

Cellulose Biodegradation Models; An Example of Cooperative Interactions in Structured Populations

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Abstract

We introduce various models for cellulose bio-degradation by micro-organisms. Those models rely on complex chemical mechanisms, involve the structure of the cellulose chains and are allowed to depend on the phenotypical traits of the population of micro-organisms. We then use the corresponding models in the context of multiple-trait populations. This leads to classical, logistic type, reproduction rates limiting the growth of large populations but also, and more surprisingly, limiting the growth of populations which are too small in a manner similar to the effects seen in populations requiring cooperative interactions (or sexual reproduction). This study thus offers a striking example of how some mechanisms resembling *cooperation* can occur in structured biological populations, even in the absence of any actual cooperation.

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1 Introduction

The goal of this article is to derive models for structured populations of micro-organisms living off cellulose degradation. Our first step is to study the mechanisms by which some micro-organisms can use cellulose. The full process is obviously complex and we have to abstract its most important features. This gives us a hierarchy of models, depending on the level of simplification that one desires.

The second step is to couple those models with the population dynamics of the corresponding micro-organisms. While the mechanism of bio-degradation that we consider is similar for each species of micro-organisms, we allow for some variability from one species to another, in the enzymes involved for instance. This leads to a population structured by a phenomenological trait that describes the exact path of bio-degradation.

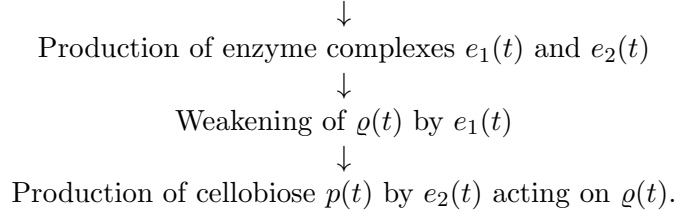
As the amount of cellulose is limited, the total growth of the population is, unsurprisingly, limited as well. More interesting are the effects when the total population or the population in a given species is small. The model does not include any actual cooperation between micro-organisms but as the bio-degradation occurs in several steps, the process is nonlinear in the population size even if cellulose is abundant. This puts small populations at a disadvantage, introducing an effect similar to classical cooperation.

Cellulose Bio-degradation. Mechanisms and Models. Cellulose is the structural component of many plants and is therefore the most abundantly produced bio-polymer; it is a homo-polymer consisting of a vast number of glucose units. The most important feature of cellulose as a substrate is its *insolubility*. As such, bacterial and fungal degradation of cellulose, (e.g. by fungi *Trichoderma reesei* or bacteria *Clostridium thermocellum*), occurs exocellularly. The products of cellulose hydrolysis are available as carbon and energy sources for microbes that inhabit environments in which cellulose is biodegraded [31, 32].

In this work we model cellulose bio-degradation as a multiple-step process, reflecting realistic mechanisms described in [32]. Let $\varrho(t)$ denote the mass of cellulose. The biodegrading microorganism is unable to consume (degrade) the cellulose ϱ directly. Instead, the individuals produce two enzyme complexes $e_1(t)$ and $e_2(t)$ that act in a two-stage process.

During the first stage, the (endoglucanase) enzyme e_1 weakens cellulose fibers in ϱ : that is, it randomly cuts the fibers, creating the so-called reducing and non-reducing ends which serve as landing sites for the (exoglucanase) enzyme e_2 . During the second stage, the enzyme e_2 locates a landing site and attaches itself to it. Once attached, it cleaves off cellobiose (a major energy source for the microorganisms) from the chain of polysaccharides. Some portion $\theta_p \in [0, 1]$ of cellobiose is consumed directly by the microorganism that produced the enzymes, and the rest is available for other individual microorganisms in the population due to diffusion. The above mechanisms can be viewed as follows:

$$\text{Growth of micro-organisms} + \text{influx of cellulose } \varrho(t)$$



The last two steps in the above diagram constitute the so-called cleaving mechanism. In our work we present two different cleaving mechanisms that differ in complexity (see Section 2). In Cleaving Mechanism 1 the enzyme e_2 that cuts off cellobiose units has two states, ‘attached to’ and ‘detached from’ cellulose. In Cleaving Mechanism 2, however, the enzyme e_2 is always detached. In this mechanism cleaving happens instantaneously once the enzyme e_2 finds a spot on the cellulose where it is able to cut off cellobiose.

In the present work we develop several models of varying complexity which incorporate these mechanisms. Even in the simplest model the aforementioned cascade of events produces a *cooperative effect*, which appears due to the fact that the cellobiose units cleaved off by the enzyme of one microorganism are available for consumption by other individuals located nearby. Mathematically, these effects are encoded in the reproduction rate $B(n)$ of the population n . In particular, for small populations, the population size $n(t)$ turns out to behave as

$$\partial_t n(\cdot, t) \sim n(B(n) - d) \quad \text{with} \quad B(n) \sim Cn^2 \quad \text{when} \quad n \ll \bar{n},$$

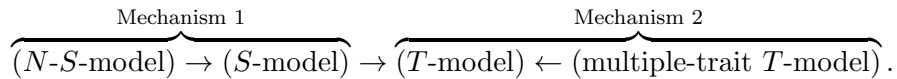
where \bar{n} is a critical threshold.

In general, the population includes various species of micro-organisms. In that case, the exact enzyme complexes used may change across species. We represent the different species x_j by traits $j \in \{1, \dots, M\}$, where the population with trait j uses enzymes complexes denoted $e_{1,j}$ and $e_{2,j}$. This can be included in a more general framework by considering continuous traits x with subpopulations $n(t, x)$ with a model of the form

$$\partial_t n(x, t) = \left(B[n](x, t) - d(x) \right) n(x, t), \quad (1.1)$$

where $B[n]$ is now an integral operator; see (5.2) for the precise formula. The case of discrete traits is included in this framework by taking $n(t, x) = \sum_j n_j(t) \delta_{x_j}(x)$ with $n_j(t)$ the population of individuals with trait x_j .

Hierarchy of Models. Let us give a brief description of the models developed in our work and their relations.



The most complex model that explicitly takes the kinetics of enzymatic reactions into account is the N - S -model. We monitor the evolution of the cellulose chains N , structured by polymer length and the total number of landing sites where the enzyme e_2 can be attached. This model incorporates cleaving Mechanism 1, in which the enzyme e_2 is either ‘attached’ (e_{2A}) or ‘detached’ (e_{2D}). In addition, the model tracks the evolution of unoccupied landing sites S and the total number of landing sites T ; these two variables are related via $T = S + e_{2A}$. Under the assumption that the cleaving rates are independent of the polymer structure, the N - S -model reduces to the

S-model. The next reduction occurs when cleaving Mechanism 1 is replaced with Mechanism 2 in which the two stages of cleaving are combined into one. Here, the enzyme e_2 is always detached (the attachment and cleaving of cellobiose occur instantaneously) while the number of unoccupied landing sites and total number of sites coincide $T = S$, leading to the *T*-model. Though this is the simplest model it still captures the basic features of cellulose biodegradation. For this reason we extend it to a multiple-trait *T*-model which allows for species structured by a parameter. Finally to study more specifically cooperative effects we modify the above models to take only time scales on which the population changes into account (see Section 4).

This framework has some interest for the analysis even when it is only applied for a finite number of traits as is the case here. Indeed our traits correspond to possible enzyme complexes and while some of them may still be unknown, we do not expect their number to be very large. We also refer to [18] for the reason that in general one can only expect a finite (if possibly very large) number of traits at the ecological equilibrium, Evolutionarily Stable Strategy or ESS.

Our model therefore resembles systems of population dynamics, see [25] for instance. However, in contrast to many of those systems, the cellulose bio-degradation process leads to both competition between individuals and species (for the resource) and cooperative interactions. This occurs at the interspecies level as the byproduct of the process, cellobiose, is the same independent of the enzyme complexes involved, and can benefit any individual in the population (and not only individuals using the same complexes). Cooperation also occurs specifically within each species (or between species that are close enough). This follows from the fact that an individual with similar enough enzyme complexes can use a landing site created in the cellulose by the endoglucanase enzyme complex of another individual. The mathematical models developed in our work thus lead to different (and hopefully improved) phenomenological results for small populations (in deterministic models) since cooperation significantly affects the dynamics, as discussed in more detail below. Those differences of behaviour for small populations may not impact the final ESS, but they are important in the transitory regime, in particular in the presence of mutations.

From the ecological point of view, an important conclusion of our modeling is that as soon as minimally complex biochemical processes are involved, one cannot simply interpret the relation between the individuals in the population (or in different sub-populations) as competitive or cooperative. When the population is very large, the interaction looks competitive because resources are limited. On the other hand when the population is very small, the interaction seems to be cooperative as the limitation on growth mostly comes from the ability of the individuals to process efficiently the several steps of the biochemical process. But this is only a caricature of the actual interaction which cannot be reduced to pure cooperation or competition.

Tail issue in deterministic selection dynamics. The cooperative nature of the interaction when populations are small also becomes important for deterministic selection models. As sub-populations may grow or decrease exponentially, there typically are several orders of magnitude between the large populations of dominant traits and smaller ones. This poses an acute problem for modeling as one would need to use deterministic model for the larger populations. But such deterministic equations do not adequately capture the stochastic nature of the dynamics of smaller populations. This problem can however be alleviated if such small populations go extinct since accurately modeling their behavior loses its relevance. This is precisely what happens if cooperation is needed when the population goes below a certain threshold: The birth rate of a small population is then necessarily too small ensuring a negative reproduction rate and extinction. We further discuss this phenomenon in the appendix.

Structure of the paper. In Section 2, we set notation and, following the seminal article [32], introduce basic processes and mechanisms that constitute cellulose biodegradation. In Section 3, we develop a series of mathematical models, that differ in complexity, for the coevolution between microorganisms which consume cellulose and the cellulose chains. In Section 4, we carry out a qualitative analysis of the models developed in Section 3 under the assumption that cellulose dynamics and enzymatic reactions occur on a faster time scale than the dynamics of the microbial population. In Section 5, the multiple-trait model, developed earlier in Section 3, is extended to a continuous-trait model. We carry out some numerical experiments in Section 6, in which we compare the models and demonstrate that the T -model can be regarded as a limit of the S -model. Finally, we discuss the tail issue in more detail in the appendix.

2 Cellulose bio-degradation: structure and mechanisms

2.1 Cellulose structure and enzyme systems

Cellulose is the most abundantly produced bio-polymer. It is a homo-polymer consisting of glucose units joined by β -1,4 bonds. In secondary walls of plants, the size of cellulose molecules (degree of polymerization) varies from seven thousand to fourteen thousand glucose moieties per molecule. Cellulose molecules are strongly associated through inter- and intra-molecular hydrogen-binding and van der Waals forces that result in the formation of microfibrils, which in turn form fibrils. Cellulose molecules are oriented in parallel, with reducing ends of adjacent glucan chains located at the same end of a micro-fibril. These molecules form highly ordered crystalline domains interspersed with more disordered, amorphous regions. Although cellulose forms a distinct crystalline structure, cellulose fibers in nature are not purely crystalline. The degree of crystallinity varies from purely crystalline to purely amorphous.

To degrade plant cell material, microorganisms produce multiple enzymes known as enzyme systems [32]. For microorganisms to hydrolyze and metabolize insoluble cellulose, extra-cellular cellulases (degradation enzymes) must be produced that are either *free* or *cell associated*. Microorganisms have adapted different approaches to effectively hydrolyze cellulose, naturally occurring in insoluble particles. Cellulosic filamentous fungi (and some types of aerobic bacteria) have the ability to penetrate cellulosic substrates through hyphal extensions, thus often presenting their *free* cellulase systems in confined cavities within cellulosic particles. In contrast, anaerobic bacteria lack the ability to effectively penetrate cellulosic material and perhaps had to find alternative mechanisms for degrading cellulose. This led to the development of *complexed* cellulase systems (called cellulosomes) which position cellulase producing cells at the site of hydrolysis, as observed for clostridia and ruminal bacteria.

Overall there are three major components of cellulase systems: (i) endoglucanases, which randomly hydrolyze β -1,4 bonds within cellulose molecules, thereby producing reducing and non-reducing ends; (ii) exoglucanases, which liberate (cleave off) either glucose (glucanohydrolases) or cellobiose (cellobiohydrolase) that serve as major products from reducing or non-reducing ends of cellulose polysaccharide chains; and (iii) β -glucosidases which hydrolyze cellobiose yielding glucose (the major product of cellulose hydrolysis used by microorganisms as energy source). For details see [32].

2.2 Quantities to monitor and two basic bio-mechanisms

We first consider the case of populations with one trait. In our analysis we let $n = n(t)$ denote the total number of the microorganism that degrades cellulose, while the total number of endoglucanases and exoglucanases produced by the microorganism are denoted by $e_1 = e_1(t)$ and $e_2 = e_2(t)$, respectively.

We view cellulose as a crystalline conglomerate of fibers (chains of polysaccharides). According to our discussion above, during the first stage of the degradation the endoglucanase enzyme e_1 weakens fibers, which means that e_1 randomly cuts the fibers by creating reducing and non-reducing ends that then serve as landing sites for exoglucanases e_2 . Viewing cellulose as a three-dimensional structure, one can imagine that structure with punctures or cuts after the first stage. It is still the same cellulose but with more ‘cuts’ that serve as landing sites for the exoglucanase enzymes e_2 .

There are two different complexes of exoglucanases that are able to cleave off (liberate) cellobiose units from the cellulose chains. These are exoglucanase CBHI and exoglucanase CBHII. The enzymes of the first type are able to attach to reducing ends, and the second to non-reducing ends (see [32, p. 512]). In our models, for simplicity, we do not distinguish between the two types; both are represented by e_2 . For this reason, we do not differentiate between reducing and non-reducing ends, and call them ‘landing sites’ instead. We add that each landing site (created by the endoglucanase e_1) always contains one reducing end and one non-reducing end. In our model, however, we allow each landing site to host only one enzyme. Once the exoglucanase e_2 lands on the chain, it cleaves off cellobiose from the chain of polysaccharides. In this treatment we do not consider the third type of enzyme (β -glucosidase) and treat cellobiose as the major product of degradation. We instead assume that some portion $\theta_p \in [0, 1]$ of cellobiose is consumed by the microorganism that produced it, while the rest diffuses and is freely available for general consumption. We let $p(t)$ denote the total of the freely available cellobiose.

