PEPTalk

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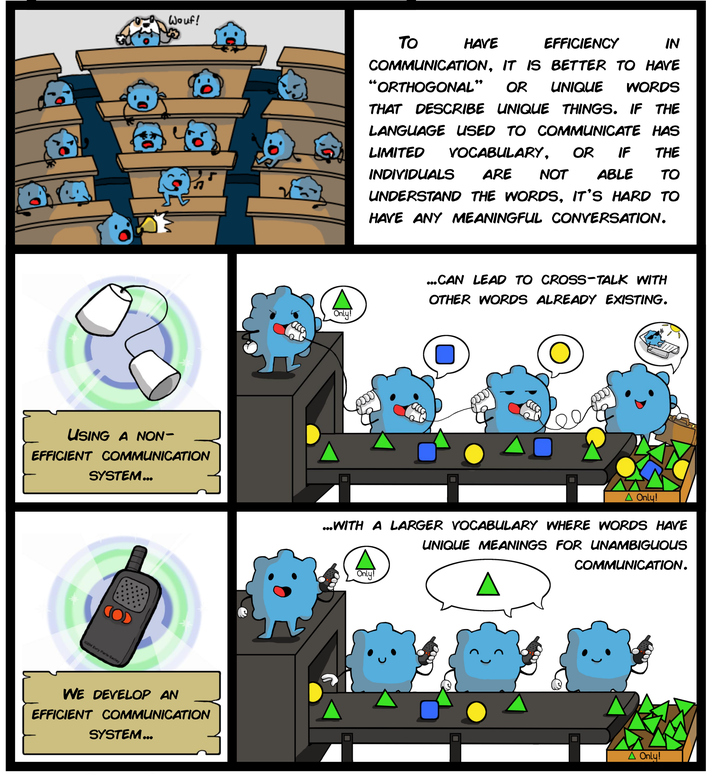
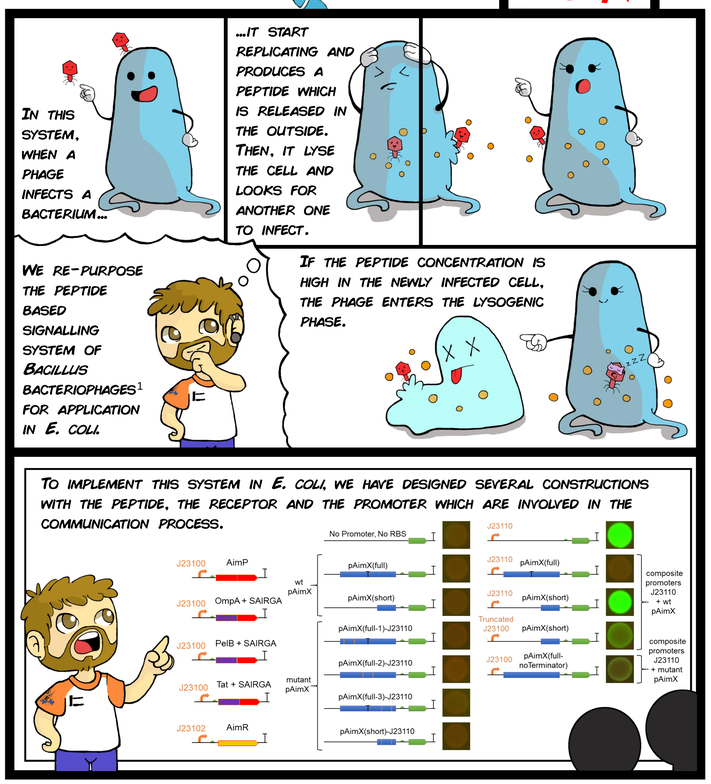
Biological engineering has turned bacteria into biosensors, nano-robots and production factories. As these applications are organised for higher-level tasks, multiple different bacteria will be needed to work in a consortium each with their own assigned sub-task. However, such division of labour can only be efficient if the bacteria can communicate with each other using unambiguous language. The aim of our project is to build a synthetic communication system with an expandable peptide vocabulary so that bacteria can send different and specific signals to communicate different things.

