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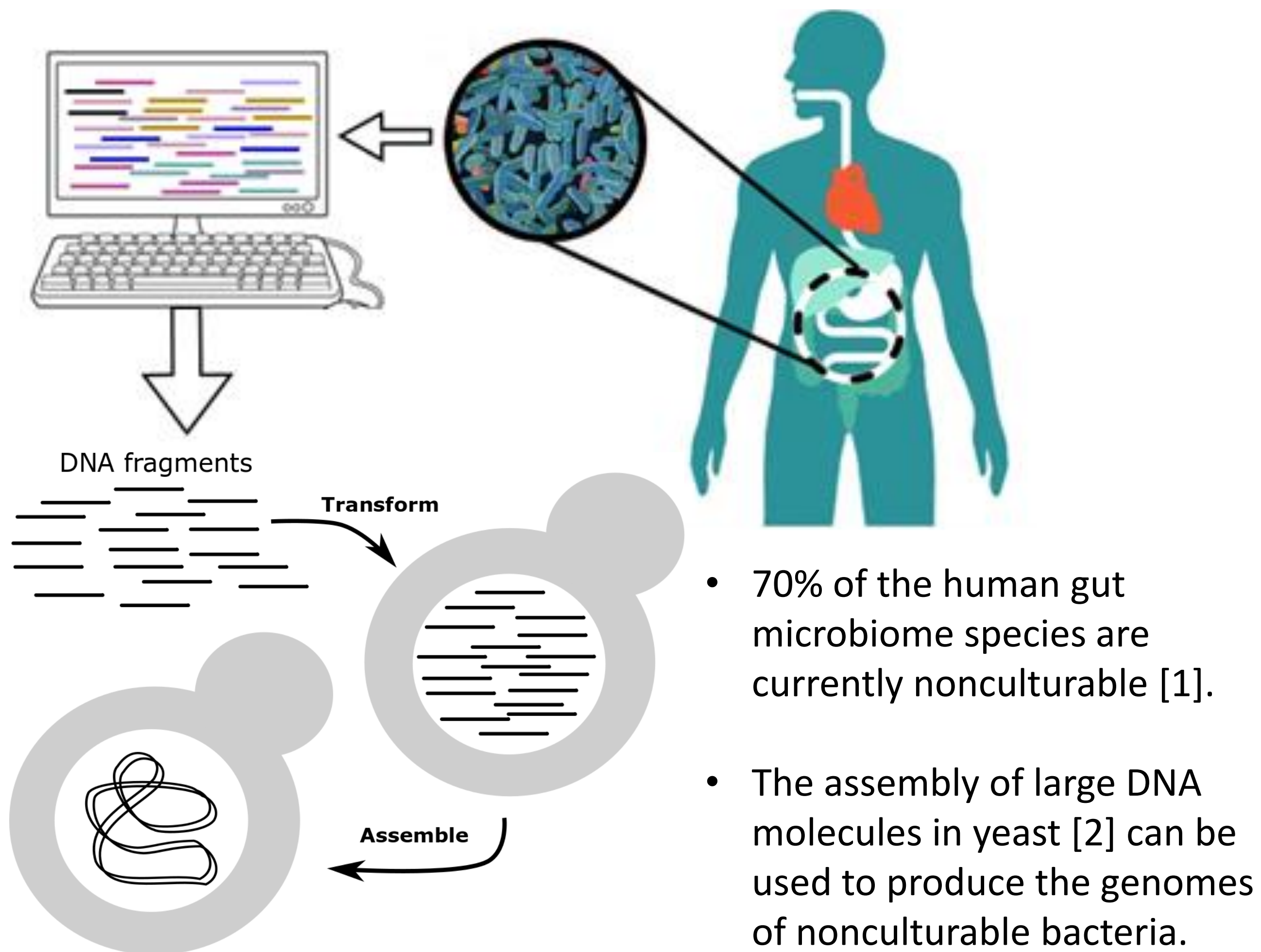
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Exploration of the transcriptional landscapes of culturable and nonculturable bacteria using *in vitro* transcription emulators