Thus in our model, there are two main stages in which the exoglucanase e_2 produces cellobiose $p(t)$: first, the enzyme locates a landing site and attaches itself to the chain there; next, it keeps cleaving off cellobiose units at a certain rate until it either disintegrates or detaches from the chain. This leads to two basic modeling approaches, which we call cleaving mechanisms.

2.2.1 Cleaving Mechanism 1

Since the time spent by an individual exoglucanase enzyme e_2 locating a landing site may differ significantly from the time it is attached to the landing site, it is useful to consider two states for exoglucanase, namely *detached* and *attached* states. In the first mechanism we distinguish them, letting $e_{2D}(t)$ represent the amount of detached e_2 (which may wander freely or on a leash, that is attached to a bacterial cell wall), and $e_{2A}(t)$ the amount attached to a landing site. Denoting the total number of landing sites by $T(t)$ and the number of *unoccupied* landing sites by $S(t)$, it then follows that

$$T(t) = S(t) + e_{2A}(t). \tag{2.1}$$

We suppose that, at any moment of time, unoccupied spots $S(t)$ become occupied (or attacked) by the detached enzymes e_{2D} at a certain rate to be described. Next, we assume that an individual attached enzyme e_{2A} cleaves off cellobiose units from the cellulose chain, again with a given rate. Also, we assume that some proportion of the (attached) enzyme e_{2A} detaches from a landing site, and that some fraction $\theta_r \in [0, 1]$ of those sites become unavailable for landing, that is, the landing sites are destroyed.

2.2.2 Cleaving Mechanism 2

The second mechanism is somewhat simplified. It may be used to describe complex cellulases where exoglucanases are not entirely free (they are attached to bacterial cell walls, and once bacteria leaves the spot the enzyme becomes detached from the landing site as well). Here we suppose that at any moment of time, all existing $T(t)$ landing sites are available for an attack by the enzyme e_2 . The landing sites $T(t)$ are attacked with a certain rate $b(T(t))$ and a certain (average) amount $q > 0$ of cellobiose units is cleaved off by each individual enzyme e_2 , after which the enzyme e_2 detaches itself. We view such an attack as instantaneous. Thus, after such an (instantaneous) attack, all $T(t)$ landing sites are again unoccupied. We will assume that after the attack a certain portion $\theta_r \in [0, 1]$ of the (attacked) landing sites become unavailable, that is, destroyed. In that scenario the two processes, finding a landing site and cleaving off cellobiose, are lumped together (with a hidden assumption that enzymes cannot remain attached to a chain for a very long time).

Remark 2.1. This first mechanism is more realistic since it takes into account time spent by the enzyme on a site. This mechanism can be employed for modeling systems where both non-complex and complex cellulases are present.

Remark 2.2. In the second mechanism the landing sites $T(t)$ serve as "prey" and e_2 as "predators", with one difference: the enzymes attack the prey, use it and leave it alone. After an attack only a certain proportion of the sites is destroyed, while the rest is still usable.

3 Cleaving Models

We now develop several models of varying complexity to describe cellulose biodegradation. We begin with a one-trait model describing cleaving mechanism 1, which retains the most detailed cellulose structure. This N - S system is too cumbersome to be effectively analyzed, so we reduce it by removing the detailed cellulose structure, to obtain the S system, a set of 7 equations which models cleaving mechanism 1. We then modify the S system to model cleaving mechanism 2, which yields the T system, consisting of 6 equations. Finally, we adapt the simplest of these, the T system, to a multiple trait model, in which there can be several species of microorganism consuming the same cellulose.

3.1 N - S -model

We first consider a model in which we monitor groups of cellulose chains consisting of $l \geq 1$ cellobiose units; in that case we say that the chain has length l . This allows us to develop a fundamental model incorporating cleaving mechanism 1.

Assumptions and notation. Cellulose chains may have different topological configurations: they could be linear or rectangular (when fibers are embedded in a lignin matrix) or they could have a random three-dimensional structure. Monitoring the topology increases the complexity, but it does not provide a better tool for studying the population dynamics. After all, it is the number of landing spots that matters rather than the configuration of the cellulose chains. Thus we make no assumption about the configuration and monitor only the length of its constituent pieces. Another assumption we make is that the enzyme e_1 produces a landing site without physically cutting the chain. This assumption decreases complexity in the model while it does not change the dynamics. Indeed, if we allow e_1 to physically cut a chain in the model, then the chain could be split into two

parts when e_1 acts. In that case, the number of landing sites would be the same as in the scenario when the landing site is created without a physical cut. Finally, we impose the requirement that at most one landing site per unit of cellobiose is allowed; this reflects the fact that cellulose chains represent systems of discrete units.

We say that a cellulose chain is in the (l, i) -state, or is an (l, i) -chain, if it has length l (so consists of $l \geq 1$ cellobiose units) and $i \in \{0, 1, \dots, l\}$ landing sites (previously made by enzyme e_1), and let $N^{l,i}(t)$ denote the number of (l, i) -chains. Recall that p denotes the number of cellobiose units available for general consumption, e_1 denotes the number of endoglucanase enzymes, which produce landing sites, and e_{2D} denotes the number of detached exoglucanase enzymes. We refine the attached exoglucanase to refer to those enzymes attached to chains in the (l, i) -state by $e_{2A}^{l,i}$, where the superscripted indices (l, i) are in the set

$$(l, i) \in I_L := \{(\tilde{l}, \tilde{i}) \in \mathbb{Z} \times \mathbb{Z} : 1 \leq \tilde{l} \leq L, 0 \leq \tilde{i} \leq \tilde{l}\}. \quad (3.1)$$

Here L stands for the maximal number of cellobiose units in cellulose chains. We also use the convention that

$$\begin{aligned} N^{l,i} &\equiv 0 && \text{if } (l, i) \notin I_L, \\ e_{2A}^{l,i} &\equiv 0 && \text{if } (l, i) \notin I_L \text{ or } i = 0. \end{aligned} \quad (3.2)$$

Enzyme dynamics. We assume that the rates of production of the enzymes e_1, e_2 by the microorganism and their degradation rates are fixed. The enzymes e_1 and e_2 are catalyzers which stay in the system as long as they “live”. Then e_1 satisfies

$$\partial_t e_1(t) = b_1 n(t) - d_1 e_1(t) \quad \text{with } b_1, d_1 > 0. \quad (3.3)$$

Next, the number of landing sites on (l, i) -chains is $T^{l,i} = i N^{l,i}$, so the number of unoccupied landing sites $S^{l,i}(t)$ is

$$S^{l,i}(t) = T^{l,i}(t) - e_{2A}^{l,i}(t) = i N^{l,i}(t) - e_{2A}^{l,i}(t). \quad (3.4)$$

Neglecting saturation effects, we suppose that unoccupied sites $S^{l,i}$ are attacked by e_{2D} with the rate $\beta^{l,i} S^{l,i}$. Also, we assume that enzyme e_2 located on a chain in (l, i) -state (randomly) detaches from the chain with rate $\sigma^{l,i} > 0$. We let $\gamma_r^{l,i} > 0$ denote the decay rate of an individual landing site (whether it is occupied or not) and assume that if an occupied landing site degrades then the attached enzyme e_{2A} disintegrates together with it. This leads to the following set of equations that monitor the dynamics of the enzyme e_2 :

$$\begin{aligned} \partial_t e_{2D}(t) &= b_2 n(t) - \sum_{l,i} \beta^{l,i} S^{l,i}(t) e_{2D}(t) + \sum_{l,i} \sigma^{l,i} e_{2A}^{l,i}(t) - d_{2D} e_{2D}(t) \\ &= b_2 n(t) - \sum_{l,i} \left[\beta^{l,i} \left(i N^{l,i}(t) - e_{2A}^{l,i}(t) \right) e_{2D}(t) - \sigma^{l,i} e_{2A}^{l,i}(t) \right] - d_{2D} e_{2D}(t) \\ \partial_t e_{2A}^{l,i}(t) &= \beta^{l,i} S^{l,i}(t) e_{2D}(t) - \left(\sigma^{l,i} + d_{2A}^{l,i} + \gamma_r^{l,i} \right) e_{2A}^{l,i} \\ &= \beta^{l,i} \left(i N^{l,i}(t) - e_{2A}^{l,i}(t) \right) e_{2D}(t) - \left(\sigma^{l,i} + d_{2A}^{l,i} + \gamma_r^{l,i} \right) e_{2A}^{l,i} \end{aligned} \quad (3.5)$$

where $d_{2D} > 0$ and $d_{2A}^{l,i} > 0$ are the degradation rates of e_{2D} and $e_{2A}^{l,i}$, respectively, and $b_2 > 0$ is the production rate of e_2 , which equals that of e_{2D} .

Chain dynamics. We neglect saturation effects and assume that the rate with which enzymes e_1 produce landing sites on chains in the (l, i) -state is

$$\alpha^{l,i}(l-i)N^{l,i}(t)e_1(t) = \widehat{\alpha}^{l,i}N^{l,i}(t)e_1(t), \quad \text{with} \quad \widehat{\alpha}^{l,i} = \alpha^{l,i}(l-i) \quad (3.6)$$

where the multiplier $(l-i)$ reflects the requirement that only one landing site per cellobiose unit is allowed. We assume that a freshly made landing site cannot be instantaneously occupied and different cuts don't occur simultaneously, so that (3.6) is the transition rate of states $(l, i) \rightarrow (l, i+1)$ due to the action of e_1 .

Recall that $\gamma_r^{l,i} > 0$ is the decay rate of an individual landing site on a chain in (l, i) -state, so that the rate of transition $(l, i) \rightarrow (l, i-1)$ due to degradation of landing sites is

$$\widehat{\gamma}^{l,i}N^{l,i}(t), \quad \text{with} \quad \widehat{\gamma}^{l,i} = i\gamma_r^{l,i}. \quad (3.7)$$

Let $q^{l,i} > 0$ denote the rate of production of cellobiose by an individual enzyme attached to an (l, i) -chain. Then, the total rate of cellobiose production by the enzymes $e_{2A}^{l,i}$ is

$$q^{l,i}e_{2A}^{l,i}(t). \quad (3.8)$$

The rate $q^{l,i}$ can be expressed as

$$q^{l,i} = c^{l,i} + p^{l,i}$$

where, $c^{l,i}$ is the rate of cleaving that results in the transition $(l, i) \rightarrow (l-1, i)$ and $p^{l,i}$ is the rate of cleaving that results in the transition $(l, i) \rightarrow (l-1, i-1)$. The latter transition occurs when an enzyme $e_{2A}^{l,i}$ cleaves off a cellobiose unit and when moving along the chain reaches the next cellobiose unit that also contains a landing site (this results in the decrease of landing sites by one on the given chain). We note that $c^{l,l} = c^{l,0} = 0$ and $p^{l,0} = p^{l,1} = 0$ for any l .

Let $\theta_r > 0$ denote the proportion of landing sites that get destroyed after $e_{2A}^{l,i}$ detaches from a chain or dies. This contributes to the transition $(l, i) \rightarrow (l, i-1)$ and the corresponding rate is

$$\widehat{\theta}^{l,i}e_{2A}^{l,i}(t) \quad \text{with} \quad \widehat{\theta}^{l,i} = \theta_r(\sigma^{l,i} + d_{2A}^{l,i}) \quad (3.9)$$

Combining (3.6)–(3.9) we obtain the equations that monitor the dynamics of $N^{l,i}(t)$, namely

$$\begin{aligned} \partial_t N^{l,i}(t) = & r^{l,i} + \left(\widehat{\alpha}^{l,i-1}N^{l,i-1}(t) - \widehat{\alpha}^{l,i}N^{l,i}(t) \right) e_1(t) + \left(\widehat{\gamma}^{l,i+1}N^{l,i+1}(t) - \widehat{\gamma}^{l,i}N^{l,i}(t) \right) \\ & + \left(c^{l+1,i}e_{2A}^{l+1,i} + p^{l+1,i+1}e_{2A}^{l+1,i+1} - (c^{l,i} + p^{l,i})e_{2A}^{l,i} \right) \\ & + \left(\widehat{\theta}^{l,i+1}e_{2A}^{l,i+1}(t) - \widehat{\theta}^{l,i}e_{2A}^{l,i}(t) \right) - \gamma_q^{l,i}N^{l,i}(t), \end{aligned} \quad (3.10)$$

where $r^{l,i}$ is the unit rate of production of cellulose, and $\gamma_q^{l,i}$ is the rate at which the cellulose naturally decays or becomes unavailable to the microorganism (that is, decay not directly attributable to the bacteria). We assume for simplicity that the cellulose provided by the environment has no landing sites, so that $r^{l,i} = 0$ for $i \geq 1$, and in particular, the sum $\sum_i i r^{l,i} = 0$.

When polymer chains are long, that is l is large, and the landing sites are spaced out, which happens when i is small relative to l , the coefficients $p^{l,i}$ can be neglected. To simplify the equation (3.10) we drop the coefficients $p^{l,i}$ except when $i = l$, corresponding to the boundary case when the number of sites l equals to the number of cellobiose units. The coefficients $p^{l,l}$ cannot be dropped

because cleaving cellobiose on the chain in state (l, l) always leads to $(l - 1, l - 1)$. Moreover, dropping the coefficients $p^{l, l}$ would lead to a loss of conservation of the total cellulose in the system when consumers are not present. This assumption leads to

$$q^{l, i} = c^{l, i} \quad \text{for } l \neq i \quad \text{and} \quad q^{l, l} = p^{l, l}$$

and hence (3.10) becomes

$$\begin{aligned} \partial_t N^{l, i}(t) = & r^{l, i} + \left(\widehat{\alpha}^{l, i-1} N^{l, i-1}(t) - \widehat{\alpha}^{l, i} N^{l, i}(t) \right) e_1(t) + \left(\widehat{\gamma}^{l, i+1} N^{l, i+1}(t) - \widehat{\gamma}^{l, i} N^{l, i}(t) \right) \\ & + \left(q^{l+1, i} e_{2A}^{l+1, i}(t) + \delta_{li} q^{l+1, i+1} e_{2A}^{l+1, i+1} - q^{l, i} e_{2A}^{l, i}(t) \right) \\ & + \left(\widehat{\theta}^{l, i+1} e_{2A}^{l, i+1}(t) - \widehat{\theta}^{l, i} e_{2A}^{l, i}(t) \right) - \gamma_{\varrho}^{l, i} N^{l, i}(t). \end{aligned} \quad (3.11)$$

where δ_{li} denotes the Kronecker delta.