Communication is Key



Design



Results

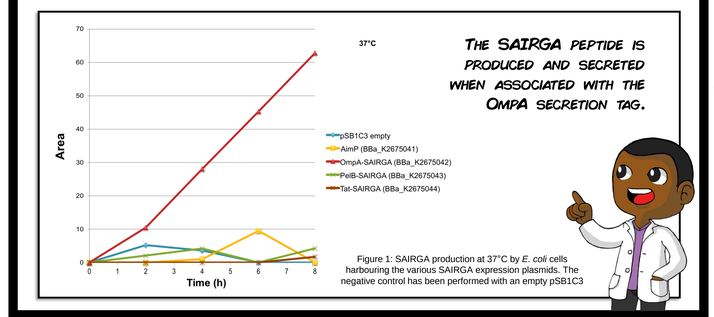


Figure 1: SAIRGA production at 37°C by *E. coli* cells harbouring the various SAIRGA expression plasmids. The negative control has been performed with an empty pSB1C3

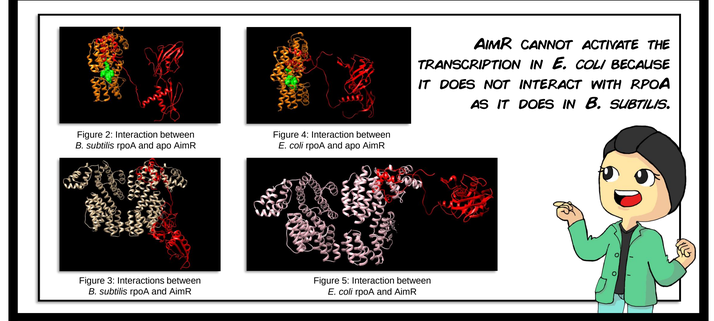


Figure 2: Interaction between *B. subtilis* rpoA and apo AimR

Figure 4: Interaction between *E. coli* rpoA and apo AimR

Figure 3: Interactions between *B. subtilis* rpoA and AimR

Figure 5: Interaction between *E. coli* rpoA and AimR

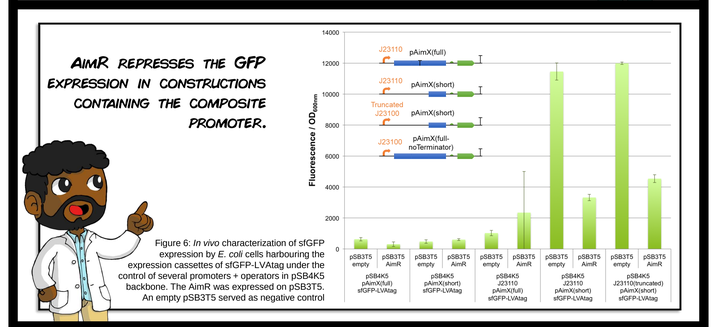


Figure 6: *In vivo* characterization of sfGFP expression by *E. coli* cells harbouring the expression cassettes of sfGFP-LVAtag under the control of several promoters + operators in pSB4K5 backbone. The AimR was expressed on pSB3T5. An empty pSB3T5 served as negative control

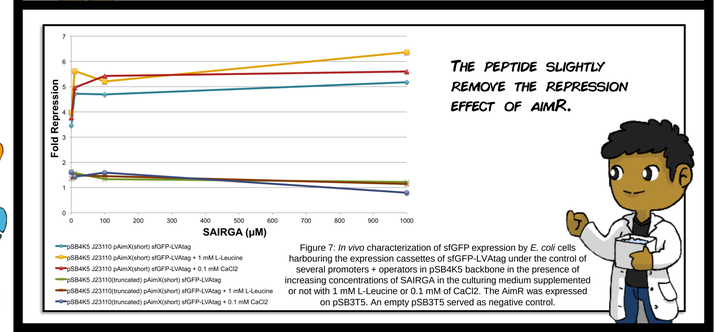


Figure 7: *In vivo* characterization of sfGFP expression by *E. coli* cells harbouring the expression cassettes of sfGFP-LVAtag under the control of several promoters + operators in pSB4K5 backbone in the presence of increasing concentrations of SAIRGA in the culturing medium supplemented or not with 1 mM L-Leucine or 0.1 mM of CaCl2. The AimR was expressed on pSB3T5. An empty pSB3T5 served as negative control.