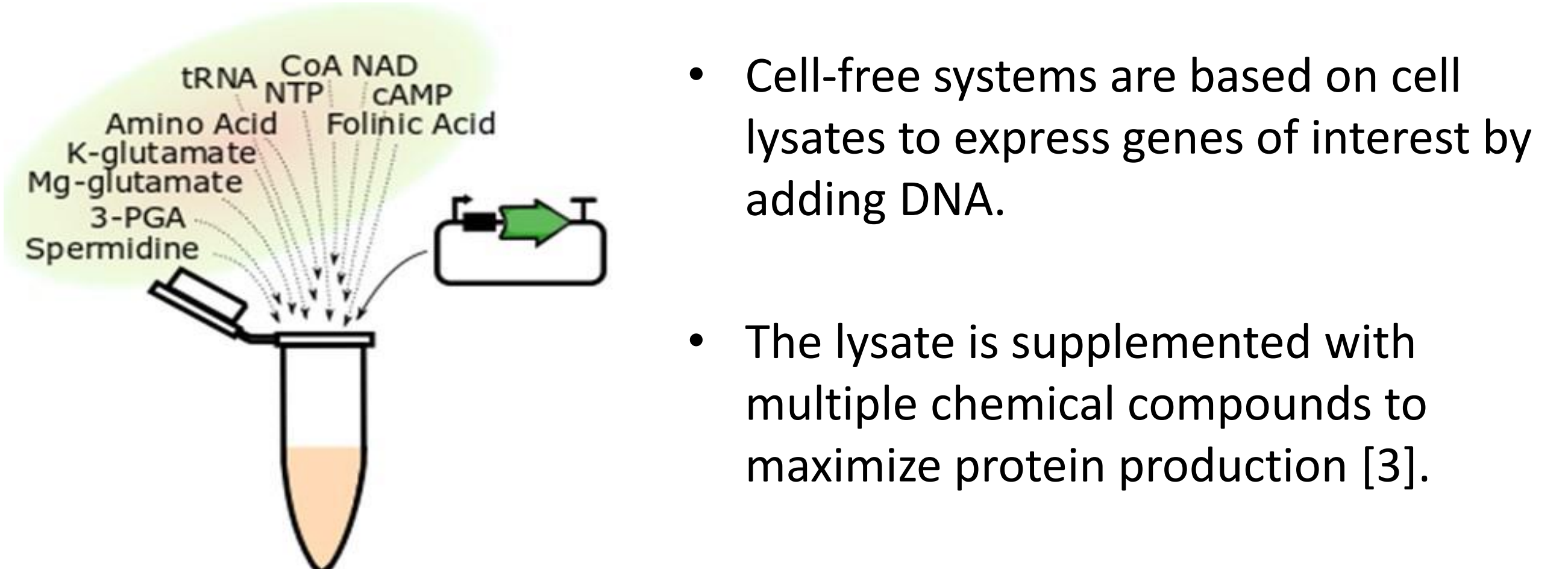
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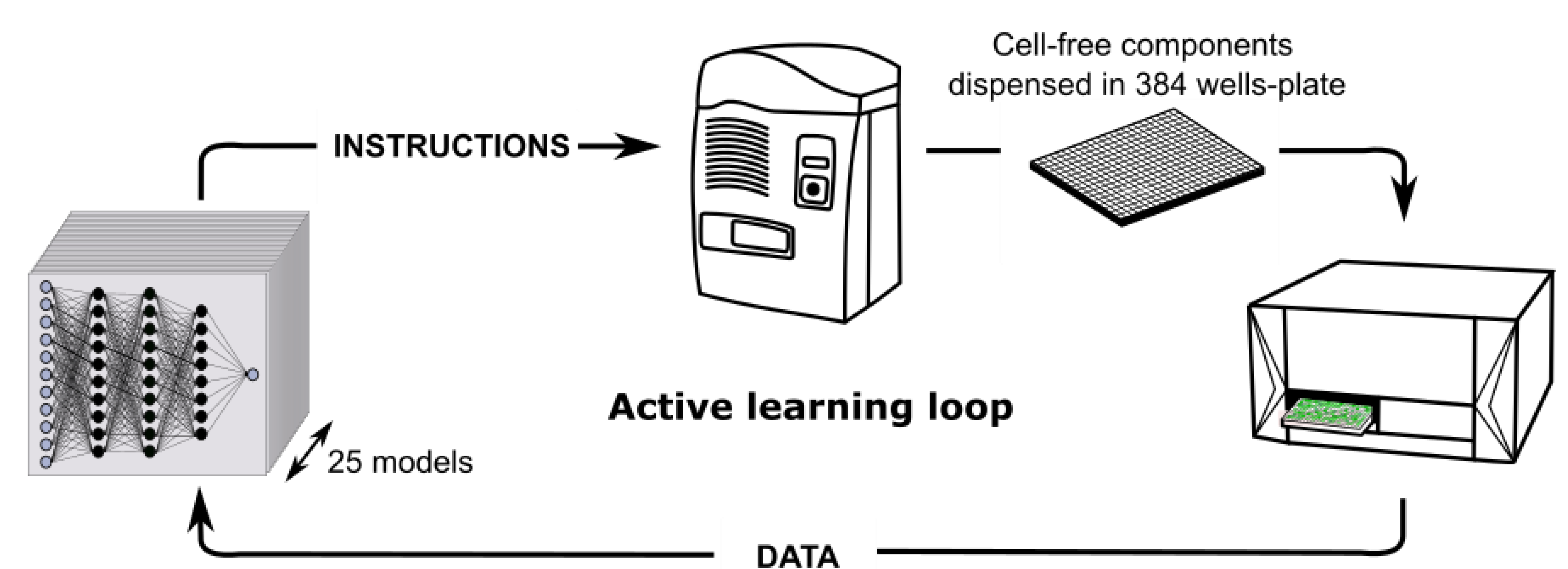
Background: Human gut microbiome