Population dynamics. Let $\theta_p \in [0, 1]$ denote the proportion of produced cellobiose that becomes available for everyone. Then, using (3.8), the equations for the total amount $p(t)$ of cellobiose available for everyone, and the total population $n(t)$ of the microorganism are respectively

$$\begin{aligned} \partial_t p(t) = & \theta_p \sum_{l, i} q^{l, i} e_{2A}^{l, i}(t) - \gamma n(t) p(t) - \gamma_p p(t), \quad \text{and} \\ \partial_t n(t) = & \frac{\mu n(t)}{\bar{n} + n(t)} \left(\gamma p(t) + (1 - \theta_p) \sum_{l, i} q^{l, i} e_{2A}^{l, i}(t) \right) - \gamma_n n(t), \end{aligned} \quad (3.12)$$

where γ is the consumption rate, μ is the conversion efficiency, and γ_p, γ_n are decay rates of p and n , respectively. Here \bar{n} represents a critical population threshold: if n is large, $n = O(\bar{n})$, the growth depends only on the cellobiose supply, while if n is small, $n \ll \bar{n}$, the growth is linear but with small growth rate, so the population is unlikely to survive (since $\mu/\bar{n} < \gamma_n$).

Summary. Figure 1 shows possible states of the resource, state transitions and the rates at which these occur.

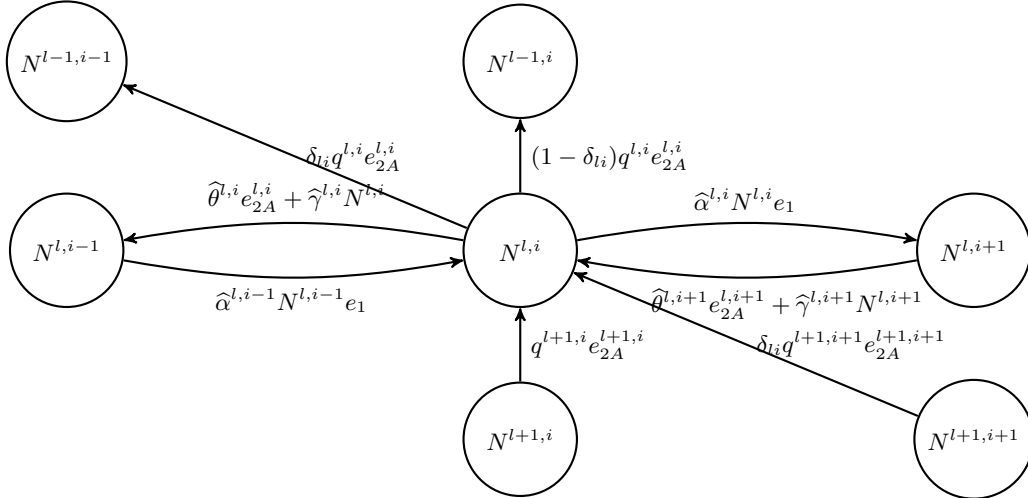


Figure 1: Transition of cellulose chains.

Remark 3.1. The processes of creating a landing site or cleaving off a cellobiose unit may depend on the configuration of the chain, the crystallinity of the cellulose as well as the lifetime of the enzymes. Thus it is possible that within a given period of time (no matter how short) more than one landing site is created or two or more cellobiose units are cleaved off from the same chain. For simplicity, we discount transitions other than $(l, i) \rightarrow (l, i + 1)$ and $(l, i) \rightarrow (l - 1, i)$, essentially assuming instantaneous transition. This approach is justified provided that the number and size of chains is very large compared to the amount of enzymes e_1, e_2 , and the likelihood that two landing sites are created or more than two cellobiose units are cleaved off from the same chain simultaneously (or during a short period of time) is extremely small.

Another way to justify this assumption is to consider a time-continuous Poisson counting process, that corresponds to the events of creating a landing site and/or cleaving off cellobiose. Any instance when a landing site is created (that is the moment it becomes available for use by e_2) or cellobiose unit is cleaved off the chain can be counted as an event. It is well-known that the probability of two or more events happening instantaneously is zero (in other words the probability that two events take place over the time Δt is $o(\Delta t)$; for details see [33, 40].

3.2 Reduction to S -model for Cleaving Mechanism 1

We now develop a simpler model by reducing the N - S -model, consisting of (3.3), (3.5), (3.11) and (3.12). It is convenient to allow the indices l and i to run through all of \mathbb{Z} . This augments the previously defined system, but by choosing appropriate constants, we can ensure that $N^{l,i}$ and $e_{2A}^{l,i}$ vanish for all times whenever $l \leq 0, i < 0$, or $i > l$ and, in addition, $e_{2A}^{l,0} = 0$ for any l . We then define the quantities

$$\begin{aligned} \varrho(t) &= \sum_{l,i} l N^{l,i}(t), & e_{2A}(t) &= \sum_{l,i} e_{2A}^{l,i}(t), \\ T(t) &= \sum_{l,i} T^{l,i}(t) = \sum_{l,i} i N^{l,i}(t), & S(t) &= \sum_{l,i} S^{l,i}(t), \end{aligned} \quad (3.13)$$

which represent the total number of cellulose units, attached exoglucanase enzymes, landing sites and unoccupied sites, respectively. Note that each of these sums is finite provided we specify appropriate initial conditions. We next assume that the constants are independent of l and i , so that for each $l, i \in \mathbb{Z}$,

$$\beta^{l,i} = \beta, \quad \sigma^{l,i} = \sigma, \quad \gamma_r^{l,i} = \gamma_r, \quad d_{2A}^{l,i} = d_{2A}, \quad \alpha^{l,i} = \alpha, \quad q^{l,i} = q, \quad \gamma_\varrho^{l,i} = \gamma_\varrho. \quad (3.14)$$

Summing over l, i in (3.5) and using (3.4), we get

$$\begin{aligned} \partial_t e_{2D}(t) &= b_2 n(t) - \beta S(t) e_{2D}(t) + \sigma e_{2A}(t) - d_{2D} e_{2D}(t), \\ \partial_t e_{2A}(t) &= \beta S(t) e_{2D}(t) - (\sigma + d_{2A} + \gamma_r) e_{2A}(t). \end{aligned} \quad (3.15)$$

To obtain equations for ϱ and T , we scale and add equations (3.11). First, we recall

$$\sum_{l,i} i r^{l,i} = 0 \quad \text{and define} \quad r = \sum_{l,i} l r^{l,i} = \sum_l l r^{l,0}, \quad (3.16)$$

so that r represents the total production of cellulose by the environment. Using (3.6) and making the change of variable $j = i - 1$ we obtain

$$\begin{aligned}
& \sum_{l,i} i \left(\widehat{\alpha}^{l,i-1} N^{l,i-1}(t) - \widehat{\alpha}^{l,i} N^{l,i}(t) \right) \\
&= \alpha \sum_{l,i} \left(i(l - (i - 1)) N^{l,i-1}(t) - i(l - i) N^{l,i}(t) \right) \\
&= \alpha \left(\sum_{l,j} (j + 1)(l - j) N^{l,j}(t) - \sum_{l,i} i(l - i) N^{l,i}(t) \right) \\
&= \alpha \left(\sum_{l,j} (l - j) N^{l,j}(t) \right) = \alpha (\varrho(t) - T(t))
\end{aligned}$$

and similarly, using (3.7) and $j = i + 1$,

$$\begin{aligned}
& \sum_{l,i} i \left(\widehat{\gamma}^{l,i+1} N^{l,i+1}(t) - \widehat{\gamma}^{l,i} N^{l,i}(t) \right) \\
&= \gamma_r \sum_{l,i} \left(i(i + 1) N^{l,i+1}(t) - i^2 N^{l,i}(t) \right) \\
&= \gamma_r \left(\sum_{l,j} (j - 1) j N^{l,j}(t) - \sum_{l,i} i^2 N^{l,i}(t) \right) \\
&= -\gamma_r \sum_{l,j} j N^{l,j}(t) = -\gamma_r T(t).
\end{aligned}$$

Next, recalling that $e_{2A}^{L+1,i} \equiv 0$ for all i , we compute

$$\begin{aligned}
& \sum_{l=1}^L \sum_{i=0}^l i \left(q^{l+1,i} e_{2A}^{l+1,i} + \delta_{li} q^{l+1,i+1} e_{2A}^{l+1,i+1} - q^{l,i} e_{2A}^{l,i} \right) \\
&= q \sum_{k=2}^L \sum_{i=0}^{k-1} i e_{2A}^{k,i} - q \sum_{l=1}^L \sum_{i=0}^l i e_{2A}^{l,i} + q \sum_{l=1}^{L-1} l e_{2A}^{l+1,l+1} \\
&= -q \sum_{l=1}^L l e_{2A}^{l,l} + q \sum_{l=2}^L (l - 1) e_{2A}^{l,l} \\
&= -q \sum_{l=1}^L e_{2A}^{l,l}.
\end{aligned} \tag{3.17}$$

and, using (3.9),

$$\begin{aligned}
& \sum_{l,i} i \left(\widehat{\theta}^{l,i+1} e_{2A}^{l,i+1}(t) - \widehat{\theta}^{l,i} e_{2A}^{l,i}(t) \right) \\
&= \theta_r(\sigma + d_{2A}) \sum_{l,i} \left(i e_{2A}^{l,i+1}(t) - i e_{2A}^{l,i}(t) \right) \\
&= \theta_r(\sigma + d_{2A}) \left(\sum_{l,j} (j-1) e_{2A}^{l,j}(t) - \sum_{l,i} i e_{2A}^{l,i}(t) \right) \\
&= -\theta_r(\sigma + d_{2A}) \sum_{l,j} e_{2A}^{l,j}(t) = -\theta_r(\sigma + d_{2A}) e_{2A}(t).
\end{aligned}$$

Combining the above identities with (3.11) and (3.13) we conclude

$$\begin{aligned}
\partial_t T(t) &= \partial_t \left(\sum_{l,i} i N^{l,i}(t) \right) \\
&= \alpha(\varrho(t) - T(t)) e_1(t) - \theta_r(\sigma + d_{2A}) e_{2A}(t) - (\gamma_r + \gamma_\varrho) T(t) - q \sum_{l=1}^L e_{2A}^{l,l}.
\end{aligned} \tag{3.18}$$

Next, referring to (3.4), subtracting $\partial_t e_{2A}$ from (3.18) and using (3.15), we obtain

$$\begin{aligned}
\partial_t S(t) &= \alpha(\varrho(t) - S(t) - e_{2A}(t)) e_1(t) - q \sum_{l=1}^L e_{2A}^{l,l} - \beta S(t) e_{2D}(t) \\
&\quad + \left((1 - \theta_r)(\sigma + d_{2A}) - \gamma_\varrho \right) e_{2A}(t) - (\gamma_r + \gamma_\varrho) S(t).
\end{aligned} \tag{3.19}$$

We now multiply each term on the right-hand side of (3.11) by l and sum to get an equation for $\varrho(t)$. First, using (3.6) and (3.7), we get

$$\begin{aligned}
\sum_{l,i} l \left(\widehat{\alpha}^{l,i-1} N^{l,i-1}(t) - \widehat{\alpha}^{l,i} N^{l,i}(t) \right) &= \alpha \left(\sum_{i,j} (l-j) N^{l,j}(t) - \sum_{l,i} (l-i) N^{l,i}(t) \right) = 0, \\
\sum_{l,i} l \left(\widehat{\gamma}^{l,i+1} N^{l,i+1}(t) - \widehat{\gamma}^{l,i} N^{l,i}(t) \right) &= \gamma_r \left(\sum_{l,j} l j N^{l,j}(t) - \sum_{l,i} l i N^{l,i}(t) \right) = 0.
\end{aligned}$$

Similarly, we compute

$$\begin{aligned}
& \sum_{l=1}^L \sum_{i=0}^l l \left(q^{l+1,i} e_{2A}^{l+1,i} + \delta_{li} q^{l+1,i+1} e_{2A}^{l+1,i+1} - q^{l,i} e_{2A}^{l,i} \right) \\
&= q \sum_{l=2}^L \sum_{i=0}^{l-1} (l-1) e_{2A}^{l,i} - q \sum_{l=1}^L \sum_{i=0}^l l e_{2A}^{l,i} + q \sum_{l=1}^{L-1} l e_{2A}^{l+1,l+1} \\
&= q \sum_{l=2}^L \sum_{i=0}^{l-1} (l-1) e_{2A}^{l,i} - q \sum_{l=1}^L \sum_{i=0}^l (l-1) e_{2A}^{l,i} - q e_{2A} + q \sum_{l=2}^L (l-1) e_{2A}^{l,l} \\
&= -q e_{2A}.
\end{aligned} \tag{3.20}$$

and, using (3.9),

$$\sum_{l,i} l \left(\widehat{\theta}^{l,i+1} e_{2A}^{l,i+1}(t) - \widehat{\theta}^{l,i} e_{2A}^{l,i}(t) \right) = \theta_r (\sigma + d_{2A}) \sum_l l \left[\sum_i e_{2A}^{l,i+1}(t) - \sum_i e_{2A}^{l,i}(t) \right] = 0.$$

Combining the above expressions and using (3.13),(3.14) and (3.16), we obtain

$$\partial_t \varrho(t) = \partial_t \left(\sum_{l,i} l N^{l,i}(t) \right) = r - q e_{2A}(t) - \gamma_\varrho \varrho(t). \quad (3.21)$$

Finally, by (3.8), (3.13) and (3.14), equations (3.12) become

$$\begin{aligned} \partial_t p(t) &= \theta_p q e_{2A}(t) - \gamma n(t) p(t) - \gamma_p p(t) \\ \partial_t n(t) &= \frac{\mu n(t)}{\bar{n} + n(t)} \left(\gamma p(t) + (1 - \theta_p) q e_{2A}(t) \right) - \gamma_n n(t). \end{aligned} \quad (3.22)$$

