Mathematical modelling of shelf life in MAP packed meat:

Coupling between oxygen dynamics, colour stability and bacterial growth

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Abstract

To understand shelf life determining processes in a modified atmosphere packaging (MAP) environment and enable more accurate predictions, colour stability and bacterial growth were modelled mathematically. This was done by coupling three distinct processes: two-way coupling of CO_2 and O_2 concentrations in the headspace to bacterial growth, transport of O_2 from the headspace into the product and chemical processes within meat. Parameters were set by extrapolation and fitting of available literature data as well as new data from validation experiments. The model reveals the nature of the competition for oxygen between bacteria and chemical oxygen-consuming processes and the different time scales governing shelf life. The model envisioned can be used as a tool for shelf life prediction. The bacterial part of the model is inspired by [1], the reaction diffusion by [2] and the latter has data validated by [3]

1. Introduction

A long shelf-life is important for the fresh meat. Two crucial phenomena influence the shelf-life of fresh meat, the colour of the meat, and the proliferation of spoilage bacteria. We seek to model both. One dimensional reaction diffusion differential equations are used to model O_2 propagation in the meat, and its reaction with myoglobin. while ordinary differential equation are used to model the proliferation of spoilage bacteria, and their O_2 consumption. The model system can be considered as a two different hierarchically systems, connected by O_2, where the biological part, i.e. the part that governs bacterial oxygen consumption dominates the chemical part i.e. the oxygen consumption within the meat, due to the biological part consumes much O_2. The differential equations for the chemical part are

$$\frac{\partial [O_2]}{\partial} = \frac{1}{1 + \frac{[Mb(II)]K_d}{(K_d + [O_2])^2}}\left(D\frac{\partial^2[O_2]}{\partial x^2} - k_{con}[O_2] - \frac{[Mb(II)]K_d}{[O_2]+K_d}\left(\frac{k_1[N][O_2]K_d}{([O_2]+K_d)^2} + \frac{k_{diss}[O_2]}{[O_2]+K_d}\right)\right) \quad (1)$$

$$\frac{\partial[Mb(II)]}{\partial t} = -k_{diss}[MbO_2] - \frac{k_b K_d[O_2]}{([O_2]+K_d)^2}[Mb(II)] + [MMb]v_{max}\frac{[NADH]}{K_m + [NADH]} \quad (2)$$

$$\frac{\partial[MMb]}{\partial t} = k_{diss}[MbO_2] + \frac{k_b K_d[O_2]}{([O_2]+K_d)^2}[Mb(II)] - [MMb]v_{max}\frac{[NADH]}{K_m + [NADH]} \quad (3)$$

$$\frac{\partial[NADH]}{\partial t} = \frac{-[MMb]v_{max}}{2}\frac{[NADH]}{K_m + [NADH]} \quad (4)$$

with

$$[MbO_2] = \frac{[Mb(II)][O_2]}{K_d + [O_2]} \quad \text{and} \quad [Mb] = \frac{[Mb(II)]K_d}{K_d + [O_2]}. \quad (5)$$

For the biological part the equations are

$$\mu_{max} = \mu_{opt}\left(1 - \frac{[CO_2]}{CO_{2max}}\right)\cdot\frac{2[O_2]k_{ox}}{k_{ox}^2 + [O_2]^2} \quad (6)$$