Background: cell-free systems

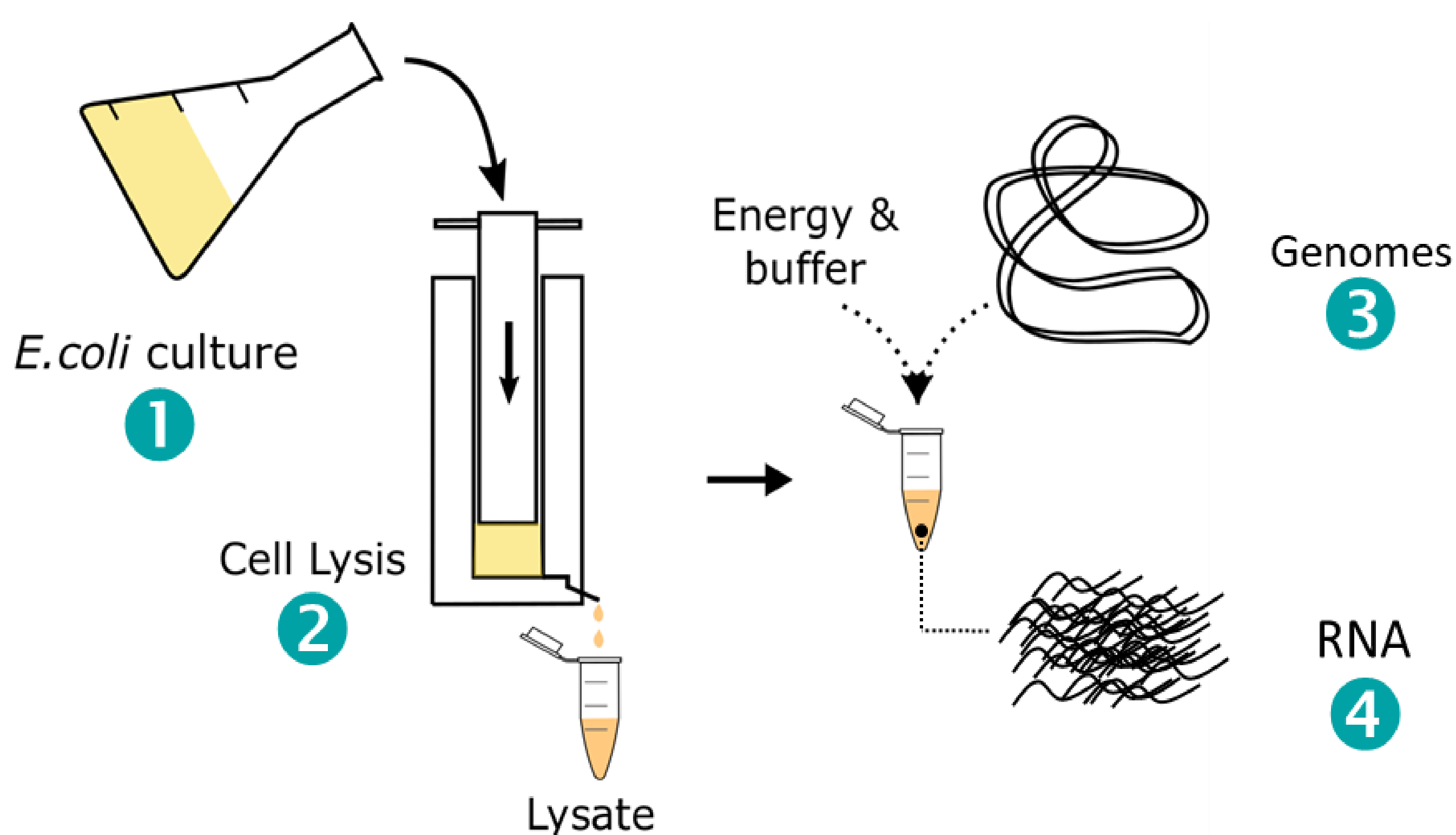


Active learning for cell-free optimization

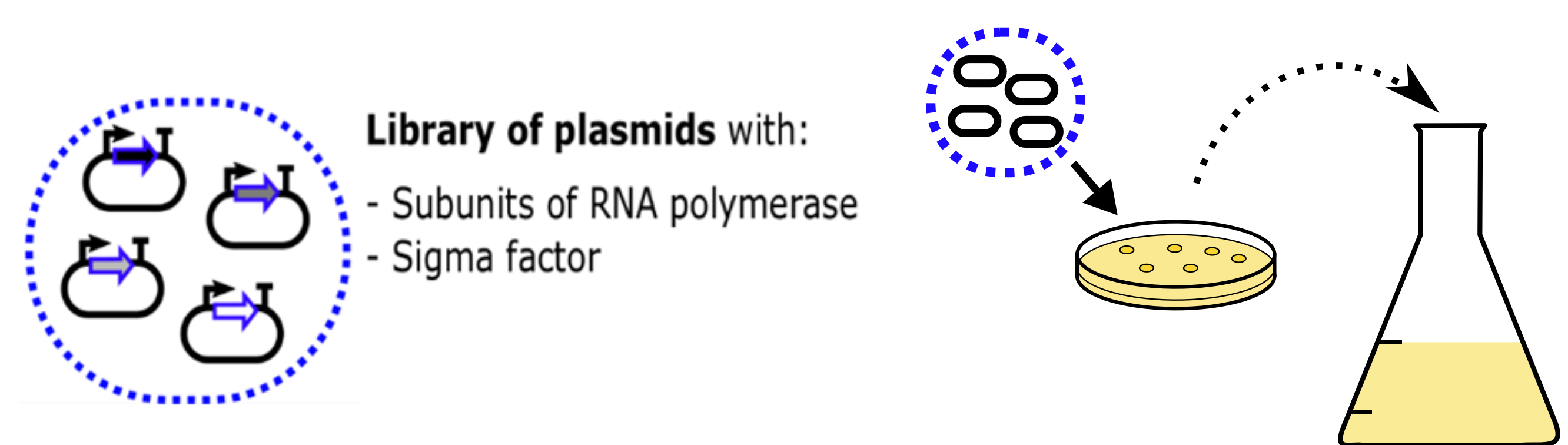


- A machine learning approach coupled with a liquid-handling robot has been used to maximize protein production in cell-free [4].
- RNA production can also be maximized by exploring a combinatorial space of ~1,000,000 cell-free compositions.