S-system. Note that the equation for S in (3.19) can be expressed as

$$\begin{cases} \partial_t S(t) = \alpha \left(\varrho(t) - S(t) - e_{2A}(t) \left(1 + \frac{q e_{2A}^b}{\alpha e_1 e_{2A}} \right) \right) e_1(t) - \beta S(t) e_{2D}(t) \\ \quad + \left((1 - \theta_r) (\sigma + d_{2A}) - \gamma_\varrho \right) e_{2A}(t) - (\gamma_r + \gamma_\varrho) S(t), \quad e_{2A}^b := \sum_{l=1}^L e_{2A}^{l,l}. \end{cases} \quad (3.23)$$

When the polymer chains are large, that is $L \gg 1$, one would expect that the proportion of cellobiose units $lN^{l,l}$ would be small compared to the total number of cellobiose $\varrho = \sum_{l,i} N^{l,i}$ and therefore one can expect $e_{2A} e_1 \gg e_{2A}^b$. Then, combining the above equations and dropping the term $\frac{q e_{2A}^b}{\alpha e_1 e_{2A}}$ in (3.23) we obtain the S -system,

Combining the above equations we obtain the S -system,

$$\begin{cases} \partial_t e_1(t) = b_1 n(t) - d_1 e_1(t) \\ \partial_t e_{2D}(t) = b_2 n(t) - \beta S(t) e_{2D}(t) + \sigma e_{2A}(t) - d_{2D} e_{2D}(t) \\ \partial_t e_{2A}(t) = \beta S(t) e_{2D}(t) - (\sigma + d_{2A} + \gamma_r) e_{2A}(t) \\ \partial_t S(t) = \alpha \left(\varrho(t) - S(t) - e_{2A}(t) \right) e_1(t) - \beta S(t) e_{2D}(t) \\ \quad + \left((1 - \theta_r) (\sigma + d_{2A}) - \gamma_\varrho \right) e_{2A}(t) - (\gamma_r + \gamma_\varrho) S(t) \\ \partial_t \varrho(t) = r - q e_{2A}(t) - \gamma_\varrho \varrho(t) \\ \partial_t p(t) = \theta_p q e_{2A}(t) - \gamma n(t) p(t) - \gamma_p p(t) \\ \partial_t n(t) = \frac{\mu n(t)}{\bar{n} + n(t)} \left(\gamma p(t) + (1 - \theta_p) q e_{2A}(t) \right) - \gamma_n n(t). \end{cases} \quad (3.24)$$

Remark 3.2. Note that system (3.24) is obtained by reduction under the assumption that rates are independent of the length of the chain and the number of landing sites. It is a closed system of seven ODE's which still keeps the important cascading structure of enzymes acting one after another on the cellulose. However, this model assumes that the topology of the cellulose chains (their length and the location of landing sites) does not affect the biodegradation process.

Remark 3.3. We make the assumption that the coefficients are constant to derive the S -system. Although this assumption is clearly non-physical, it yields a useful model. We justify dropping the extra correction term which is small relative to other terms, in the expectation that the mathematical error in doing so is much smaller than the modeling errors made by taking the mean coefficient; this is justified by the numerical experiments in Section 6.

3.2.1 S -system with fast transitions of e_{2A} and e_{2D}

In this section we will get a modified version of the S -system given by (3.24) assuming that the transitions $e_{2D} \rightarrow e_{2A}$ and $e_{2A} \rightarrow e_{2D}$ are fast.

Recall that βS is the rate of transition of e_{2D} to e_{2A} and σ is the rate of transition to e_{2D} . Thus, if one assumes that $\beta, \sigma \rightarrow \infty$ so that $\frac{\beta}{\sigma}$ stays bounded, then the equation (3.24)₃ tends to the equilibrium relation

$$0 = (\beta/\sigma)S(t) e_{2D}(t) - e_{2A}(t) \quad \text{or} \quad e_{2A}(t) = \omega S(t) e_{2D}(t) \quad \text{with} \quad \omega := \frac{\beta}{\sigma}. \quad (3.25)$$

Thus, the total number of enzymes e_2 can be written as

$$e_2 = e_{2D} + e_{2A} = e_{2D} + \omega S e_{2D} = e_{2D}(1 + \omega S),$$

so we obtain

$$e_{2D} = e_2 R_D(\omega S) \quad \text{and} \quad e_{2A} = e_2 R_A(\omega S) \quad \text{where} \quad R_D(x) := \frac{1}{1+x}, \quad R_A(x) := \frac{x}{1+x}. \quad (3.26)$$

Assume next that $d_{2A} = d_{2D}$. Then the total number of enzymes e_2 satisfies the equation

$$\partial_t e_2 = b_2 n - d_2 e_2 - \gamma_r e_{2A} = b_2 n - (d_2 + \gamma_r R_A(\omega S)) e_2 \quad (3.27)$$

where we have set $d_2 = d_{2A} = d_{2D}$.

Thus, replacing (3.24)_{2,3} with (3.25) and (3.27) we obtain the system, called the S_2 system,

$$\left\{ \begin{array}{l} \partial_t e_1(t) = b_1 n(t) - d_1 e_1(t) \\ \partial_t e_2(t) = b_2 n(t) - (d_2 + \gamma_r R_A(\omega S)) e_2 \\ \partial_t S(t) = \alpha \left(\varrho(t) - S(t) - e_2 R_A(\omega S) \right) e_1(t) - \beta S(t) e_2 R_D(\omega S) \\ \quad + \left((1 - \theta_r) (\sigma + d_{2A}) - \gamma_\ell \right) e_2 R_A(\omega S) - (\gamma_r + \gamma_\ell) S(t) \\ \partial_t \varrho(t) = r - q e_2 R_A(\omega S) - \gamma_\ell \varrho(t) \\ \partial_t p(t) = \theta_p q e_2 R_A(\omega S) - \gamma n(t) p(t) - \gamma_p p(t) \\ \partial_t n(t) = \frac{\mu n(t)}{\bar{n} + n(t)} \left(\gamma p(t) + (1 - \theta_p) q e_2 R_A(\omega S) \right) - \gamma_n n(t). \end{array} \right. \quad (3.28)$$

The system (3.28) is a version of the S -system with fast transitions of e_{2A} and e_{2D} .

3.3 Cleaving Mechanism 2: T -model

We now modify the S_2 -system derived for the cleaving Mechanism 1 to a model derived for the cleaving Mechanism 2. We directly work from the already reduced S_2 -system (3.28). Note that it is of course possible to derive this model from a more fundamental model in which we directly implement a corresponding cleaving mechanism on chains of length l , similar to our derivation of the N - S model above.

In Mechanism 2, we do not distinguish between attached and detached enzymes e_2 . In addition, we do not distinguish between occupied and unoccupied sites, preferring to count the total number of available landing sites $T(t)$, which satisfies (2.1). Our goal is to rewrite the S_2 -system (3.24) in terms of $T(t)$ rather than $S(t)$.

Recall that the S_2 -system (3.28) is a version of the S -system obtained under the assumption that transitions of the enzyme e_2 happen fast, which is equivalent to the requirement (3.25). Thus, adding (3.24)₃ and (3.24)₄ and using the equilibrium relation (3.25), we conclude that the total number of landing sites $T = S + e_{2A}$ (with fast e_2 transitions) satisfies the equation

$$\partial_t T(t) = \alpha (\varrho(t) - T(t)) e_1(t) - \theta_r (\sigma + d_2) e_2(t) R_A(\omega S) - (\gamma_r + \gamma_\varrho) T(t), \quad (3.29)$$

where we employed the relationship $e_{2A} = e_2 R_A(\omega S)$ and $e_{2D} = e_2 R_D(\omega S)$, and the assumption $d_2 = d_{2D} = d_{2A}$.

We next consider the action of the enzyme e_2 in the Mechanism 2. In this model, the concentration of e_{2A} enzymes is always low as those enzymes are used and degraded immediately after they are produced. The landing, cleaving off of a cellobiose unit, and detaching all occur at approximately the same instant. Thus all enzymes e_2 should be considered unattached, so should most closely resemble e_{2D} . To model this scenario we consider the S_2 -system in the asymptotic regime in which

$$\omega = \frac{\beta}{\sigma} \rightarrow 0 \quad \text{and} \quad q\omega = q\frac{\beta}{\sigma} \rightarrow \hat{q}. \quad (3.30)$$

The first assumption makes sure that the enzyme e_2 detaches immediately after the attack and as a consequence the proportion between e_{2A} and e_{2D} tends to zero, while the second one is necessary for the population $n(t)$ to survive.

Observe that under assumptions (3.30)

$$R_{2A}(\omega S) \sim \omega S, \quad T = S + e_2 R_A(\omega S) \sim S, \quad (\sigma + d_2) e_2 R_A(\omega S) \sim \beta e_2 T, \quad q e_2 R_A(\omega S) \sim q(\beta/\sigma) e_2 T$$

and so the S_2 -system transforms into the T -system for Mechanism 2:

$$\begin{cases} \partial_t e_1(t) = b_1 n(t) - d_1 e_1(t) \\ \partial_t e_2(t) = b_2 n(t) - d_2 e_2(t) \\ \partial_t T(t) = \alpha (\varrho(t) - T(t)) e_1(t) - \theta_r \beta e_2(t) T(t) - \hat{\gamma}_T T(t) \\ \partial_t \varrho(t) = r - \hat{q} T(t) e_2(t) - \gamma_\varrho \varrho(t) \\ \partial_t p(t) = \theta_p \hat{q} T(t) e_2(t) - \gamma n(t) p(t) - \gamma_p p(t) \\ \partial_t n(t) = \frac{\mu n(t)}{\bar{n} + n(t)} (\gamma p(t) + (1 - \theta_p) \hat{q} e_2(t) T(t)) - \gamma_n n(t). \end{cases} \quad (3.31)$$

where we have set $\hat{q} = q(\beta/\sigma)$ and $\hat{\gamma}_T = \gamma_r + \gamma_\varrho$.

Comparing this system to (3.24) modeling Mechanism 1, we make the following observations: first, the dynamics of e_2 and T are simpler than those of e_{2A} , e_{2D} and S , because we do not have to account for the different processes for e_{2D} and e_{2A} . On the other hand, the cleaving rate changes from the linear term $q e_{2A}$ in the S -system, to the nonlinear term $\hat{q} T e_2$ which models simultaneously finding and attacking a landing site. Note that the coefficient $\hat{q} = q (\beta/\sigma)$ combines those coefficients corresponding to finding sites and cleaving off in Mechanism 1, while $\hat{\gamma}_T = \gamma_r + \gamma_\varrho$ is the combined rate of degradation of landing sites.

3.4 Multiple trait T -model

We now extend the T -model to a model that allows for several species of microorganisms feeding on the same cellulose. Specifically, we introduce populations n^i , with $i \in \{1, \dots, M\}$, equipped with different traits x^i ; throughout this section, we use superscripts to distinguish traits. We assume that Mechanism 2 is used by each population to cleave off cellobiose, while the different populations have different rates for the various actions.

As in the T -model, we assume that microorganism n_i produces endoglucanases enzymes e_1^i that make landing sites, and exoglucanases enzymes e_2^i that cleave off cellobiose from the cellulose chains. In analogy with (3.31)_{1,2}, we suppose that the enzymes e_1^i , e_2^i are produced by the microorganism n_i and degrade with fixed rates. This gives the equations

$$\begin{aligned}\partial_t e_1^i(t) &= b_1^i n^i(t) - d_1^i e_1^i(t) \\ \partial_t e_2^i(t) &= b_2^i n^i(t) - d_2^i e_2^i(t)\end{aligned}\tag{3.32}$$

where b_1^i , b_2^i and d_1^i , d_2^i are, respectively, the enzyme generation and death rates, $i \in \{1, \dots, M\}$.

Next, for simplicity we will not differentiate between landing sites created by the enzymes of different species. In other words, the landing sites made by e_1^i are allowed to be used by any enzyme e_2^j for all j . Then, following Mechanism 2, and neglecting saturation effects, we assume that enzymes e_1^i make landing sites on the cellulose ϱ with the rate

$$\alpha^i (\varrho(t) - T(t)) e_1^i(t),$$

where α^i is the probability of an individual enzyme e_1^i finding a spot among the $\varrho(t) - T$ available cellobiose units (reflecting the requirement that only one landing site per cellobiose unit is allowed), and making a landing site. Next, we suppose that the landing sites T are attacked by enzymes e_2^i with the rate

$$\beta^i T(t) e_2^i(t)$$

where β^i is the probability of an individual e_2^i finding and attaching to a landing spot. Finally, as above, we let $\gamma_r > 0$ be the decay rate of an individual landing site and suppose that the portion $\theta_r^i \in [0, 1]$ of those ends is not usable after an attack by e_2^i . Then, in analogy with (3.31)₃, we obtain the equation for T for multiple trait populations:

$$\partial_t T(t) = \sum_j \alpha^j (\varrho(t) - T(t)) e_1^j(t) - \sum_j \theta_r^j \beta^j T(t) e_2^j(t) - \hat{\gamma}_T T(t).\tag{3.33}$$

Next, we let q^i be the number of cellobiose units cleaved off by e_2^i during an attack. In analogy with (3.31)₄, the dynamics of cellulose ϱ is then given by

$$\partial_t \varrho(t) = r - \sum_j \hat{q}^j T(t) e_2^j(t) - \gamma_\varrho \varrho(t)\tag{3.34}$$

where we set $\hat{q}^i = q^i \beta^i$, the combined rate of attack of e_2^i .

We next let $\theta_p^i \in [0, 1]$ denote the proportion of produced cellobiose produced by e_2^i that is made available to everyone. Then, as in (3.31)₅, the equation for the total amount $p(t)$ of cellobiose available to everyone is

$$\partial_t p(t) = \sum_j \theta_p^j \hat{q}^j e_2^j(t) T(t) - \sum_j \gamma^j n^j(t) p(t) - \gamma_p p(t). \quad (3.35)$$

where γ^j is the predation rate of p by n^j , and γ_p is the decay rate of p .