$$\frac{dn}{dt} = \mu_{max}n\frac{N-n}{N} \quad (7)$$

$$\frac{dn_{O_2}}{dt} = -k_{pbc}n^{-\alpha}\frac{dn}{dt} \quad (8)$$

$$\frac{dn_{CO_2}}{dt} = -\frac{dn_{O_2}}{dt} \quad (9)$$

A surprising result is $\alpha > 0$. This means that as the density of bacteria increases the O_2 consumption per bacteria decreases in such a way that the total O_2 consumption $\approx \sqrt{n}$. A diagram of our model can be seen in Fig 1
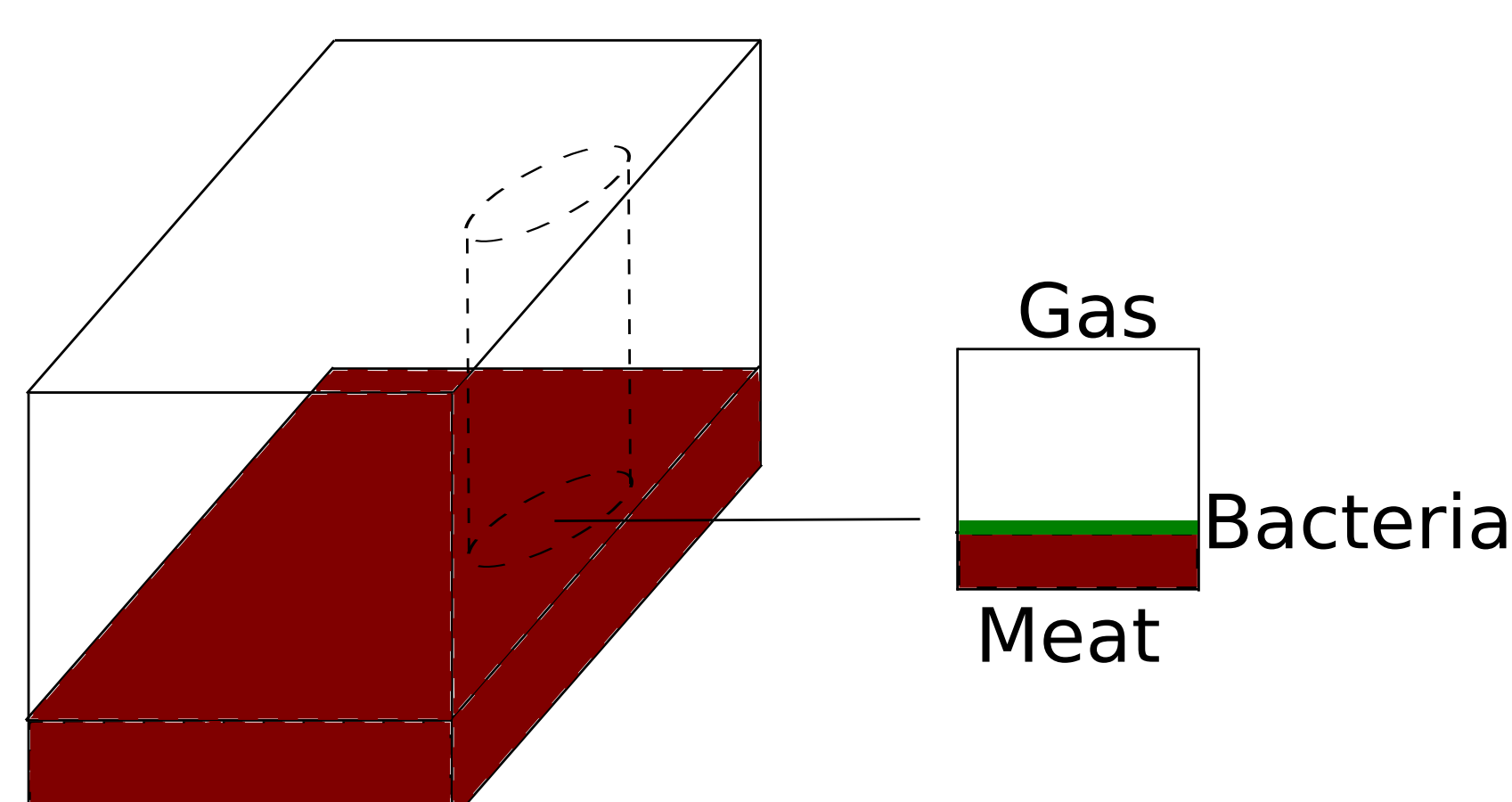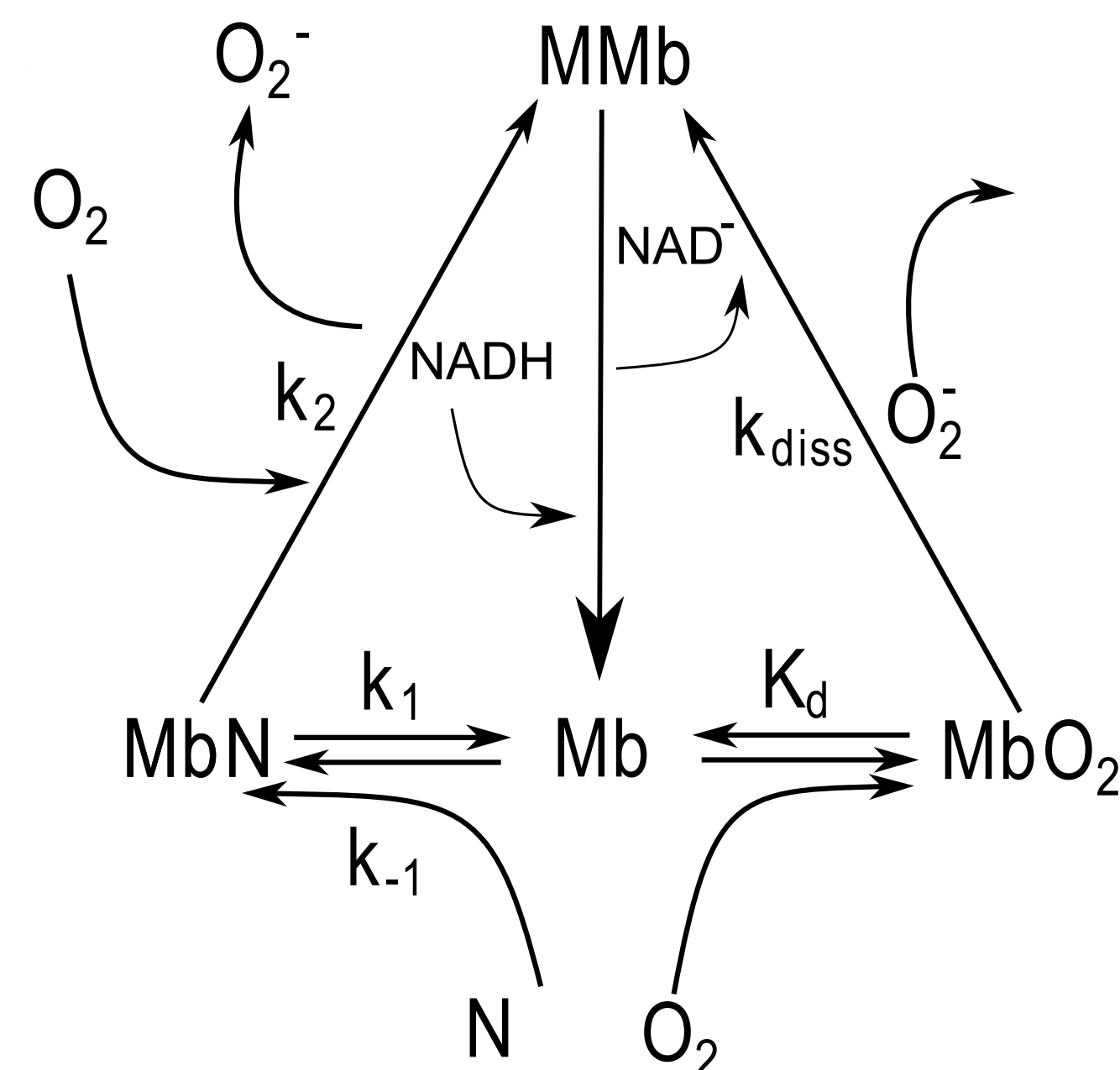
Figure 1: Diagram of our model

