}+\frac{\mathrm{d}X_2}{\mathrm{d}t}=r_1X_1+r_2X_2.$$

Let us focus on the instantaneous growth rate

$$r_1=\varrho_1+\eta_{1,1}X_1+\eta_{1,2}X_2+\gamma_{1,1}Y_1-\sigma_{1,1}Z_1+\gamma_{1,2}Y_2-\sigma_{1,2}Z_2.$$

Applying (22) on both genotypes, we have

$$r_1=\varrho_1+\eta_{1,1}X_1+\eta_{1,2}X_2+\left(\gamma_{1,1}-\sigma_{1,1}\frac{v_1}{u_1}\right)Y_1+\left(\gamma_{1,2}-\sigma_{1,2}\frac{v_2}{u_2}\right)Y_2.$$

Because of assumption (17), $\gamma_{1,1}-\sigma_{1,1}\frac{v_1}{u_1}>0$. If we assume as well that $\gamma_{1,2}-\sigma_{1,2}\frac{v_2}{u_2}>0$, the following inequality holds:

$$r_1 \geq \varrho_1 + \eta_{1,1}X_1 + \eta_{1,2}X_2.$$

Using the same arguments for r_2, we have

$$\begin{aligned}\frac{\mathrm{d}X}{\mathrm{d}t} &\geq \left(\varrho_1 + \eta_{1,1}X_1 + \eta_{1,2}X_2\right)X_1 + \left(\varrho_2 + \eta_{2,2}X_2 + \eta_{2,1}X_1\right)X_2,\\ &= \varrho_1 X_1 + \varrho_2 X_2 + \eta_{1,1}X_1^2 + \eta_{2,2}X_2^2 + \left(\eta_{1,2}+\eta_{2,1}\right)X_1X_2.\end{aligned}$$

By defining $\underline{X} := \min(X_1, X_2) \geq 0$ (which is a continuous function of time), $\underline{\varrho} := \min\left(\varrho_1, \varrho_2\right) > 0$ and $\underline{\eta} := \min\left(\eta_{1,1}, \eta_{2,2}\right) < 0$ and noticing that $X_1^2 + X_2^2 = X^2 - 2X_1X_2$, it follows that

$$\frac{\mathrm{d}X}{\mathrm{d}t} \geq \left(\underline{\varrho} + \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)\underline{X}\right)\underline{X}.$$

Let $\underline{X}$ satisfy $\frac{\mathrm{d}\underline{X}}{\mathrm{d}t} = \left(\underline{\varrho} + \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)\underline{X}\right)\underline{X}$, $\underline{X}(0) = \varepsilon < X(0) \geq 2\varepsilon > 0$. Defining $f := \frac{1}{\underline{X}}$, f satisfies the following ODE,

$$\frac{\mathrm{d}f}{\mathrm{d}t} = -\underline{\varrho}f - \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right),$$

the solution of which is

$$f(t) = \left(f(0) + \frac{\left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)}{\underline{\varrho}}\right)e^{-\underline{\varrho}t} - \frac{\left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)}{\underline{\varrho}},$$

yielding

$$\underline{X}(t) = \frac{\underline{\varrho}\varepsilon}{\left(\underline{\varrho} + \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)\varepsilon\right)e^{-\underline{\varrho}t} - \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)\varepsilon}.$$

But $\underline{X_i}(t)$ is not defined for t^* such that

$$\left(\underline{\varrho} + \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)\varepsilon\right)e^{-\underline{\varrho}t^*} - \left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)\varepsilon = 0,$$

i. e.

$$t^* = \frac{1}{\underline{\varrho}}\log\left(1 + \frac{\underline{\varrho}\varepsilon}{\left(\eta_{1,2}+\eta_{2,1}+2\underline{\eta}\right)}\right).$$

Assuming that $\min\left(\eta_{1,1}, \eta_{2,2}\right) \leq -\frac{\eta_{1,2}+\eta_{2,1}}{2}$ makes $t^* \in \mathbb{R}_+^\star$. Therefore $\lim_{t\to t^*}\underline{X}(t) = +\infty$.