Finally, we consider the dynamics of the population n^i . First, recall that cellobiose $p(t)$ is available to all species n^j , $j = 1, \dots, M$. Since every species n^j hunts with the predation rate γ^j on the cellobiose p , the growth rate of n^i may be expressed via the logistic term

$$\mu^i n^i(t) \frac{\gamma^i p(t)}{\bar{n}^i + \frac{1}{\gamma^i} \sum_j \gamma^j n^j} \quad (3.36)$$

where μ^i is the conversion efficiency.

Next, comparing to (3.35), the production rate of cellobiose which is produced by e_2^j and consumed directly on the spot is given by

$$(1 - \theta_p^j) \hat{q}^j e_2^j(t) T(t).$$

We assume that in view of the homogeneity and close proximity of species, the cellobiose produced by e_2^j , $j = 1, \dots, M$, can be consumed by the n^i ; this manifests the cross species interaction. We express this as

$$\mu^i (1 - \theta_p^j) \frac{\nu^{ij} n^i}{\nu^{ij} \bar{n}^i + \sum_s \nu^{sj} n^s} \hat{q}^j e_2^j(t) T(t), \quad \text{with} \quad \sum_s \nu^{sj} = 1,$$

representing the contribution of the energy obtained from the direct consumption of cellobiose cleaved off by e_2^j to the growth rate of n^i . Combining these leads to the equation for the dynamics of the population n^i ,

$$\partial_t n^i(t) = \mu^i n^i(t) \left(\frac{\gamma^i p(t)}{\bar{n}^i + \frac{1}{\gamma^i} \sum_j \gamma^j n^j} + \sum_j \frac{(1 - \theta_p^j) \nu^{ij}}{\nu^{ij} \bar{n}^i + \sum_s \nu^{sj} n^s} \hat{q}^j e_2^j(t) T(t) \right) - \gamma_n^i n^i(t) \quad (3.37)$$

where γ_n^i is the death rate of the population n^i .

We collect the above equations to obtain the *multiple trait T-system*,

$$\left\{ \begin{array}{l} \partial_t e_1^i(t) = b_1^i n^i(t) - d_1^i e_1^i(t) \\ \partial_t e_2^i(t) = b_2^i n^i(t) - d_2^i e_2^i(t) \\ \partial_t T(t) = (\varrho(t) - T(t)) \sum_j \alpha^j e_1^j(t) - \sum_j \theta_r^j \beta^j e_2^j(t) T(t) - \widehat{\gamma}_T T(t) \\ \partial_t \varrho(t) = r - \sum_j \widehat{q}^j e_2^j(t) T(t) - \gamma_\varrho \varrho(t) \\ \partial_t p(t) = \sum_j \theta_p^j \widehat{q}^j e_2^j(t) T(t) - \sum_j \gamma^j n^j(t) p(t) - \gamma_p p(t) \\ \partial_t n^i(t) = \mu^i n^i(t) \frac{\gamma^i p(t)}{\bar{n}^i + \frac{1}{\gamma^i} \sum_j \gamma^j n^j} \\ \quad + \mu^i n^i(t) \sum_j (1 - \theta_p^j) \frac{\nu^{ij}}{\nu^{ij} \bar{n}^i + \sum_s \nu^{sj} n^s} \widehat{q}^j e_2^j(t) T(t) - \gamma_n^i n^i(t) \end{array} \right. \quad (3.38)$$

where $i = 1, \dots, M$.

3.4.1 Compatibility with the single trait model

We now show that the multiple trait T -model directly generalizes the single trait T -model by considering two special cases of the multiple trait model, and confirming that these reduce to the single trait model.

Our first test is to assume that all but one species (say the i -th) are absent. That is, we begin with data $n^j(0) = 0$, and similarly $e_1^j(0) = e_2^j(0) = 0$, for $j \neq i$. Then (3.38) implies that for all $t > 0$, $j \neq i$, we have $n^j(t) = 0$. It is then evident that equations (3.38)_{1,2,3,4,5} reduce to (3.31)_{1,2,3,4,5} (for $n = n^i$, etc), and (3.38)₆ becomes

$$\partial_t n^i(t) = \mu^i n^i \frac{\gamma^i p}{\bar{n}^i + n^i} + \mu^i n^i (1 - \theta_p^i) \frac{\widehat{q}^i e_2^i T}{\bar{n}^i + n^i} - \gamma_n^i n^i,$$

which is exactly (3.31)₆.

Our second test is to assume that even though there are M different traits, the coefficients are independent of i, j , so there is no way to distinguish different populations in the model. In this case, we check the dynamics for the total population $n(t) = \sum_i n^i(t)$, and similarly $e_1 = \sum_i e_1^i$ and $e_2 = \sum_i e_2^i$. It is then clear that (3.38)_{3,4,5} become (3.31)_{3,4,5}, and adding (3.38)_{1,2} over i gives (3.31)_{1,2}. Finally, adding (3.38)₆ over i yields

$$\partial_t (\sum_i n^i) = \mu \sum_i n^i \frac{\gamma p}{\bar{n} + \sum_j n^j} + \mu \sum_i n^i \frac{1 - \theta_p}{\bar{n} + \sum_s n^s} \widehat{q} \sum_j e_2^j T - \gamma_n \sum_i n^i,$$

which is again exactly (3.31)₆.

4 Cooperation

4.1 Cooperation in the T -model

In this section we consider the system (3.31) on different time scales. We assume that production of enzymes, consumption and creation of landing sites occurs at a much faster rate than changes in the population of the microorganism. In this case, over time scales on which the population changes, we can assume that equations (3.31)_{1,2,3,4,5} are at equilibrium, and the dynamics is driven by the population change (3.31)₆. This gives the system

$$\left\{ \begin{array}{l} 0 = b_1 n(t) - d_1 e_1(t) \\ 0 = b_2 n(t) - d_2 e_2(t) \\ 0 = \alpha (\varrho(t) - T(t)) e_1(t) - \theta_r \beta T(t) e_2(t) - \widehat{\gamma}_T T(t) \\ 0 = r - \widehat{q} T(t) e_2(t) - \gamma_\varrho \varrho(t) \\ 0 = \theta_p \widehat{q} T(t) e_2(t) - \gamma n(t) p(t) - \gamma_p p(t) \\ \partial_t n(t) = \frac{\mu n(t)}{\bar{n} + n(t)} \left(\gamma p(t) + (1 - \theta_p) \widehat{q} T(t) e_2(t) \right) - \gamma_n n(t). \end{array} \right. \quad (4.1)$$

We use (4.1) to eliminate all the fast variables, to obtain a single equation for the population n , so that the population growth rate can be understood. The first two equations give

$$e_i = k_i n \quad \text{with} \quad k_i := \frac{b_i}{d_i}, \quad i = 1, 2, \quad (4.2)$$

and from (4.1)₄, we have

$$\varrho = \frac{r}{\gamma_\varrho} - \frac{\widehat{q}}{\gamma_\varrho} T e_2 = \frac{r}{\gamma_\varrho} - \frac{\widehat{q} k_2}{\gamma_\varrho} T n.$$

Plugging these into (4.1)₃, we get

$$0 = \frac{\alpha r k_1}{\gamma_\varrho} n - T \left(\frac{\alpha \widehat{q} k_2 k_1}{\gamma_\varrho} n^2 + (\alpha k_1 + \theta_r \beta k_2) n + \widehat{\gamma}_T \right),$$

so that

$$T = \frac{\alpha r k_1}{\gamma_\varrho} \frac{n}{P_2(n)}, \quad (4.3)$$

where $P_2(n)$ is the quadratic polynomial

$$\begin{aligned} P_2(n) &= c_2 n^2 + c_1 n + c_0, \\ c_2 &= \frac{\alpha \widehat{q} k_2 k_1}{\gamma_\varrho}, \quad c_1 = \alpha k_1 + \theta_r \beta k_2, \quad c_0 = \widehat{\gamma}_T. \end{aligned} \quad (4.4)$$

Next, using these in (3.31)₅, it follows that

$$p = \theta_p \widehat{q} k_2 \frac{T n}{\gamma n + \gamma_p} = \theta_p \widehat{q} k_2 \frac{\alpha r k_1}{\gamma_\varrho} \frac{n^2}{(\gamma n + \gamma_p) P_2(n)}. \quad (4.5)$$

Finally, we use (4.3), (4.5) in (4.1)₆ to get the scalar population equation

$$\partial_t n(t) = n(t) \left[B(n) - \gamma_n \right], \quad (4.6)$$

where

$$\begin{aligned}
B(n) &= \frac{\mu}{\bar{n} + n} \left(\gamma p + (1 - \theta_p) \hat{q} k_2 T n \right) \\
&= \mu \hat{q} k_2 \frac{T n}{\bar{n} + n} \left(\frac{\gamma \theta_p}{\gamma n + \gamma_p} + (1 - \theta_p) \right) \\
&= K n^2 \Phi(n),
\end{aligned} \tag{4.7}$$

where the function $\Phi(n)$ and constant K are given by

$$\begin{aligned}
\Phi(n) &= \left(\frac{\theta_p}{n + \gamma_p/\gamma} + 1 - \theta_p \right) \frac{1}{(n + \bar{n}) P_2(n)}, \\
K &= \mu \hat{q} k_2 \frac{\alpha r k_1}{\gamma_e} = \frac{\mu q \beta \alpha r b_1 b_2}{\gamma_e d_1 d_2}.
\end{aligned} \tag{4.8}$$

4.2 Asymptotics of $B(n)$

We are interested in the structure of $B(n)$ for small populations, $n \ll \bar{n}$. First, we note that the birth rate $B(n)$ is positive and satisfies

$$B(0) = 0 \quad \text{and} \quad \lim_{n \rightarrow \infty} B(n) = 0,$$

so that B is globally bounded.

For n small, using (4.7), (4.8) and (4.4), we have

$$\frac{B(n)}{n^2} = K \Phi(n) \approx K \Phi(0) = \frac{K}{\bar{n} \hat{\gamma}_r} \left(\theta_p \frac{\gamma}{\gamma_p} + 1 - \theta_p \right), \tag{4.9}$$

so that $B(n) \sim n^2$ for $n \ll \bar{n}$. Thus for small populations, $B(n)$ is convex, and so superlinear. This superlinear birth rate is indicative of cooperative behavior.

More generally, the growth rate $B(n)/n$ increases as long as $\log(n \Phi(n))$ does, and

$$\frac{\partial}{\partial n} \left(\frac{B(n)}{n} \right) = \frac{\partial}{\partial n} \left(K n \Phi(n) \right) = K n \Phi(n) \left(\frac{1}{n} + \frac{\partial_n \Phi}{\Phi} \right) = K n \Phi(n) \left(\frac{\partial}{\partial n} \log(n \Phi) \right),$$

so the system exhibits cooperative behavior as long as

$$\frac{\partial}{\partial n} \log(n \Phi) = \frac{1}{n} - \frac{\theta_p}{(n + \gamma_p/\gamma)^2} \left(\theta_p \frac{1}{n + \gamma_p/\gamma} + 1 - \theta_p \right)^{-1} - \frac{1}{n + \bar{n}} - \frac{2c_2 n + c_1}{P_2(n)} > 0.$$

This condition is at least true for $n \in (0, n_*)$, where n_* is the smallest positive root of this expression; combining the fractions, it is evident that n_* is the smallest positive root of a fifth-order polynomial.

Moreover, referring to (4.9), we see that

$$\frac{\partial}{\partial \theta_p} K \Phi(n) \Big|_{n=0} = \frac{K}{\bar{n} \hat{\gamma}_r} \left(\frac{\gamma}{\gamma_p} - 1 \right),$$

which is positive if and only if $\gamma > \gamma_p$. For small population n , we expect this to persist: that is,

$$\frac{\partial}{\partial \theta_p} \left(\frac{B(n)}{n^2} \right) = \frac{\partial}{\partial \theta_p} K \Phi(n) > 0 \quad \text{if and only if} \quad \gamma > \gamma_p.$$

Since $\theta_p \in [0, 1]$ is the proportion of produced cellulose which is shared, this last inequality suggests that for small populations *sharing food is beneficial* in terms of growth as long as the consumption rate γ is greater than the decay rate γ_p of the cleaved off cellobiose.