Genome expression in cell-free

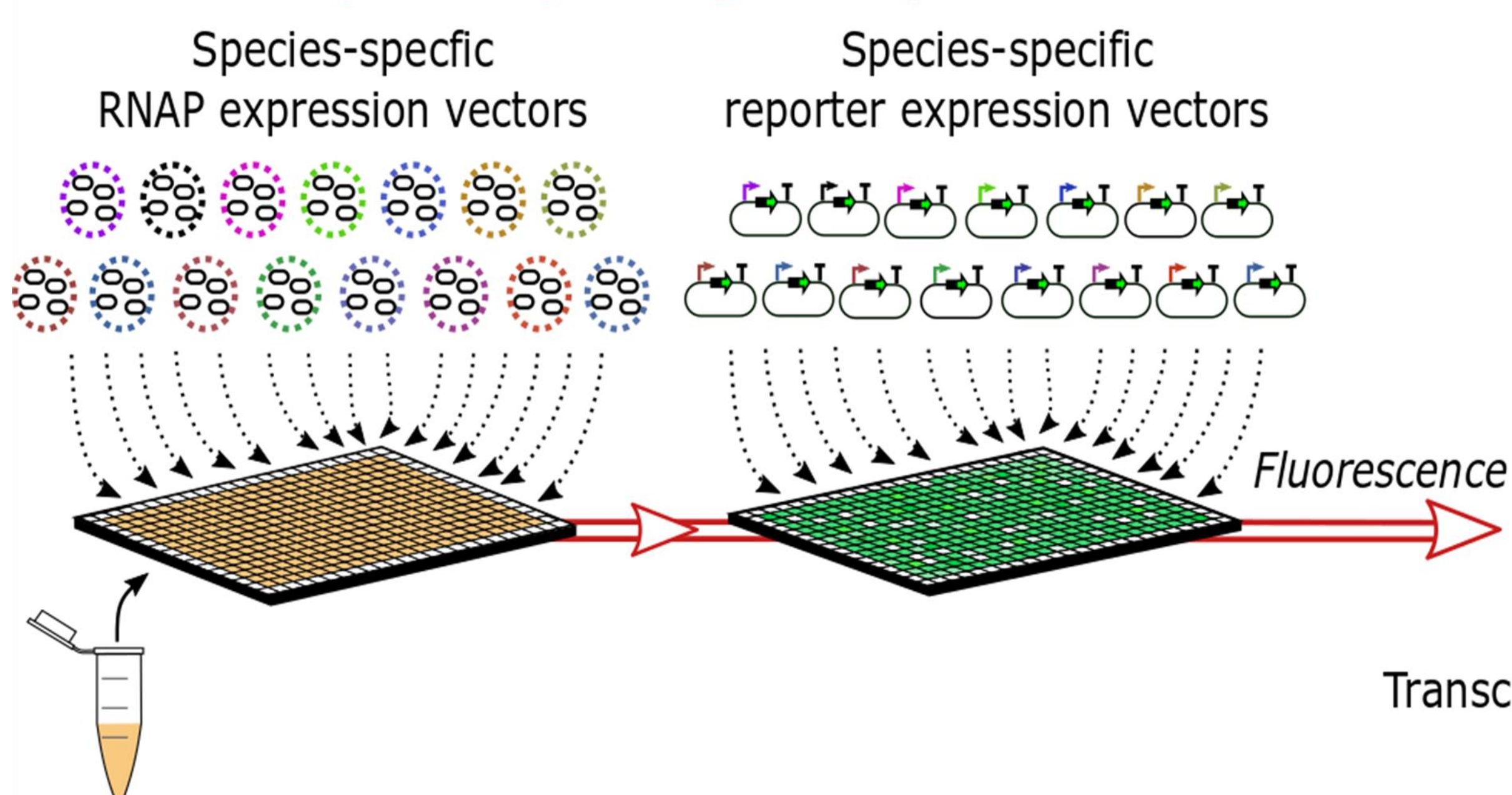


Production of RNAP from nonculturable bacteria

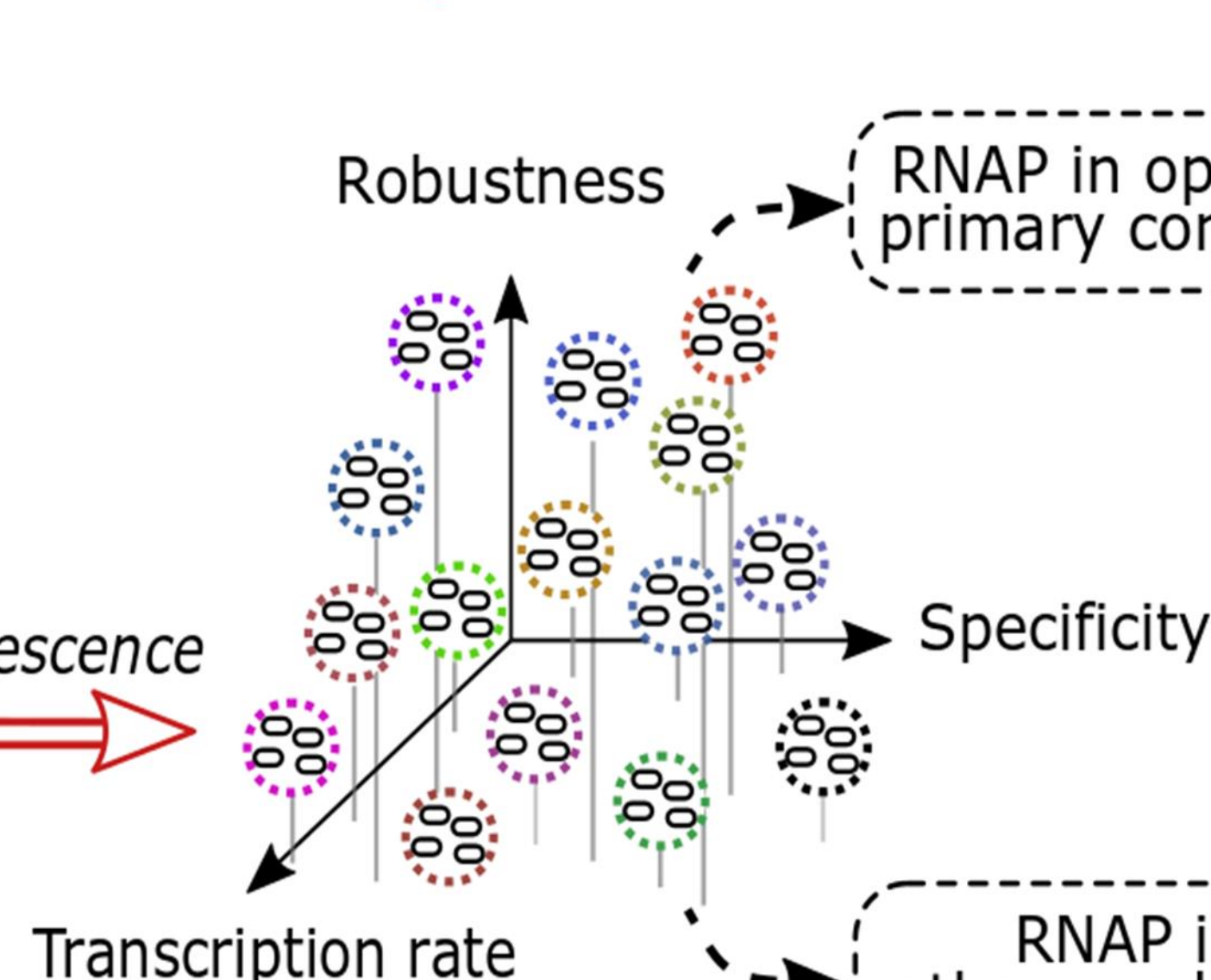