Because $\frac{\mathrm{d}X}{\mathrm{d}t} \geq \frac{\mathrm{d}\underline{X}}{\mathrm{d}t}$ and $\underline{X}(0) < X(0)$, it follows that $\lim_{t \to t^*} X(t) = +\infty$ as well under the previous assumptions. Moreover we have numerically checked that the dynamics behave similarly for cases where $\varpi = \emptyset$ and relaxed assumptions on the parameters.

To conclude, if the parasite traits are such that no fixed point is feasible and LAS in the DIS, the total parasite load blows up in finite time.

D.4 Threshold adaptation to explosive infections

In order to take into account explosive infections and keep the model outputs biologically relevant for all parameter sets or to avoid numerical complications, one should add the following rule to the dynamical system:

$$\exists T \in \mathbb{R}_+^\star : X_1(T) + X_2(T) = x_{\max} > 0 \Longrightarrow \forall t > T, X_1(t) = X_2(t) = 0,$$

where $x_{\max}$ is a new parameter of the model defined as the total parasite load threshold a host can bear before either dying or triggering an acute immune response that leads to recovery.

E Generated infection pattern identification

E.1 Compatible sets of FLAS fixed points

Let $\boldsymbol{\omega}_i$ and $\boldsymbol{\omega}$ be the set of feasible and LAS ('FLAS') fixed points in the SIS ($\mathcal{W}_i$) and the DIS ($\mathcal{W}$) respectively.

$$\boldsymbol{\omega}_i := \left\{ \widehat{\mathbf{w}} \in \widehat{\mathcal{W}_i} : (\widehat{\mathbf{w}} \geq 0) \wedge \left(\widehat{\mathbf{w}} \text{ LAS in } \mathcal{W}_i \right) \right\},$$

$$\boldsymbol{\omega} := \left\{ \widehat{\mathbf{w}} \in \widehat{\mathcal{W}} : (\widehat{\mathbf{w}} \geq 0) \wedge \left(\widehat{\mathbf{w}} \text{ LAS in } \mathcal{W} \right) \right\}.$$

From the results obtained in section C and summarised in table S9, one can derive four rules satisfied by these sets:

$$\widehat{\mathbf{w}}_i \in \boldsymbol{\omega} \implies \widehat{\mathbf{w}}_i \in \boldsymbol{\omega}_i, \tag{23}$$

$$\widehat{\mathbf{w}}_0 \in \boldsymbol{\omega} \implies \widehat{\mathbf{w}}_0 \in \boldsymbol{\omega}_1 \cap \boldsymbol{\omega}_2, \tag{24}$$

$$\widehat{\mathbf{w}}_0 \in \boldsymbol{\omega} \implies \{\widehat{\mathbf{w}}_1, \widehat{\mathbf{w}}_2\} \not\supseteq \boldsymbol{\omega}, \tag{25}$$

$$\widehat{\mathbf{w}}_3 \in \boldsymbol{\omega} \implies \{\widehat{\mathbf{w}}_1, \widehat{\mathbf{w}}_2\} \not\supseteq \boldsymbol{\omega}. \tag{26}$$

Rule (23) states that if the SIFP$_i$ is FLAS in the DIS then it is also FLAS in the SIS. Its proof is obvious from (19) and (20). Rule (24) states that if the UFP is FLAS in the DIS then it is also FLAS in the SIS and its proof is obvious from (15) and (16). Rule (25) states that if the UFP is FLAS in the DIS, then none of the SIFPs are FLAS in the DIS and its proof is obvious from (15) and (20).

Rule (26) states that if the DIFP is FLAS in the DIS, then it is the only FLAS fixed point in the DIS. We could not prove this rule analytically because of the size of the local asymptotic stability conditions. However, numerical explorations always satisfied this rule.

A consequence of (26) is that if any fixed point other than the DIFP is both feasible and LAS in the DIS, then the DIFP is not FLAS in the DIS.