4.3 Cooperation in multiple-trait T -model

As in Section 4.1, we consider the system (3.38) on a generational time scale. We again assume that production of enzymes, consumption and creation of landing sites happens at a much faster rate than change in the populations n^i . In other words, we assume that the equations (3.38)_{1,2,3,4,5} are at equilibrium, and the dynamics of the system is driven by the population equations (3.38)₆. This results in the system

$$\left\{ \begin{array}{l} 0 = b_1^i n^i(t) - d_1^i e_1^i(t), \\ 0 = b_2^i n^i(t) - d_2^i e_2^i(t), \\ 0 = (\varrho(t) - T(t)) \sum_j \alpha^j e_1^j(t) - \sum_j \theta_r^j \beta^j e_2^j(t) T(t) - \widehat{\gamma}_T T(t), \\ 0 = r - \sum_j \widehat{q}^j e_2^j(t) T(t) - \gamma_\varrho \varrho(t), \\ 0 = \sum_j \theta_p^j \widehat{q}^j e_2^j(t) T(t) - \sum_j \gamma^j n^j(t) p(t) - \gamma_p p(t), \\ \partial_t n^i(t) = \mu^i n^i(t) \frac{\gamma^i p(t)}{\bar{n}^i + \frac{1}{\gamma^i} \sum_j \gamma^j n^j} \\ \quad + \mu^i n^i(t) \sum_j (1 - \theta_p^j) \frac{\nu^{ij}}{\nu^{ij} \bar{n}^i + \sum_s \nu^{sj} n^s} \widehat{q}^j e_2^j(t) T(t) - \gamma_n^i n^i(t). \end{array} \right. \quad (4.10)$$

We wish to understand the growth rate of n^i as a function of $n = (n_1, \dots, n_M) \in \mathbb{R}^M$. The first two equations of (4.10) give

$$e_1^i(t) = k_1^i n^i(t), \quad e_2^i = k_2^i n^i, \quad \text{with } k^i := \frac{b^i}{d^i}, \quad i = 1, \dots, M. \quad (4.11)$$

We next write n as a vector and introduce the coefficient vectors

$$\begin{aligned} A &= (\alpha^j k_1^j), \quad B = (\theta_r^j \beta^j k_2^j), \quad Q = (\widehat{q}^j k_2^j), \\ \Theta &= (\theta_p^j \widehat{q}^j k_2^j), \quad \Gamma = (\gamma^j), \quad N^k = (\nu^{jk}), \end{aligned} \quad (4.12)$$

and denote the scalar product by $\langle \cdot, \cdot \rangle$. We can then rewrite (4.10)_{3,4,5} as

$$\begin{aligned} 0 &= (\varrho(t) - T(t)) \langle A, n \rangle - \langle B, n \rangle T(t) - \widehat{\gamma}_T T(t), \\ 0 &= r - \langle Q, n \rangle T(t) - \gamma_\varrho \varrho(t), \\ 0 &= \langle \Theta, n \rangle T(t) - \langle \Gamma, n \rangle p(t) - \gamma_p p(t). \end{aligned}$$

These immediately yield

$$\varrho(t) = \frac{1}{\gamma_\varrho} (r - T(t) \langle Q, n \rangle) \quad \text{and} \quad p(t) = \frac{\langle \Theta, n \rangle}{\langle \Gamma, n \rangle + \gamma_p} T(t), \quad (4.13)$$

and, plugging in, we get

$$0 = \frac{r}{\gamma_\varrho} \langle A, n \rangle - \tau(n) T(t), \quad \text{so that} \quad T(t) = \frac{r}{\gamma_\varrho} \frac{\langle A, n \rangle}{\tau(n)}, \quad (4.14)$$

where we have set

$$\tau(n) = \frac{1}{\gamma_\varrho} \langle A, n \rangle \langle Q, n \rangle + \langle A, n \rangle + \langle B, n \rangle + \widehat{\gamma}_T. \quad (4.15)$$

Finally, using (4.13) and (4.14) in (4.10)₆, we can write our population system as

$$\partial_t n^i = n^i (B^i(n) - \gamma_n^i), \quad (4.16)$$

where the i -th population's birth rate is

$$\begin{aligned} B^i(n) &= \frac{\mu^i \gamma^i p(t)}{\bar{n}^i + \frac{1}{\gamma^i} \langle \Gamma, n \rangle} + \mu^i \sum_j \frac{(1 - \theta_p^j) \nu^{ij} \widehat{q}^j k_2^j n^j}{\nu^{ij} \bar{n}^i + \langle N^j, n \rangle} T(t) \\ &= \mu^i T(t) \left(\frac{\gamma^i \langle \Theta, n \rangle}{(\bar{n}^i + \frac{1}{\gamma^i} \langle \Gamma, n \rangle) (\langle \Gamma, n \rangle + \gamma_p)} + \sum_j \frac{(1 - \theta_p^j) \nu^{ij} \widehat{q}^j k_2^j n^j}{\nu^{ij} \bar{n}^i + \langle N^j, n \rangle} \right) \\ &= \frac{\mu^i r \langle A, n \rangle}{\gamma_\varrho \tau(n)} \left(\frac{\gamma^i \langle \Theta, n \rangle}{(\bar{n}^i + \frac{1}{\gamma^i} \langle \Gamma, n \rangle) (\langle \Gamma, n \rangle + \gamma_p)} + \sum_j \frac{(1 - \theta_p^j) \nu^{ij} \widehat{q}^j k_2^j n^j}{\nu^{ij} \bar{n}^i + \langle N^j, n \rangle} \right). \end{aligned} \quad (4.17)$$

Here the two terms in the growth rate correspond to intentionally shared food and food consumed as it's produced, respectively.

Asymptotic behavior of $B^i(n)$. Assuming the coefficients are positive, we make the following observations about the birth rate $B^i(n)$. According to (4.15) $\tau(n)$ is quadratic in n , while all inner products in (4.16) are linear. It follows immediately that $B^i(n) \rightarrow 0$, and in fact $B^i(n) = O(\frac{1}{n})$ as $n \rightarrow \infty$.

We are more interested in the behavior for small populations, $n \sim 0$. Since $\tau(0) = \widehat{\gamma}_T$, no denominators vanish, and (4.17) yields

$$B^i(n) = O((\sum n)^2) \quad \text{for } n \sim 0.$$

More precisely, recalling that

$$\nabla_n \langle V, n \rangle = V \quad \text{and} \quad D_n^2 (\langle V, n \rangle \langle W, n \rangle) = V W^T + W V^T,$$

we see that at $n = 0$, the gradient of B^i vanishes, $\nabla_n B^i(0) = 0$, and the Hessian of B^i is the symmetric matrix

$$D_n^2 B^i(0) = \frac{\mu^i r}{\gamma_\varrho \widehat{\gamma}_T \bar{n}^i} \left(\frac{\gamma^i}{\gamma_p} (A\Theta^T + \Theta A^T) + A(Q - \Theta)^T + (Q - \Theta)A^T \right).$$

We cannot conclude that B^i is convex as the matrix $D_n^2 B^i(0)$ is not positive definite, but because all the entries are positive, we can conclude that the directional derivative is increasing in any direction in the positive orthant $\{n^k \geq 0\}$, which indicates cooperative behavior.

Special Case. Now, we consider the special case when $\nu^{ij} = 0$ for $i \neq j$; in this case, there is no competition for cellobiose that is not intentionally shared. In this special case, (4.17) becomes

$$\begin{aligned} B^i(n) &= \frac{\mu^i r \langle A, n \rangle}{\gamma_\varrho \tau(n)} \left(\frac{\gamma^i \langle \Theta, n \rangle}{(\bar{n}^i + \frac{1}{\gamma^i} \langle \Gamma, n \rangle) (\langle \Gamma, n \rangle + \gamma_p)} + \frac{(1 - \theta_p^i) \widehat{q}^i k_2^i n^i}{\bar{n}^i + n^i} \right) \\ &=: B_1^i(n) + B_2^i(n). \end{aligned}$$

As in the single-trait case, we again see an indication that for small populations, more sharing (represented by the coefficient vector Θ) would be beneficial for the i -th population provided $\gamma^i > \gamma_p$, because it increases the derivative $\nabla_n B^i(n)$: this can be seen by differentiating with respect to the vector parameter Θ . Recall that $\gamma^i > \gamma_p$ means that cellobiose is consumed (by n^i) faster than it decays.

Lemma 4.1. *Suppose that $\nu^{ij} = 0$ for $i \neq j$. Let $i \in \{1, \dots, M\}$ be fixed and let*

$$n_0 = (n_0^1, n_0^2, \dots, n_0^{i-1}, 0, n_0^{i+1}, \dots, n_0^M) \in \mathbb{R}^M \quad \text{with} \quad n_0^j \geq 0.$$

Then

$$\frac{\partial B_2^i}{\partial n^i}(n_0) = \frac{\mu^i r}{\gamma_\varrho} \frac{\langle A, n_0 \rangle}{\tau(n_0)} \frac{(1 - \theta_p^i) \widehat{q}^i k_2^i}{\bar{n}^i} > 0. \quad (4.18)$$

Furthermore, suppose $\min_j \bar{\alpha}^j > 0$ and $\min_j \gamma^j > 0$. Then there exists $\varepsilon > 0$ such that for all $\max_j \theta_p^j < \varepsilon$, we have

$$\frac{\partial B^i}{\partial n^i}(n_0) > 0 \quad \text{for all } n_0 \neq 0.$$

Idea of proof. Equation (4.18) follows immediately by differentiation. When we differentiate B_1^i , we introduce negative terms each time the derivative falls on a denominator. However, each such term introduces a higher power in the denominator, so each of those terms can be represented as a product of $\langle A, n_0 \rangle / \tau(n_0)$ with terms uniformly bounded in n_0 . Comparing these to (4.18), it follows that by choosing $\max_j \theta_p^j < \varepsilon$ with ε small enough, the sum will be positive. \square

Remark 4.1. The key conclusion in Lemma 4.1 is that the birth rate $B^i(n)$ includes some form of *cooperation*. Namely, the cooperative effect is not eliminated in the multiple trait population T -model provided that $\nu_{ij} = 0$ for $i \neq j$. In other words, when interspecies competition for ‘ready to be digested’ resource p is not involved then there is an Allee effect for each species. Compare it for instance with simple logistic terms like $r - n_0^i$ which decreases with n_0^i . In contrast $B^i(n)$ actually penalizes populations which are too small (and populations which are too large of course just like a logistic term). Finally, even if the conditions of Lemma 4.1 do not hold a cooperative effect still maybe present depending on the differential $DB(0)$.

4.4 Cooperative interactions in N - S -model

We now consider cooperation in the N - S -model as we did for the simpler models. We are interested in the situation that the production of enzymes, consumption and creation of landing sites occurs much faster than changes in the population of the microorganism. Thus we again assume that equations (3.3), (3.5), (3.11) and (3.12)₁ are at equilibrium, and the dynamics is driven by the population change (3.12)₂. We also assume that the length of the cellulose chains does not exceed

a given number $L > 0$. Then we obtain the system

$$\left\{ \begin{array}{l} 0 = b_1 n(t) - d_1 e_1(t) \\ 0 = b_2 n(t) - \sum_{l,i} \left[\beta^{l,i} \left(i N^{l,i}(t) - e_{2A}^{l,i}(t) \right) e_{2D}(t) - \sigma^{l,i} e_{2A}^{l,i}(t) \right] - d_{2D} e_{2D}(t) \\ 0 = \beta^{l,i} \left(i N^{l,i}(t) - e_{2A}^{l,i}(t) \right) e_{2D}(t) - \left(\sigma^{l,i} + d_{2A}^{l,i} + \gamma_r^{l,i} \right) e_{2A}^{l,i}(t) \\ 0 = r^{l,i} + \left(\hat{\alpha}^{l,i-1} N^{l,i-1}(t) - \hat{\alpha}^{l,i} N^{l,i}(t) \right) e_1(t) + \left(\hat{\gamma}^{l,i+1} N^{l,i+1}(t) - \hat{\gamma}^{l,i} N^{l,i}(t) \right) \\ \quad + \left(q^{l+1,i} e_{2A}^{l+1,i}(t) - q^{l,i} e_{2A}^{l,i}(t) \right) + \delta_{li} q^{l+1,l+1} e_{2A}^{l+1,l+1} \\ \quad + \left(\hat{\theta}^{l,i+1} e_{2A}^{l,i+1}(t) - \hat{\theta}^{l,i} e_{2A}^{l,i}(t) \right) - \gamma_\varrho^{l,i} N^{l,i}(t) \\ 0 = \theta_p \sum_{l,i} q^{l,i} e_{2A}^{l,i}(t) - \gamma n(t) p(t) - \gamma_p p(t) \\ \partial_t n(t) = \frac{\mu n(t)}{\bar{n} + n(t)} \left(\gamma + \frac{1 - \theta_p}{\theta_p} (\gamma n(t) + \gamma_p) \right) p(t) - \gamma n(t), \end{array} \right. \quad (4.19)$$

for $(l, i) \in I_L$, where δ_{li} is the Kronecker delta, the rates $r^{l,i} = 0$ when $i \neq 0$ and we use the convention (3.2); here we have used (4.19)₅ to simplify (4.19)₆.

To describe the dynamics, it is sufficient to express p in terms of n , which will in turn provide a scalar autonomous differential equation for $n(t)$. For small populations the equations (4.19)₁₋₅ can be solved uniquely in terms of n , yielding the following theorem.

Theorem 4.1. *There are $m, \bar{m} > 0$ and C^∞ functions*

$$\hat{e}_1(n), \quad \hat{e}_{2D}(n), \quad \hat{e}_{2A}^{l,i}(n), \quad \hat{N}^{l,i}(n), \quad \hat{p}(n) : (-m, \bar{m}) \rightarrow \mathbb{R} \quad (4.20)$$

such that:

- (i) *For each $n \in (-m, \bar{m})$ the equations (4.19)₁₋₅ can be solved uniquely for $e_1, e_{2D}, e_{2A}^{l,i}, N, p$ in terms of n ,*

$$e_1 = \hat{e}_1(n), \quad e_{2D} = \hat{e}_{2D}(n), \quad e_{2A}^{l,i} = \hat{e}_{2A}^{l,i}(n), \quad N^{l,i} = \hat{N}^{l,i}(n), \quad p = \hat{p}(n).$$

- (ii) *The functions from (4.20) are given to leading order as*

$$\hat{N}^{l,i}(n) = \nu^{l,i} n^i + O(n^{i+1}), \quad (4.21)$$

with

$$\nu^{l,0} = \frac{r^{l,0}}{\gamma_\varrho^{l,0}} \quad \text{and} \quad \nu^{l,i} = \nu^{l,i-1} \frac{\hat{\alpha}^{l,i-1}}{\hat{\gamma}^{l,i} + \gamma_\varrho^{l,i}} \frac{b_1}{d_1}, \quad i \geq 1,$$

and with

$$\begin{aligned}
\widehat{e}_1(n) &= \frac{b_1}{d_1}n, & \widehat{e}_{2D}(n) &= \frac{b_2}{d_{2D}}n + O(n^2) \\
\widehat{e}_{2A}^{l,i}(n) &= i \left(\frac{b_2 \beta^{l,i} \nu^{l,i}}{d_{2D}(\sigma^{l,i} + d_{2A}^{l,i} + \gamma_r^{l,i})} + O(n) \right) n^{i+1} \\
\frac{\gamma_p}{\theta_p} \widehat{p}(n) &= \bar{p}(n)n^2, & \text{where } \bar{p}(n) &= \frac{b_2}{d_{2D}} \sum_l q^{l,1} \frac{\beta^{l,1} \nu^{l,1}}{(\sigma^{l,1} + d_{2A}^{l,1} + \gamma_r^{l,1})} + O(n). \tag{4.22}
\end{aligned}$$

Proof. For fixed t , we regard (4.19)₁-(4.19)₅ as an algebraic system, which can be solved uniformly in t , for small n . First, (4.19)₁ yields

$$e_1 = k_1 n, \quad \text{with } k_1 = \frac{d_1}{b_1},$$

and subtracting all of (4.19)₃ from (4.19)₂ and solving gives

$$e_{2D} = \frac{b_2}{d_{2D}} n - \sum_{l,i} \frac{d_{2A}^{l,i} + \gamma_r^{l,i}}{d_{2D}} e_{2A}^{l,i}. \tag{4.23}$$