Figure 2: Reaction diagram of the chemical model. The left part of the model gives rise to the $\frac{K_b K_d[O_2]}{([O_2]+K_d)^2}\cdot[Mb + MbO_2]$ term

2. Results and discussion

The model goes through five distinct phases, separated by four times. The first is defined to be the time when the O_2 has diffused into the meat enough that a quasi-steady state is reached where it is consumed as fast as it diffuses in. At this point, the number of bacteria is still low, so the O2 concentration in the headspace is more or less constant, and there is still plenty of NADH left to reduce all the MMb. The model denotes the time when this phase ends t1. The second phase ends when, at the point of maximum oxidation rate, $[NADH] << [Mb] + [MbO_2]$. At this time, all the Mb and MbO_2 located where the maximum oxidation takes place will be oxidized, spreading outwards as time progresses. This time is called t_2. When enough bacteria have accumulated, and the O_2 consumption of their growth is starting to consume the significant amounts of O_2 in the headspace, the third phase ends. This time is called t3. It is not necessarily the case that $t_2 < t_3$. Whichever occurs first marks the end of the quasi-steady state, where either the amount of MMb begins to increase or the amount of O_2 in the headspace begins to decrease. The fourth phase ends at the "beginning of the end" of the model. Either the bacteria have consumed all the O_2, or the bacteria reached the carrying capacity. This happens at t_4. In the fifth and final phase, nothing happens on the time scales that is meaningful for meat storage. For a starting concentration of 70% O_2 and 30% CO_2 , t_1 occurs around 8 h, t_2 around 36 h, t_3 around 380 h and t_4 around 900 h.

To get the parameters values seen in table 2 we fit the chemical parameters to data from [3] and the bacterial data from unpublished results from the Danish Meat Research Institute(DMRI), results from the fit can be seen in Figs 3, 4 and 5

Table 1: Characteristic phases

End of phase	Time	Characteristic of phase
t_1	8	Only [NADH] changes
t_2	36	Somewhere [NADH]=0
t_3	380	Bacteria start consuming O2
t_4	900	"End" of model

References

[1] Garcia-Ochoa, F., Gomez, E., Santos, V. and Merchuk, J. (2010). Oxygen uptake rate in microbial processes: An overview, Biochemical Engineering Journal 79: 289-307.

[2] Brantley et al., Biochem. J. **268**, 6695-7010 (1993).

[3] Saenz et al.,Eur Food Res Technol. **227**, 1329-1338 (2008).

