# Summary Of Modeling Marathon 30.03

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We discussed few issues and then went to Food Engineering Library. Pictures of the whiteboard are available here.

Our biggest progress was resolving some disputes we had for quite long time. Our discussion was mostly about the problems I've described in this document. Therefore, I shall elaborate only our decisions and insights.

1. The infamous In/Out Dispute: Well, I'm not sure how to put it. What we argued about in the 'In/out dispute' wasn't what 'in' and 'out' are actually about. We thought 'in' stands for the amounts in the scale of a single cell and 'out' for the amounts in the scale of the whole organism, and we should use 'out' where it's possible because we don't want to assume the materials are uniformly distributed. Well, that's not what they are about. As Nitzan explained to Chen few weeks ago, 'in' is supposed to stand for the amounts inside a single cell, and 'out' for all the materials that are outside all cells. You may say now that although we used the wrong names to describe it, we still should account for the total amount of the material in the whole system the same way we did hitherto. I and Chen thought it over and concluded that we have to assume uniformity between cells, drop all references to 'out' except in AHL and the enzyme X. We owe you an explanation to these decisions, but I'm too lazy to do it. I assigned this task to Chen, and he wrote this assay. I want to stress that we don't claim to make the decision for all the team and our statement isn't the last word, but we think we understand the subject better than we did when we disputed about issue at the time. If you have any questions, you are welcome to contact me or Chen.

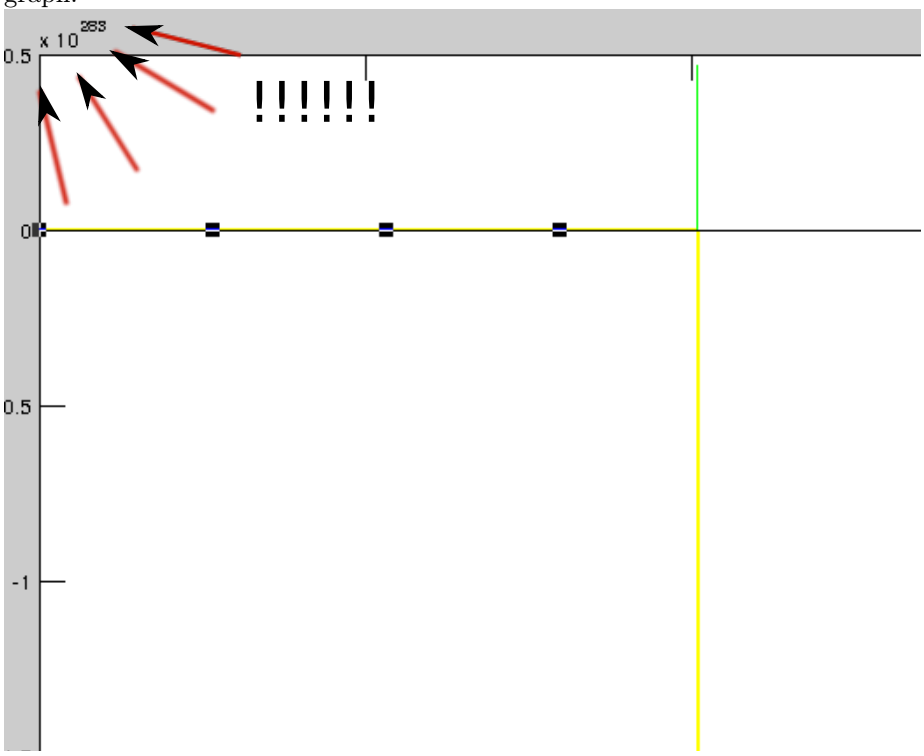
2. Diffusion: I'll elaborate just one aspect of our decision, which is ditching $AHL_{out}$in favour of $AHL_{in}$. Of all the materials in the cell, AHL is the only one that moves freely between cells' inside and outside. It's the only material that its out-y thing is worth speaking of. Lets describe the process hereby: We put a certain amount of AHL, say $A_0$, in a bottle with the bacteria, put it in a refrigerator for some time and then apply it on one's head. The AHL doesn't get immediately into the cells, like we have assumed hitherto, because it's not how nature works. It enters them in a slow process, presumably diffusion. I don't know what's the rate of diffusion under low temperatures and whether we can assume by the time