Research objectives of the project

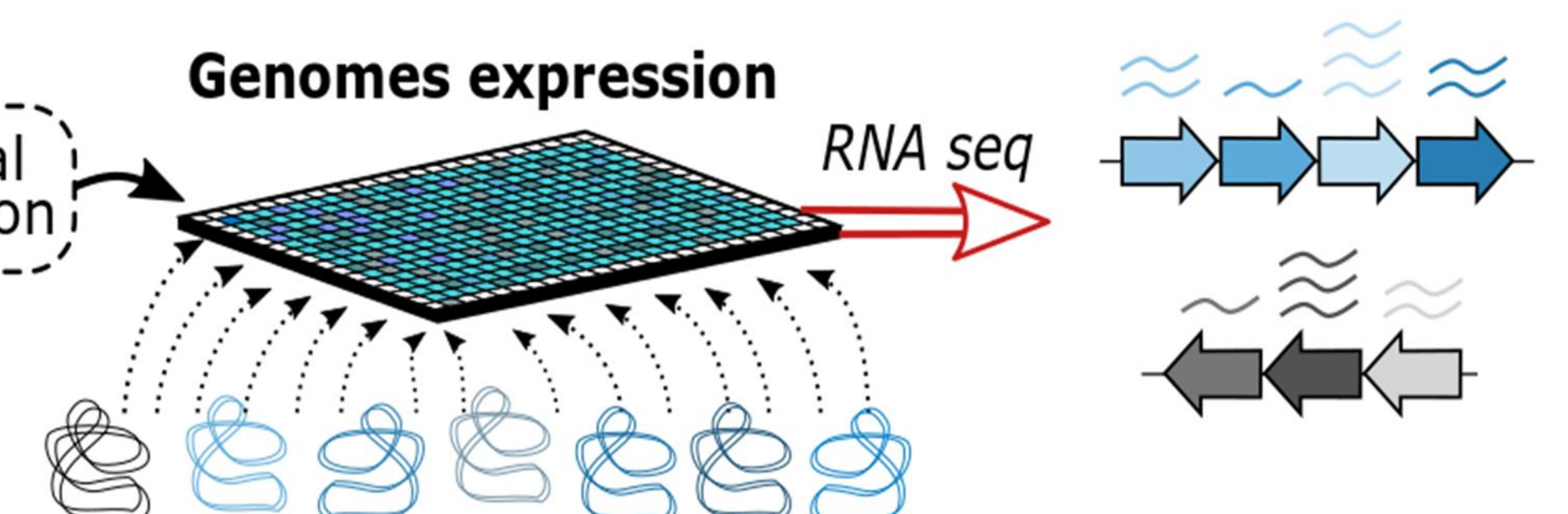
RO1. Development of an *in vitro* platform for species-specific gene expression