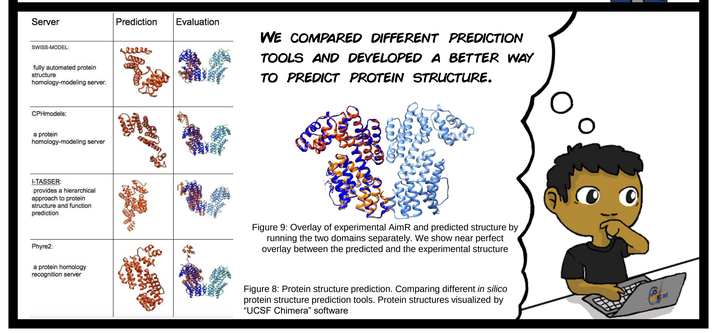
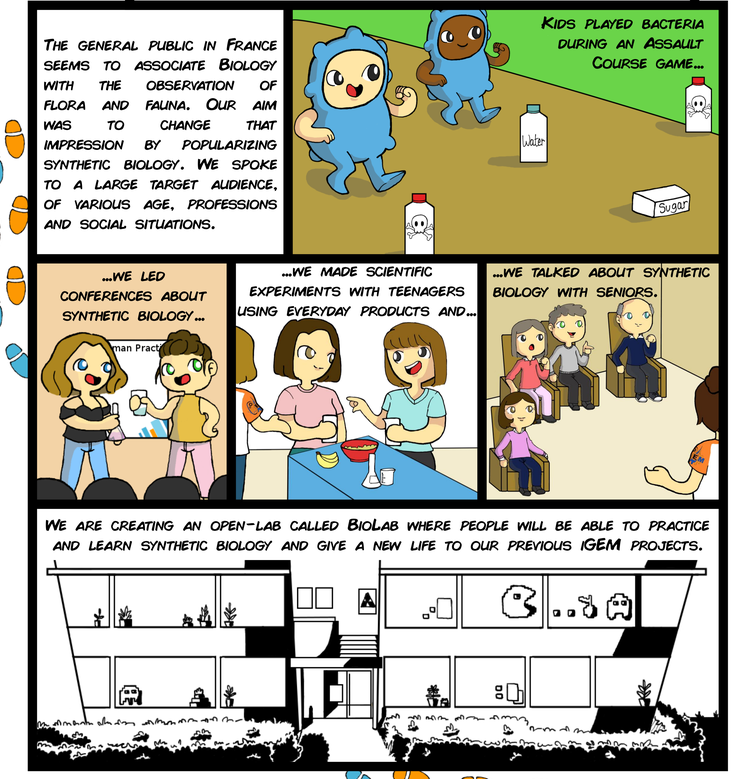


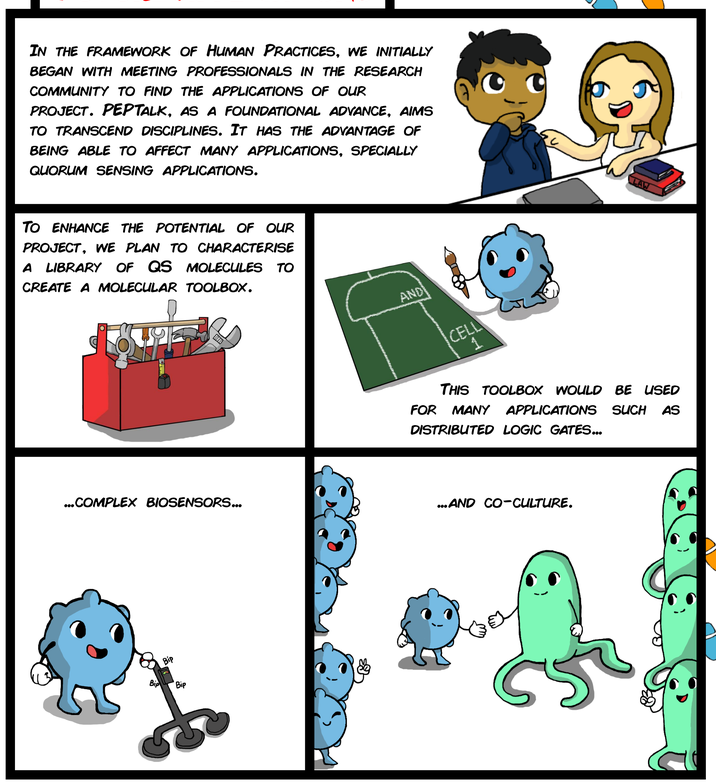
Figure 9: Overlay of experimental AimR and predicted structure by running the two domains separately. We show near perfect overlay between the predicted and the experimental structure

Figure 8: Protein structure prediction. Comparing different *in silico* protein structure prediction tools. Protein structures visualized by "UCSF Chimera" software

Education and Public Engagement



Future Applications



[1] Erez et al., Nature (2017) 541, 488-493.