Next, (4.19)₅ yields

$$p = \frac{\theta_p}{\gamma n + \gamma_p} \sum_{l,i} q^{l,i} e_{2A}^{l,i},$$

while (4.19)₃ gives

$$e_{2A}^{l,i} = i N^{l,i} \left(1 + \frac{\sigma^{l,i} + d_{2A}^{l,i} + \gamma_r^{l,i}}{\beta^{l,i} e_{2D}} \right)^{-1} = \eta^{l,i} N^{l,i}, \tag{4.24}$$

where we have set

$$\begin{aligned}
\eta^{l,i} &= i \left(1 - \frac{1}{1 + \zeta^{l,i} e_{2D}} \right) = i \zeta^{l,i} e_{2D} (1 + O(e_{2D})), \quad \text{with} \\
\zeta^{l,i} &= \frac{\beta^{l,i}}{\sigma^{l,i} + d_{2A}^{l,i} + \gamma_r^{l,i}}.
\end{aligned}$$

Now, regarding n and e_{2D} as fixed, we use (4.24) in (4.19)₄ to get

$$\begin{aligned}
0 &= r^{l,i} + \left(\widehat{\alpha}^{l,i-1} N^{l,i-1} - \widehat{\alpha}^{l,i} N^{l,i} \right) k_1 n + \left(\widehat{\gamma}^{l,i+1} N^{l,i+1} - \widehat{\gamma}^{l,i} N^{l,i} \right) \\
&+ \left(q^{l+1,i} \eta^{l+1,i} N^{l+1,i} - q^{l,i} \eta^{l,i} N^{l,i} \right) + \delta_{l,i} q^{l+1,l+1} \eta^{l+1,l+1} N^{l+1,l+1} \\
&+ \left(\widehat{\theta}^{l,i+1} \eta^{l,i+1} N^{l,i+1} - \widehat{\theta}^{l,i} \eta^{l+1,i} N^{l,i} \right) - \gamma_\rho^{l,i} N^{l,i}, \tag{4.25}
\end{aligned}$$

which we regard as a linear system,

$$\mathbf{A} \mathbf{N} = \mathbf{r}, \quad \text{for } \mathbf{N}^T = (N^{1,0}, N^{1,1}, N^{2,0}, N^{2,1}, N^{2,2}, N^{3,0}, \dots, N^{L,L}).$$

When expressed in matrix form, the matrix A is sparse and upper Hessenberg, with subdiagonal entries $-\widehat{\alpha}^{l,i-1}k_1n$. It follows that the matrix is upper triangular for $n = 0$, so invertible for small n , and we get a unique solution $N^{l,i} = N^{l,i}(n, e_{2D})$.

Setting $n = e_{2D} = 0$, and recalling that $r^{l,i} = 0$ for $i > 0$ and $\widehat{\gamma}^{l,0} = 0$, (4.25) gives the initial solution

$$N^{l,0}(0,0) = \frac{r^{l,0}}{\gamma_\rho^{l,0}}, \quad N^{l,i}(0,0) = 0, \quad i > 0,$$

and so using (4.24) and (4.23), we get in particular $e_{2A}^{l,i} = \eta^{l,i} = 0$ whenever $n = e_{2D} = 0$.

We now plug the solution $N^{l,i} = N^{l,i}(n, e_{2D})$ into (4.24), (4.23) to get

$$G(n, e_{2D}) := e_{2D} - \frac{b_2}{d_{2D}}n + \sum_{l,i} \frac{d_{2A}^{l,i} + \gamma_r^{l,i}}{d_{2D}} \eta^{l,i} N^{l,i}(n, e_{2D}) = 0,$$

relating e_{2D} to n . We calculate

$$\left. \frac{\partial G}{\partial e_{2D}} \right|_{(0,0)} = 1,$$

so the implicit function theorem implies that, for n small enough, there is a unique function $e_{2D}(n)$ such that $G(n, e_{2D}(n)) = 0$, and moreover,

$$e_{2D} = \frac{b_2}{d_{2D}}n + O(n^2).$$

Finally, we have

$$N^{l,i}(n) = N^{l,i}(0,0) + O(n) \quad \text{and} \quad \eta^{l,i} = i \frac{b_2 \zeta^{l,i}}{d_{2D}}n + O(n^2),$$

so according to (4.24), we have

$$e_{2A}^{l,i} = O(n^2), \quad \text{so also} \quad p = O(n^2).$$

Moreover, for small n , we can write (4.25) for $i \geq 1$ as

$$\begin{aligned} 0 &= \widehat{\alpha}^{l,i-1} k_1 n N^{l,i-1} - (\widehat{\gamma}^{l,i} + \gamma_\rho^{l,i} + O(n)) N^{l,i} \\ &\quad + (\widehat{\gamma}^{l,i+1} + O(n)) N^{l,i+1} + \delta_{l,i} q^{l+1,l+1} \eta^{l+1,l+1} N^{l+1,l+1}, \end{aligned}$$

and we can solve this inductively in i , to get

$$N^{l,i} = \frac{\widehat{\alpha}^{l,i-1} k_1}{\widehat{\gamma}^{l,i} + \gamma_\rho^{l,i}} N^{l,i-1} n (1 + O(n)),$$

from which the result follows. □

Birth rate $B[n]$. By Theorem 4.1, and using (4.19)₆ and (4.22), we conclude that for small populations $n \in [0, \bar{m})$, the dynamics is again driven by the equation

$$\partial_t n(t) = n(t)(B(n) - \gamma_n),$$

where now the birth rate $B(n)$ is given by

$$\begin{aligned} B(n) &= \frac{\mu}{\bar{n} + n(t)} \left(\gamma + \frac{\theta_p - 1}{\theta_p} (\gamma n + \gamma_p) \right) \widehat{p}(n) \\ &= \frac{\mu n^2}{\bar{n} + n(t)} \left(\frac{\gamma}{\gamma_p} \theta_p + (1 - \theta_p) \left(\frac{\gamma}{\gamma_p} n + 1 \right) \right) \bar{p}(n). \end{aligned} \tag{4.26}$$

We now divide $B(n)$ by n^2 and differentiate with respect to θ_p . Since \bar{p} is independent of θ_p , we obtain

$$\left. \frac{\partial}{\partial \theta_p} \left(\frac{B(n)}{n^2} \right) \right|_{n=0} = \frac{\mu}{\bar{n}} \left(\frac{\gamma}{\gamma_p} - 1 \right) \frac{b_2}{d_{2D}} m_c \sum_l q^{l,1} \frac{\beta^{l,1} \nu^{l,1}}{(\sigma^{l,1} + d_{2A}^{l,1} + \gamma_r^{l,1})},$$

so that

$$\left. \frac{\partial}{\partial \theta_p} \left(\frac{B(n)}{n^2} \right) \right|_{n=0} > 0 \quad \text{if and only if} \quad \gamma > \gamma_p.$$

Thus we arrive at a similar conclusion to that of the T -model: that is, for small populations, sharing food (within the species) is beneficial in terms of growth as long as the consumption rate γ is greater than the decay rate γ_p of the cleaved off cellobiose.

5 A Model in the Continuous Setting

In this section, by analogy with our multiple trait T -model (4.16), we develop a model for a population with any number of traits, which we write for convenience in the continuous setting. We should say again that in our context, we do not expect the number of possible enzymes for cellulose degradation to be that large but note that this model includes finite trait models by appropriate use of δ -functions,

$$n(t, x) = \sum_j n_j(t) \delta_{x_j}(x).$$

We hence present the continuous model here for its generality and because the resulting equation may be more amenable to analysis.

We think of the multiple-trait population as having M traits indexed by $x_1 < \dots < x_M$, so we write

$$n^i(t) = n(x^i, t) \Delta x, \quad e_1^i(t) = e_1(x^i, t), \quad e_2^i(t) = e_2(x^i, t),$$

for some functions $n(x, t)$, $e_1(x, t)$, $e_2(x, t)$, representing the population and enzyme densities. We now simply assume that the variable x takes on a continuous range of values.

We similarly translate the coefficient vectors (4.12), so that these become continuous parameters: that is, we allow the parameters b_i , d_i , α , β , \widehat{q} , θ_p , etc, to depend on x , and in analogy to (4.12)_{1,2,3} we set

$$A(x) = \alpha(x) \frac{b_1(x)}{d_1(x)}, \quad B(x) = \theta_r(x) \beta(x) \frac{b_2(x)}{d_2(x)}, \quad Q(x) = \widehat{q}(x) \frac{b_2(x)}{d_2(x)}, \tag{5.1}$$

where these are now positive functions. In particular, we interpret α , β and \widehat{q} as the rates of landing site generation, occupation, and the rate of cellobiose production, per individual, respectively.

We now simply follow the development that led to (4.16), but reinterpreting the inner product, so that for each function $W(x)$,

$$\langle W, n \rangle = \int W(y) n(y, t) dy.$$

Then (4.13), (4.14) and (4.15) are unchanged. To express the population equation, we define the functional

$$\tau[n] := \frac{1}{\gamma_\varrho m_c} \langle A, n \rangle \langle Q, n \rangle + \langle A, n \rangle + \langle B, n \rangle + \gamma_p,$$

and the convolution

$$N[n](x, t) = \int \nu(s, x) n(s, t) ds,$$

which is an inner product in the first variable.

We must now model the last term in (4.17). In analogy with that term, we define

$$\Xi(z; x, t) = \frac{\nu(x, z) Q(z)}{\nu(x, z) \bar{n}(x, t) + N[n](z, t)}.$$

Now, in analogy with (4.16), (4.17), we write the population equation as

$$\partial_t n(x, t) = n(x, t) \left(B[n](x, t) - \gamma_n(x) \right),$$

where the birth rate is now the functional

$$B[n] = \frac{\mu(x) r}{\gamma_\varrho m_c} \frac{\langle A, n \rangle}{\tau[n]} \left(\frac{\langle \theta_p Q, n \rangle \gamma(x)}{\left(\bar{n}(x) + \frac{1}{\gamma(x)} \langle \gamma, n \rangle \right) (\langle \gamma, n \rangle + \gamma_p)} + \left\langle (1 - \theta_p) \Xi(\cdot; x, t), n \right\rangle \right). \quad (5.2)$$

6 Numerical experiments

In this section we use numerical experiments to test and compare the various models that we have derived.

N-S and S models. First, we compare the *N-S*-model with the *S*-model. The results of the numerical computations are presented in Figure 2. The coefficients of the *S*-system are chosen as

$$\begin{aligned} b_1 = 0.5, \quad b_2 = 0.5, \quad d_1 = 0.5, \quad d_{2A} = 0.5, \quad d_{2D} = 0.5 \\ \beta = 0.5, \quad \sigma = 0.1, \quad \gamma_r = 0.01, \quad \gamma_p = 0.001, \quad \gamma_\varrho = 0.001 \\ \gamma_n = 0.1, \quad \alpha = 0.05, \quad r = 1000, \quad \theta_r = 0.05, \quad \theta_p = 0.75 \\ q = 1, \quad \gamma = 0.005, \quad \mu = 0.5, \quad \bar{n} = 100. \end{aligned} \quad (6.1)$$

The coefficients of the *N-S*-system are chosen randomly as follows. For each coefficient of the *S*-system, let us call it ‘ c ’, the corresponding coefficient $c^{l,i}$ of the *N-S*-system (which explicitly depends on the state of the chain (l, i)) is chosen as

$$c^{l,i} = cX \quad \text{where} \quad X \sim \text{gamma}(k, \theta), \quad k = p^{-2}, \theta = p^2. \quad (6.2)$$

Here the value p is the standard deviation of X . Thus all samples approximately lie in $(c-3p, c+3p)$.

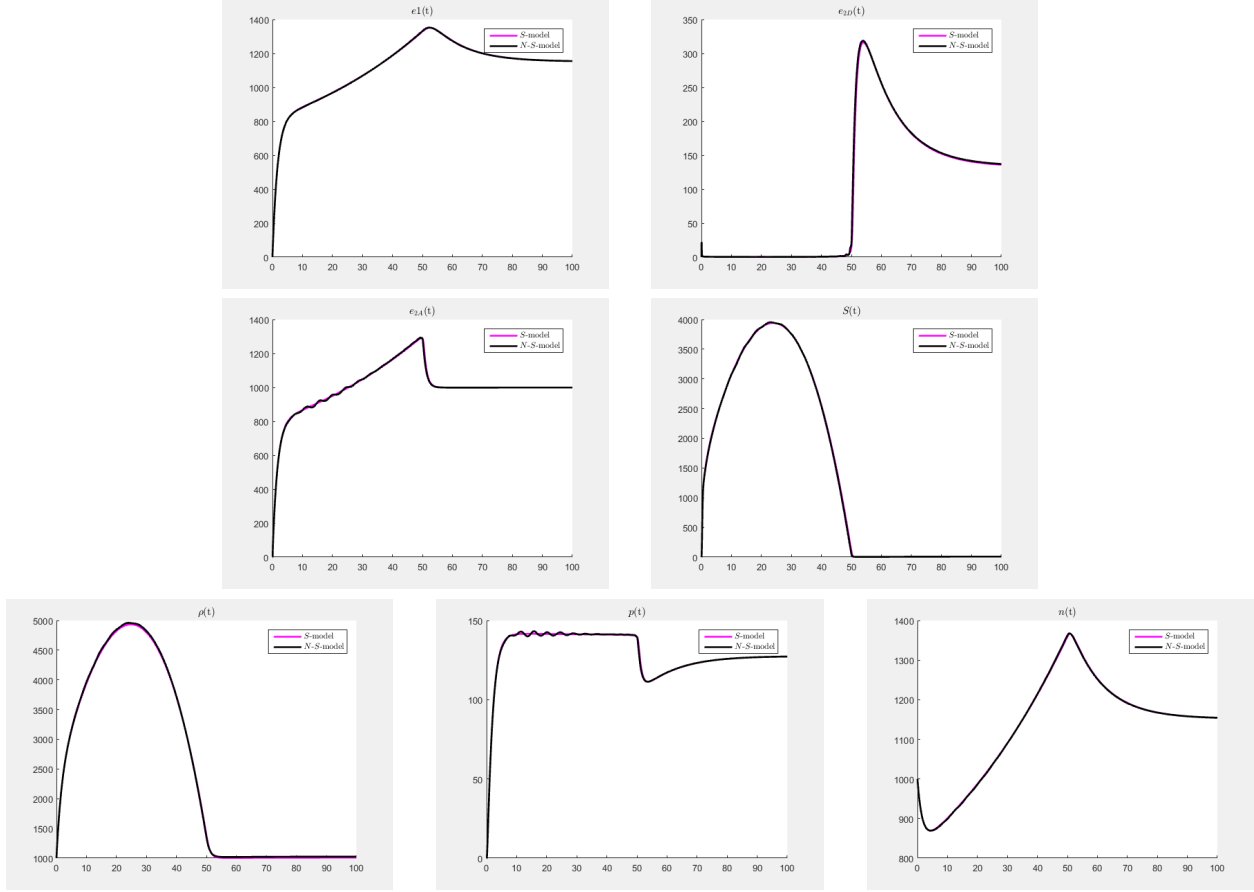


Figure 2: Solutions of S and NS systems with $3p = 0.05$

S and T models. We next compare the *T* and *S* systems numerically. The coefficients of the *S*-system are chosen as