Table 2: Parameters values from the fitting function

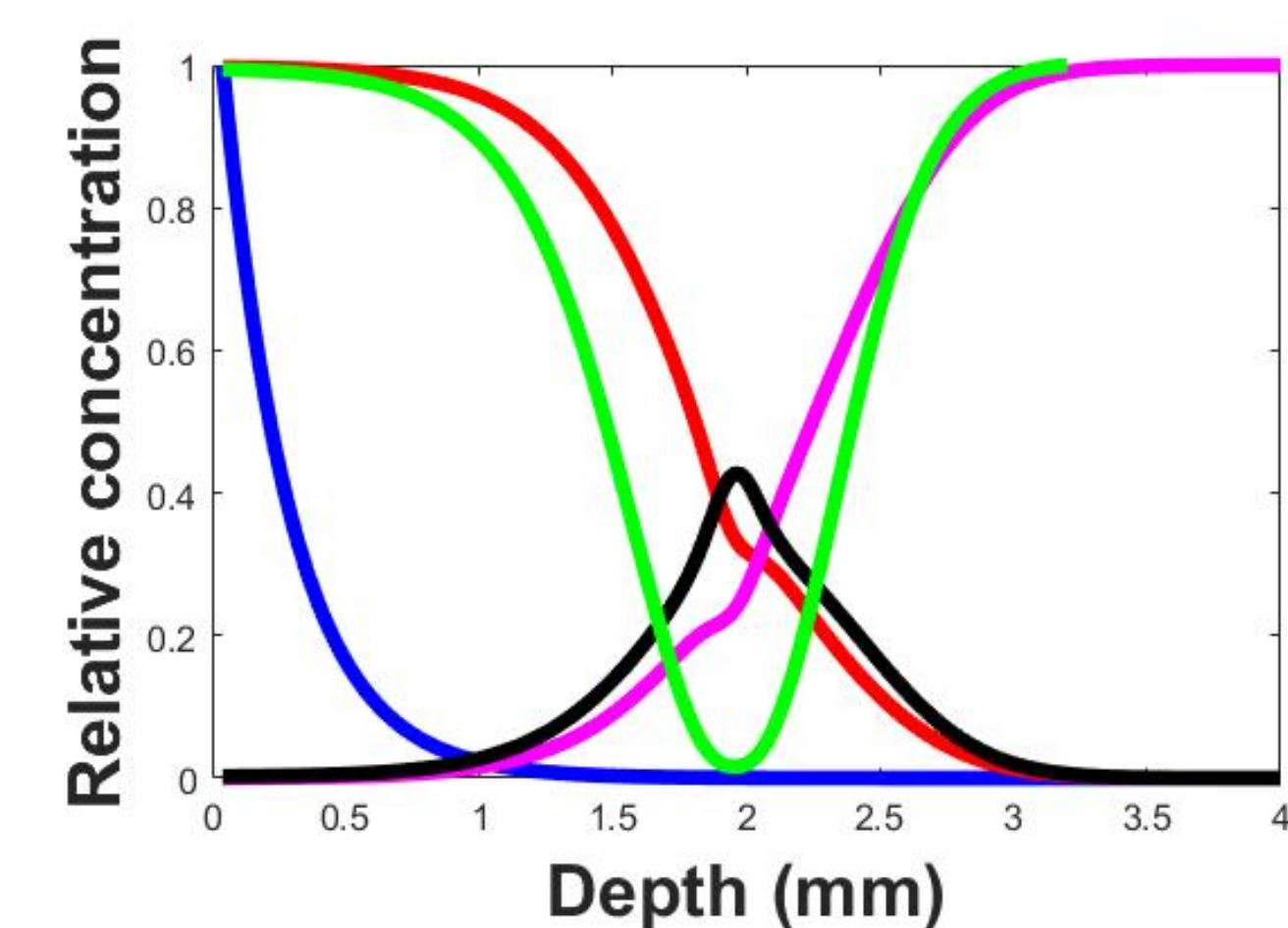|	0 °C	5 °C
μ_{opt}	0.0112 h^{-1}	0.0307h^{-1}
k_s	0.0042 M	0.0053 M
CO_{2max}	1.67 M	4.27 M
N	$10^{6.36}$CFU cm^{-2}	$10^{7.41}$ CFU cm^{-2}
$\sqrt{K_{con}D}$	$6.41\cdot10^{-2}$ m h^{-1}	12.9 m h^{-1}
k_{pbc}	$9.77\cdot10^{-7}$mol CFU$^{-1+\alpha}$	$6.98\cdot10^{-7}$ mol CFU$^{-1+\alpha}$
α	0.509	0.543
D	NA	2.6 mm^{2}h^{-1}
k_{diss}	NA	$1.8\cdot10^{-3}$ h^{-1}
K_d	NA	$3.5\cdot10^{-7}$h^{-1}
k_{con}	NA	40 h^{-1}
k_{red}	NA	0.95h^{-1}
K_m	NA	$3.3\cdot10^{-5}$ mol L^{-1}
k_b	NA	1.5 h^{-1}
$[Mb2]_0$	NA	$2.4\cdot10^{-4}$mol L^{-1}
$[NADH]_0$	NA	$1\cdot10^{-3}$mol L^{-1}

