











Escherichia coli-based physical reservoir computing: potential and applications

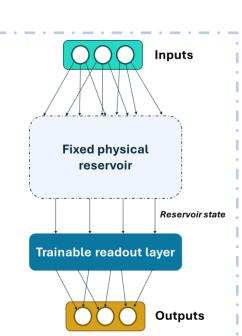
BioRetroSynth and Ekinocs teams

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Context

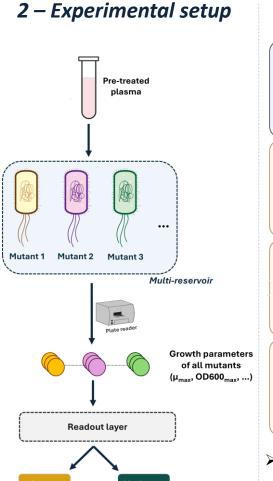
- Computation using bacteria has mostly relied on synthetic circuits since the early days of synthetic biology
- These circuits allowed to implement relatively complex functions in cells but displayed serious limitations [1] restricting the complexity of the tasks they can perform
- Reservoir computing might outperform these circuits
- Jones et al. [2] already used bacteria as reservoirs to solve a XOR problem. Bacteria-based reservoirs exploit the bacterial natural non-linear dynamics to project features from the growth medium to the observable space
- Here, we go further and demonstrate that bacterial metabolism can be used as a reservoir to solve regression and classification machine learning (ML) problems
- To showcase some potential applications of this new biocomputing method, an Escherichia coli multi-reservoir will be constructed to perform prognosis on COVID-19 infected patients

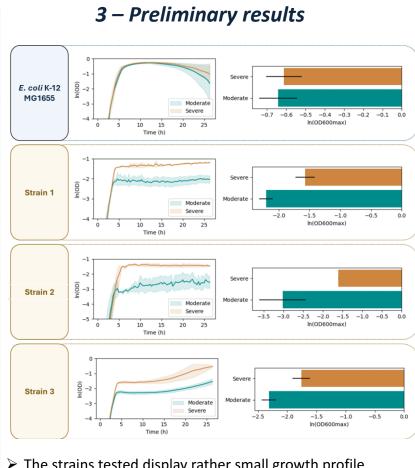


Resolution of machine learning problems 1 – Framework presentation White Vine quality prediction (regression problem) DensitypHSulfatesglucose | inorganic phosphate 0.99563.13 0.9956 0.43E.coli C_1 Output: C_2 Note on 10 Inputs: Trainable or layer C_p Translating machine learning problem into growth condition vector Trained AMN: weights have been frozen after training on experimental data Proxy of E. coli's behavior

3 – Assessing the contribution 2 – Benchmark with other ML methods of the bacteria **Ablation:** 0.8 Ablation: replace bacteria by a linear combination of C elements 0.0 **Substitution:** Linear Reg The AMN-based reservoir outperforms linear methods, but is still less performant than XGBoost Substitute to bacteria non-trainable NN

Application: prediction of COVID-19 severity 1 – Construction of the reservoir Predicted growth COVID-19 patients Strain 1 (\triangle gene1, \triangle gene2, \triangle gene3, \triangle g Strain 2 (∆gene5, ∆gene6) ••• Predicted growth Strain 3 (∆gene7, ∆gene8, ∆gene9 rates on both plasma soon-to-be severe COVID-19 patients differences between the 2 categories of deletion C Mass spectrometry signals Media nding to *E. coli* entry Predicted growth





- The strains tested display rather small growth profile differences when grown on the 2 categories of plasma
- > But all together, they might create a more powerful classifier

Take-home messages

- A reservoir based on bacterial metabolism can perform complex computational tasks (solve ML problems) at low cost for the cell (no circuit constructed) in an easy-to-use framework
- Combining the unique features of living systems with physical reservoir computing could have potential applications in diagnostics and prognosis

References

[1] Meyer, A.J., Segall-Shapiro, T.H., Glassey, E. et al. Escherichia coli "Marionette" strains with 12 highly optimized small-molecule sensors. Nat Chem Biol 15, 196-204 (2019). https://doi.org/10.1038/s41589-018-0168-3

[2] Jones, B., Stekel, D., Rowe, J., Fernando, C., 2007. Is there a Liquid State Machine in the Bacterium Escherichia Coli?, in: 2007 IEEE Symposium on Artificial Life. Presented at the 2007 IEEE Symposium on Artificial Life, pp. 187–191 https://doi.org/10.1109/ALIFE.2007.367795