of the aforementioned application all the AHL that can get into the cells have already done it. Anyway, we definitely can't assume that all the AHL we put reach the cells, again because that's not how nature works. We can hope that the amount that gets into the cells is propositional to the amount we've put, and that's what we're going to do for now. In fact, we are going to assume: $AHL_{in}(t = 0) = A_0/N_0$. Otherwise, we can toy around with diffusion equations, but I wouldn't recommend it to my worst enemies.

3. We talked about the differences in the description of the kinetics between us and the former IGEMs, especially regarding the reaction [LA+LA->LA2]. We decided that the inconsistency between the past IGEMs (that has been described in the document 'problems') shows that they didn't know what they were doing, and we shouldn't trust them. We'll keep using our model to describe the processes.

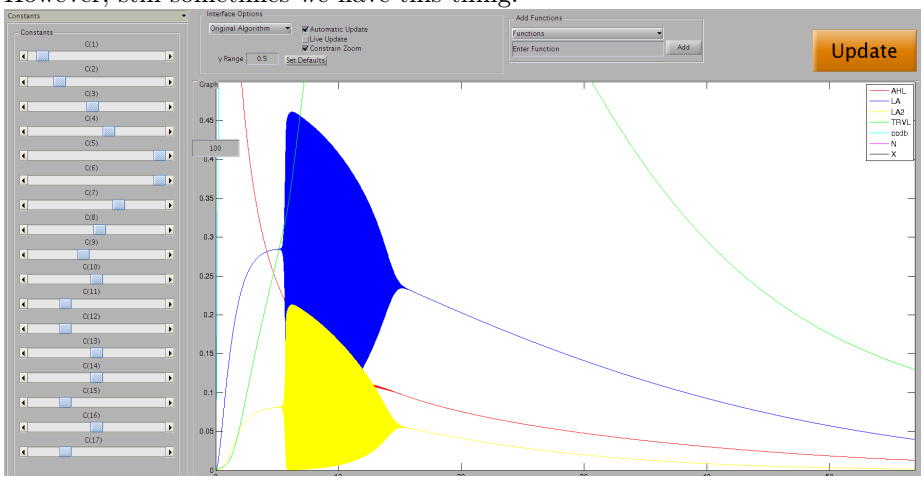
4. We still need to understand better what TRLV is and how the transcription happens, but apparently our model is pretty accurate anyway,

5. And Another Mistake: in the aforementioned document ('problems'), I mentioned that the matlab programme still diverges pretty often, both in my algorithm and in Matlab's. As I've already said few times, the strange bit about it is the fact the mass in the system isn't conserved, like in this graph:



So, while we were talking about kinetics we noticed that there is a mistake in our first equation, in which we forgot to take into account that the formation of LA reduces the amount of free AHL. That adds a term to the first equation. After updating the equations and the programme accordingly there aren't more divergences for any input. Wohoo!

6. However, still sometimes we have this thing:




Yeah. I'd not be too worried about it, because it happens only for a very certain parameters and is apparently programmatic bug somewhere in my algorithm (in Matlab's algorithm it doesn't happen). Anyway, you must admit that it looks interesting. I'll check it sometime.

7. If I've already deviated from the topic, I'll mention here that there is a new version of the programme in Drive here. You can see it in all its glory above. The change log is available here.

After that, we went to the library and tried SimBiology. It's nice and all, but not a game-changer. I started implementing our algorithm using it anyway, but it's going to take some time because the computers in that library are super slow.

## Future Research

We need to decide what we're going to do now. There are no planned marathons on the horizon. We can set a marathon before the urgent meeting Tal and Ealeal arranged on Monday the 13th of April. Anyway, we need to decide regarding a work plan. Here is my suggestion: We should assign for each sub-team a team leader, who will be in charge for arranging team's meetings, appoiting tasks for team members and reporting on their progress to the rest of the team. What do you think?