$$\begin{aligned}
 b_1 &= 0.1, & b_2 &= 0.1, & d_1 &= 0.1, & d_{2A} &= 0.1, & d_{2D} &= 0.1 \\
 \gamma_r &= 0.01, & \gamma_p &= 0.005, & \gamma_e &= 0.005, & \gamma_n &= 0.01, & \alpha &= 0.05 \\
 r &= 1000, & \theta_r &= 0.05, & \theta_p &= 0.75, & \gamma &= 0.01, & \mu &= 0.5, \\
 \bar{n} &= 100
 \end{aligned} \tag{6.3}$$

and

$$\begin{aligned}
 \{\beta\}_{i=1}^6 &= \{0.6668, 0.8394, 1.0567, 1.3304, 1.6748, 2.1085\} \\
 \{\sigma\}_{i=1}^6 &= \{17.7828, 177.828, 1778.28, 17782.8, 177828, 1778280\} \\
 \{q\}_{i=1}^6 &= \{0.0007, 0.0053, 0.0421, 0.3342, 2.6544, 21.0848\}.
 \end{aligned} \tag{6.4}$$

The pictures on Figure 3 correspond to the limiting procedure where

$$q_i \frac{\beta_i}{\sigma_i} = q_0 = 0.000025 \quad \text{and} \quad \frac{\beta_i}{\sigma_i} \rightarrow 0.$$

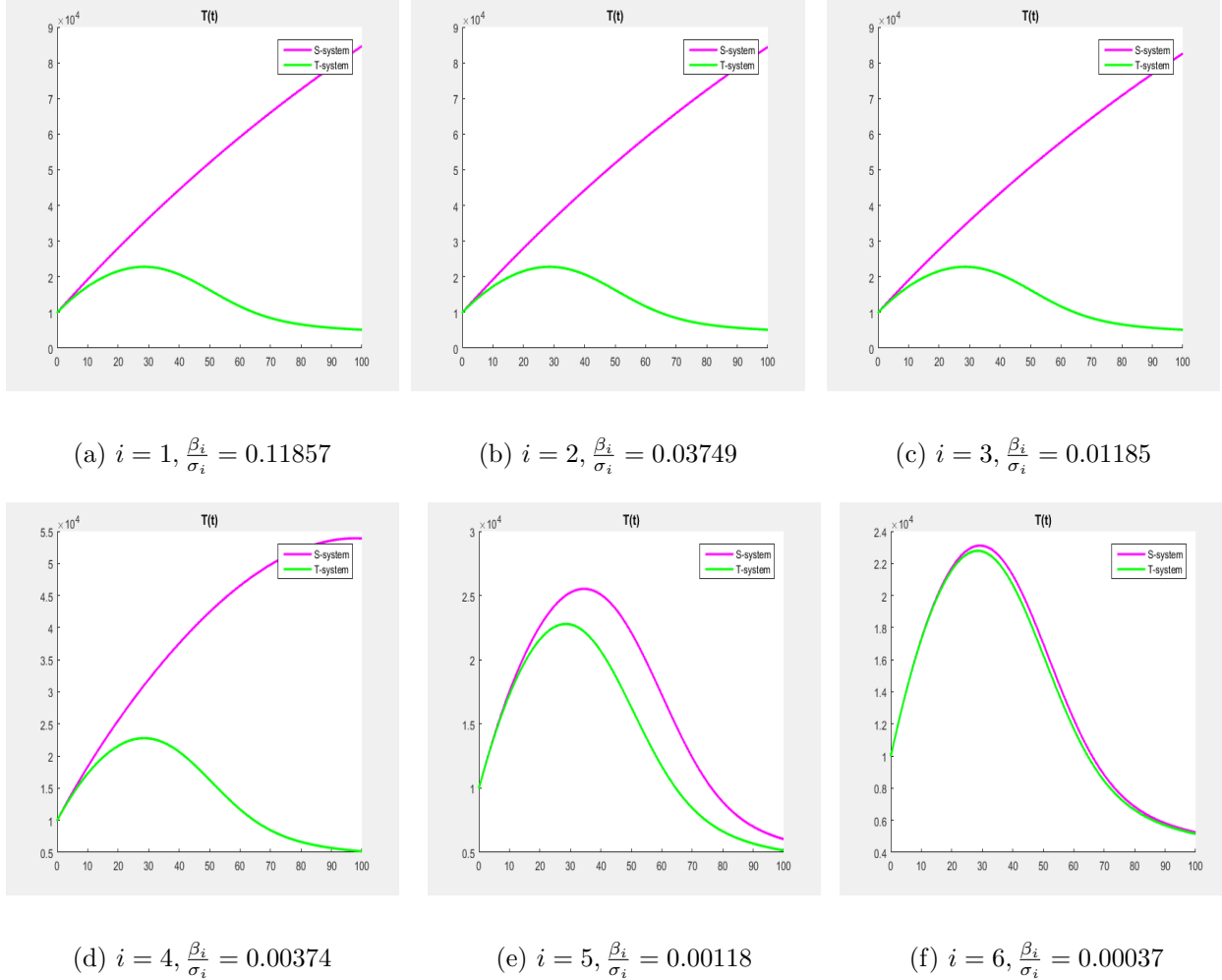


Figure 3: $T(t)$ of T -model and S -model for $q_i \frac{\beta_i}{\sigma_i} = q_0 = 0.000025$ and $\frac{\beta_i}{\sigma_i} \rightarrow 0$.

7 Appendix

7.1 Tail issue in deterministic selection dynamics

Models in population dynamics focus on selection because it is rightfully viewed as the main mechanism to explain the survival of populations and the evolution of traits. The selection mechanism in these models is often driven by competition between individuals, possibly combined with mutations to create new traits. In addition competition is well understood from the modeling point of view.

On the other hand cooperative effects are harder to model, especially at the level of micro-organisms. Several well-known cooperative effects (such as sexual reproduction for large animals) do not take place for all micro-organisms. Nevertheless, the importance of such effects has long been recognized: see for instance the works [14, 23, 24, 28] on mutualism that discuss interspecies interactions yielding reciprocal benefits.

In this paper we introduce biological mechanisms, by the example of cellulose bio-degradation,

that lead to reproduction rates encoding both (intra-species) cooperative effects and competition between individuals; see Section 4. This suggests that reproduction rates that only incorporate competition may fail to describe many biochemical processes, especially at the level when $B[n]$ significantly deviates from traditional logistic terms, that is for small populations.

There are several approaches to study the phenotypical evolution driven by small mutations in replication, the main objective being to describe the dynamics of the fittest (or dominant) trait in the population. The main mechanisms affecting dynamics are usually a) the selection principle (due to competition, birth and death), and b) small mutations. These two mechanisms influence the trait dynamics on two different scales. The selection effect becomes evident on the reproduction timescale t_R , while the effect of small mutations is evident on a generation timescale $t_M \gg t_R$. The drastic difference between the two scales introduces both small and large parameters into models (mutations can be small or rare for instance, population is usually large and death rates could vary) and this causes various difficulties.

One of the best known approaches is the so-called adaptive dynamics theory, see for instance [10, 12, 3, 16, 36]. Adaptive dynamics considers evolution as a series of invasions by a small mutant population of the dominant trait population, a process which is classically modeled by a system of ODE's. Depending on the relative fitness of the mutant, this can lead to the replacement of the dominant trait or the extinction of the invading population (the cases of co-existence are usually harder to handle at this level).

Other very popular models are stochastic, or individual-centered models, see for instance [14, 5, 5] among many. Probabilistic models are natural because they take natural fluctuations of births, deaths, and mutations into account at the individual level, and are therefore considered to be the most realistic. They consist in life and death processes for each individual X_i . A typical example consists in taking Poisson processes with birth rates $b(X_i)$ and death rates increasing with the competition between individuals, for example $d_i = d(X_i) + \sum_{j \neq i} I(X_i - X_j)$.

When a birth occurs, it simply adds another individual with the same trait, unless a mutation takes place, generally with small probability. In that case, the new individual has a different random trait, obtained through some distribution. In general of course competition could influence both the birth rate and the mortality rate. Under the right scalings, stochastic models can lead to the classical adaptive dynamics [34, 26].

When the total number of individuals is too large (it can easily reach $10^{10} - 10^{12}$ for some micro-organisms), stochastic models can become cumbersome and prohibitive to compute numerically for instance. In that case, one expects to be able to derive a deterministic model as a limit of large populations which would be simpler to use. Such a derivation was provided in [7] for example, leading to integro-differential equations such as

$$\partial_t n(x, t) = \left(r(x) - \int I(x - y) n(t, y) dy \right) n(x, t) + M[n](t, x), \quad (7.1)$$

where $r(x) = b(x) - d(x)$ and $M[\cdot]$ is the mutation kernel, a diffusion or integral operator. This is the level of modeling that we are interested in this article.

Even though deterministic models of type (7.1) are obtained from stochastic ones, simulations for these two types of models typically produce different behaviors in terms of evolutionary speeds and branching patterns. In stochastic simulations, in which a single individual represents a minimal unit necessary for survival, demographic stochasticity (the variability in population growth rates among individuals) acts drastically on small populations, leading to complete extinction of small populations with negative reproduction rates. In deterministic models however, sub-populations

can never go completely extinct and can “rebound” later on if their reproduction rate becomes positive.

It is an open and difficult question of how to keep the stochastic effects for the small populations in the deterministic models. Perthame and Gauduchon [26] made an attempt in truncating the populations with less than one individual by introducing an analog of stochastic mortality for models of type (7.1), a survival threshold, which allows phenotypical traits in the small population to vanish in finite time. In [26] this is achieved by modifying (7.1) as follows

$$\partial_t n(x, t) = \left(r(x) - I \star n \right) n - \sqrt{\frac{\bar{n}}{n}} + M[n](t, x). \quad (7.2)$$

The new term enables the population to vanish for some traits when the population density is too low in comparison with \bar{n} , which disallows densities corresponding to fewer than one individual.

As one wishes to see the evolution of traits generated by mutations, one needs to rescale the above equation in time. This leads to large deviation type phenomena which can be observed by defining $n_\varepsilon(t, x) = \exp(\phi_\varepsilon(t, x)/\varepsilon)$, with ε the ratio of the reproduction and mutation time scales (see [26, 13]). One now has two scales for the populations, the small population threshold \bar{n} and the exponential scale $\exp \phi/\varepsilon$.

Often, the aim is to analyze the population behavior in the limit as $\varepsilon \rightarrow 0$ and therefore \bar{n} should be chosen in terms of ε . Numerical simulations for the corresponding equation with initial data of monomorphic type, see [26], indicate that the evolution speeds and time of branching depend on this choice of \bar{n} in terms of ε . When ε is fixed, too large a value of \bar{n} leads to extinction, while too small a value of \bar{n} leads to spontaneous jumps in branching, see [26, 13].

A complete mathematical analysis of the general equations is currently intractable. One of the few situations that is currently understood [26] is when the mortality threshold is chosen as $\bar{n}_\varepsilon = \exp(-\frac{\bar{\varphi}}{\varepsilon})$. However, the scaling $\bar{n}_\varepsilon = \exp(-\frac{\bar{\varphi}}{\varepsilon})$ for a fixed $\bar{\varphi}$ is often much too small. Recall that the threshold \bar{n}_ε should correspond to a single individual in stochastic modeling. Thus, if we come back to the starting point, which means a total population $\int n(x, t) dx$ of $10^{10} - 10^{12}$, then for $\varepsilon = 10^{-4}$ (a typical value for many applications) and threshold \bar{n}_ε of order $\exp(-\frac{1}{\varepsilon})$, an aggregate population over any fixed interval of traits would still represent much less than one individual.

Another type of correction has been proposed by Jabin [22]. The author allows the threshold \bar{n}_ε to be polynomial in ε and introduces special cooperative term D_ε in the (rescaled) model

$$\partial_t n_\varepsilon(x, t) = \left(r(x) - \int I(x - y)n(t, y) - D_\varepsilon[n] \right) n(x, t) + M[n](t, x). \quad (7.3)$$

This term does not handle the small populations as precisely, but the new model still corrects all the abnormal behaviors of (7.1) near the limit. The cooperative effects in [22] were, however, more intuited than derived. For example, the typical cooperative term D_ε has the form

$$-D_\varepsilon[n_\varepsilon](x, t) = -D_0 + \max \left(0, D_0 - K(x) d(x, \{n_\varepsilon \geq \bar{n}_\varepsilon\}) \right) \quad (7.4)$$

where $K(x)$ is a symmetric positive kernel. In that respect, the present work puts the approach in [22] on a more solid framework by actually deriving those effects from realistic biochemical processes.

The present work aims at introducing cooperative terms, similar to those of [22], that arise naturally (directly from biological processes), rather than *ad hoc* mathematical terms. The cooperative

effects in the integral operator $B[n]$ in (1.1) appear naturally in the process of model construction and give a hint of what such terms should look like.

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