We want to reveal the infection patterns this model generates. This requires enumerating all the $(\varpi_i, \varpi_k, \varpi)$ triplets that satisfy rules (23) to (26), with the addition that explosive single infections should be treated as failed infections (that is $\boldsymbol{\omega}_i = \emptyset$ is epidemiologically equivalent to $\boldsymbol{\omega}_i = \{\widehat{\mathbf{w}}_0\}$). The resulting list is given in Table S10, each combination corresponding to a distinct infection pattern.

$\boldsymbol{\omega}_i =$	$\boldsymbol{\omega}_k =$	$\boldsymbol{\omega} =$	pattern
$\{\widehat{\mathbf{w}}_0\}$ or $\emptyset$	$\{\widehat{\mathbf{w}}_0\}$ or $\emptyset$	$\{\widehat{\mathbf{w}}_0\}$ or $\{\widehat{\mathbf{w}}_0, \widehat{\mathbf{w}}_3\}$ or $\emptyset$	**no infection**
		$\{\widehat{\mathbf{w}}_3\}$	***ambinfection***
$\{\widehat{\mathbf{w}}_i\}$		$\{\widehat{\mathbf{w}}_i\}$ or $\emptyset$	***latinfection*** (k)
		$\{\widehat{\mathbf{w}}_3\}$	***suprainfection*** (k)
	$\{\widehat{\mathbf{w}}_k\}$	$\emptyset$	***ultrainfection***
		$\{\widehat{\mathbf{w}}_i\}$	**superinfection** (i)
		$\{\widehat{\mathbf{w}}_1, \widehat{\mathbf{w}}_2\}$	***priorinfection***
		$\{\widehat{\mathbf{w}}_3\}$	**coinfection**

Table S10: FLAS fixed points set combination and corresponding infection patterns.
For the sake of concision, twin infection patterns (*latinfection* i, *suprainfection* i and *superinfection* k) are not shown.

E.2 Logical viewpoint

If the steady presence of genotype 1 in a given host is denoted by the logical proposition p, and if q denotes the same for genotype 2, then the host classes S, I_1, I_2, I_3 are equivalent to $\{\neg p, \neg q\}$, $\{p, \neg q\}$, $\{\neg p, q\}$, $\{p, q\}$ respectively. If we attribute to each class a value 1 if epidemiologically observed or 0 if not, there exists an application that associates one binary operator (also called logical connective) to each infection pattern. Because the susceptible class is, by definition, always observed (the value of $\{\neg p, \neg q\}$ is always 1), only half of the sixteen different binary operators do match. Restrained to this set, this application is surjective, as shown in Table S11.

infection pattern	S $\{\neg p, \neg q\}$	I_1 $\{p, \neg q\}$	I_2 $\{\neg p, q\}$	I_3 $\{p, q\}$	**logical connective equivalence**	
no infection	1	0	0	0	$p \downarrow q$	joint denial
ambinfection	1	0	0	1	$p \leftrightarrow q$	biconditional
latinfection 1	1	0	1	0	$\neg p$	negation of p
suprainfection 1	1	0	1	1	$p \rightarrow q$	material implication
latinfection 2	1	1	0	0	$\neg q$	negation of q
suprainfection 2	1	1	0	1	$p \leftarrow q$	converse implication
ultrainfection, priorinfection, superinfection 1, superinfection 2	1	1	1	0	$p \uparrow q$	alternative denial
coinfection	1	1	1	1	$\top$	tautology

Table S11: Infection patterns and their binary operators (logical connectives) equivalents.

However, the infection pattern-to-logical connective map is not injective since ultrainfection, priorinfection and the two superinfections match with the alternative denial. This yields two lessons. The first one is that the world of (formal) infection patterns is richer than the logical one. The second is that if only prevalence data is available for a host-parasite system, then it is impossible to distinguish between these four infection patterns. This requires the knowledge of the within-host dynamics or, at least, the outcome of cross-inoculations.

Additional references

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