Figure 3: The chemical part of the model, after 36 hours around t_2, for 70% O_2 and 5° C. Green is [NADH], blue is $[O_2]$ black is [MMb] red is [MbO_2] and purple is [Mb]
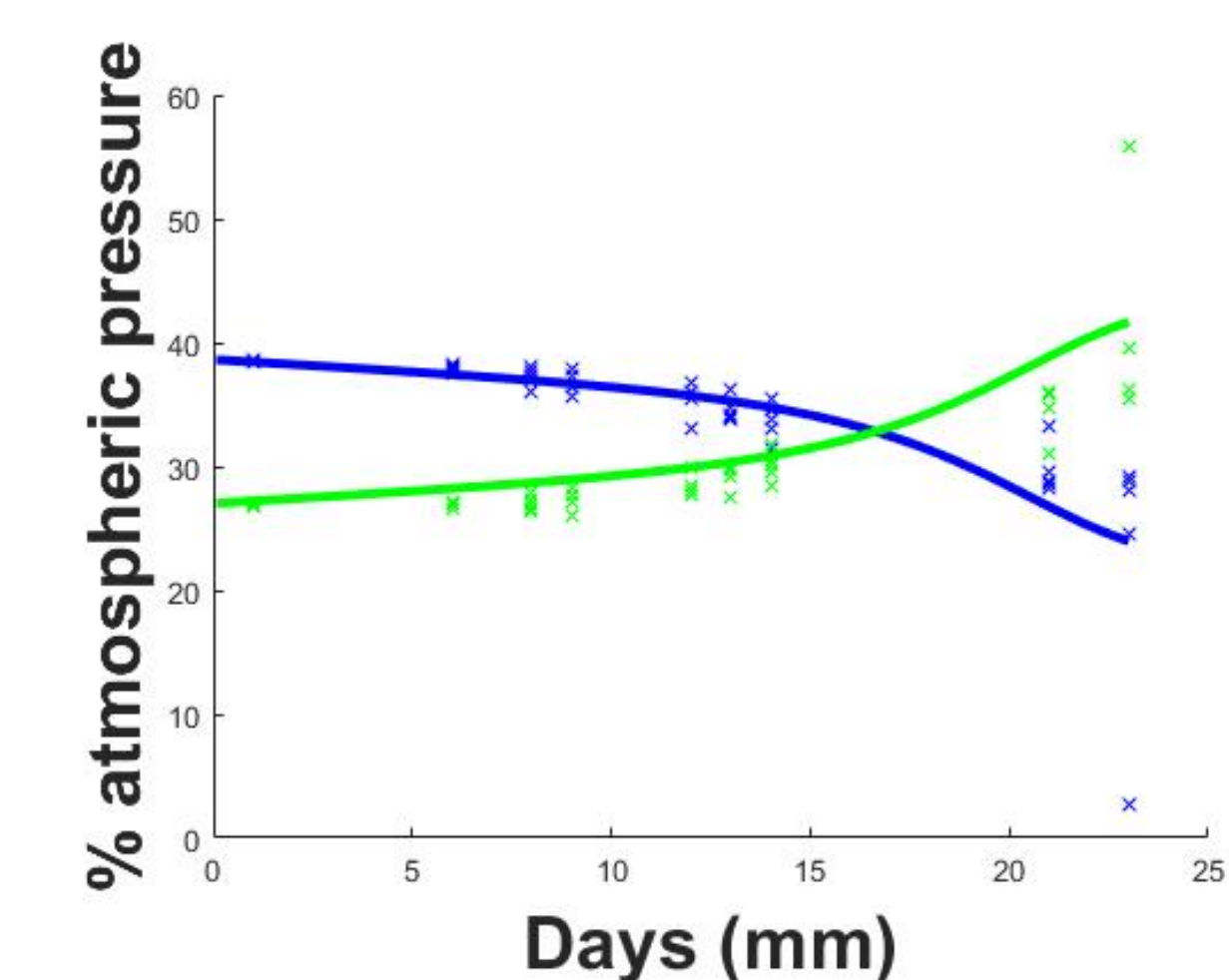