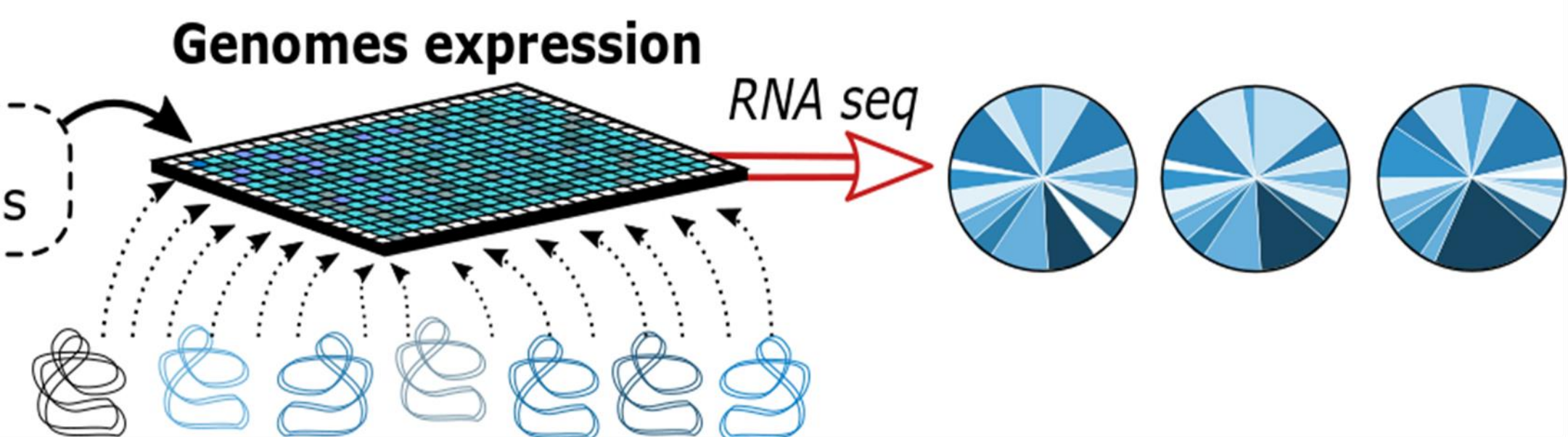
RO2. Characterization of transcription machineries



RO3. Identification of new transcription units and regulatory sequences



RO4. Analysis of transcriptome reorganisation in different conditions



- What are the full transcriptional landscapes of nonculturable bacteria of the human gut?
- To what extent nonculturable bacteria in the human gut can reorganize their genomes activity?
- Which regulations and molecular mechanisms are involved in such reorganization?

References

1. Almeida, A. et al., 2021. A unified catalog of 204,938 reference genomes from the human gut microbiome. *Nature biotechnology*, 39(1), pp.105-114.
2. Gibson, D.G., et al., 2008. One-step assembly in yeast of 25 overlapping DNA fragments to form a complete synthetic *Mycoplasma genitalium* genome. *Proceedings of the National Academy of Sciences*, 105(51), pp.20404-20409.
3. Sun, Z.Z. et al., 2013. Protocols for implementing an *Escherichia coli* based TX-TL cell-free expression system for synthetic biology. *JoVE (Journal of Visualized Experiments)*, (79), p.e50762.
4. Borkowski, O. et al., 2020. Large scale active-learning-guided exploration for *in vitro* protein production optimization. *Nature communications*, 11(1), p.1872.