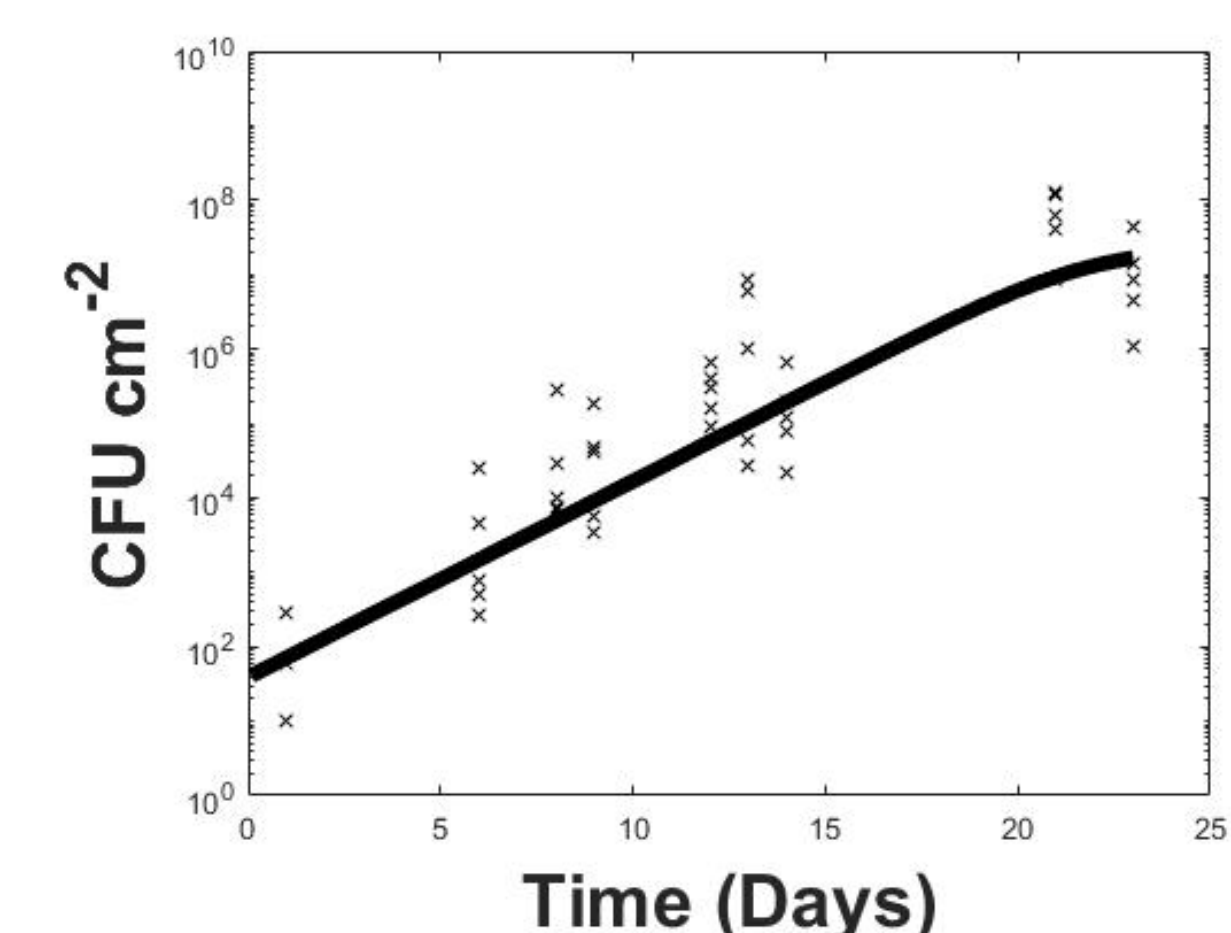**Figure 4:** The O_2 and CO_2 in the head space for our model, for a starting concentration 40% O_2 and 5° C.

Figure 5: The number of bacteria for our model for our model, for a starting concentration 40% O_2 and 5° C.

3. Acknowledgements