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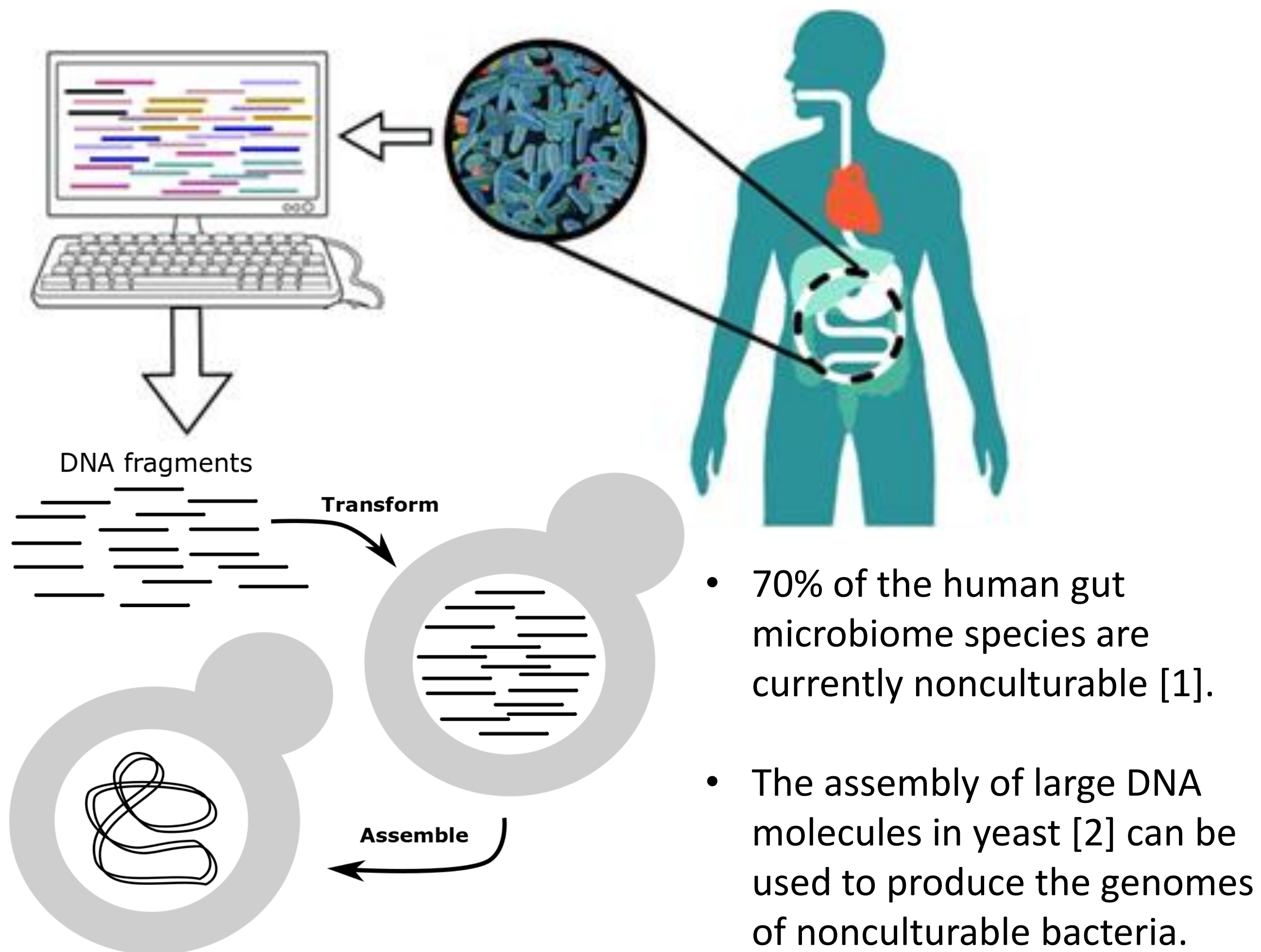
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Exploration of the transcriptional landscapes of culturable and nonculturable bacteria using *in vitro* transcription emulators

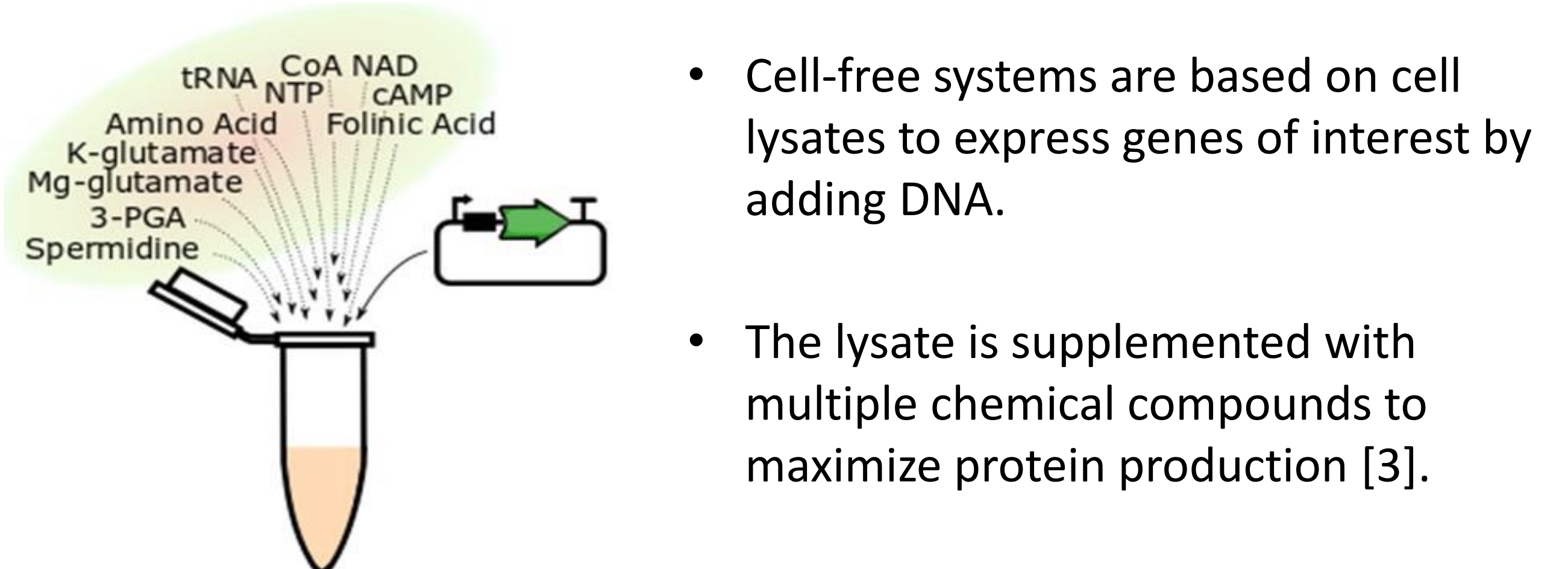
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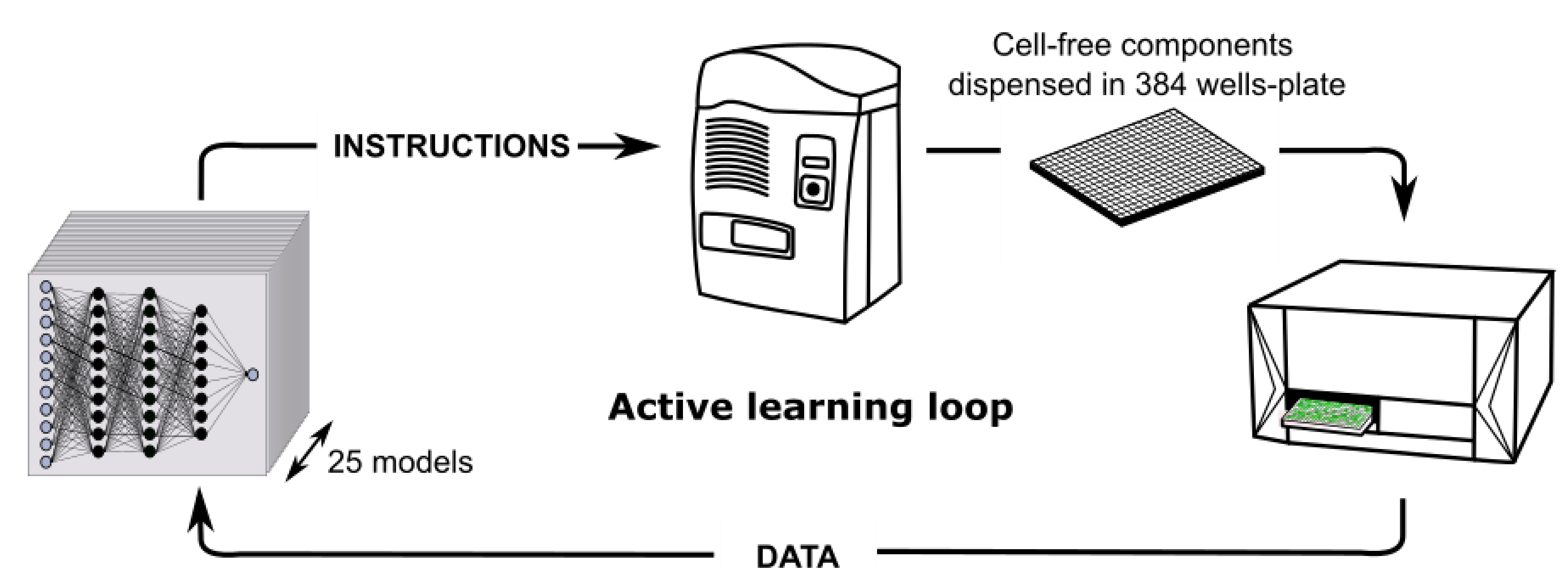
Background: Human gut microbiome



Background: cell-free systems

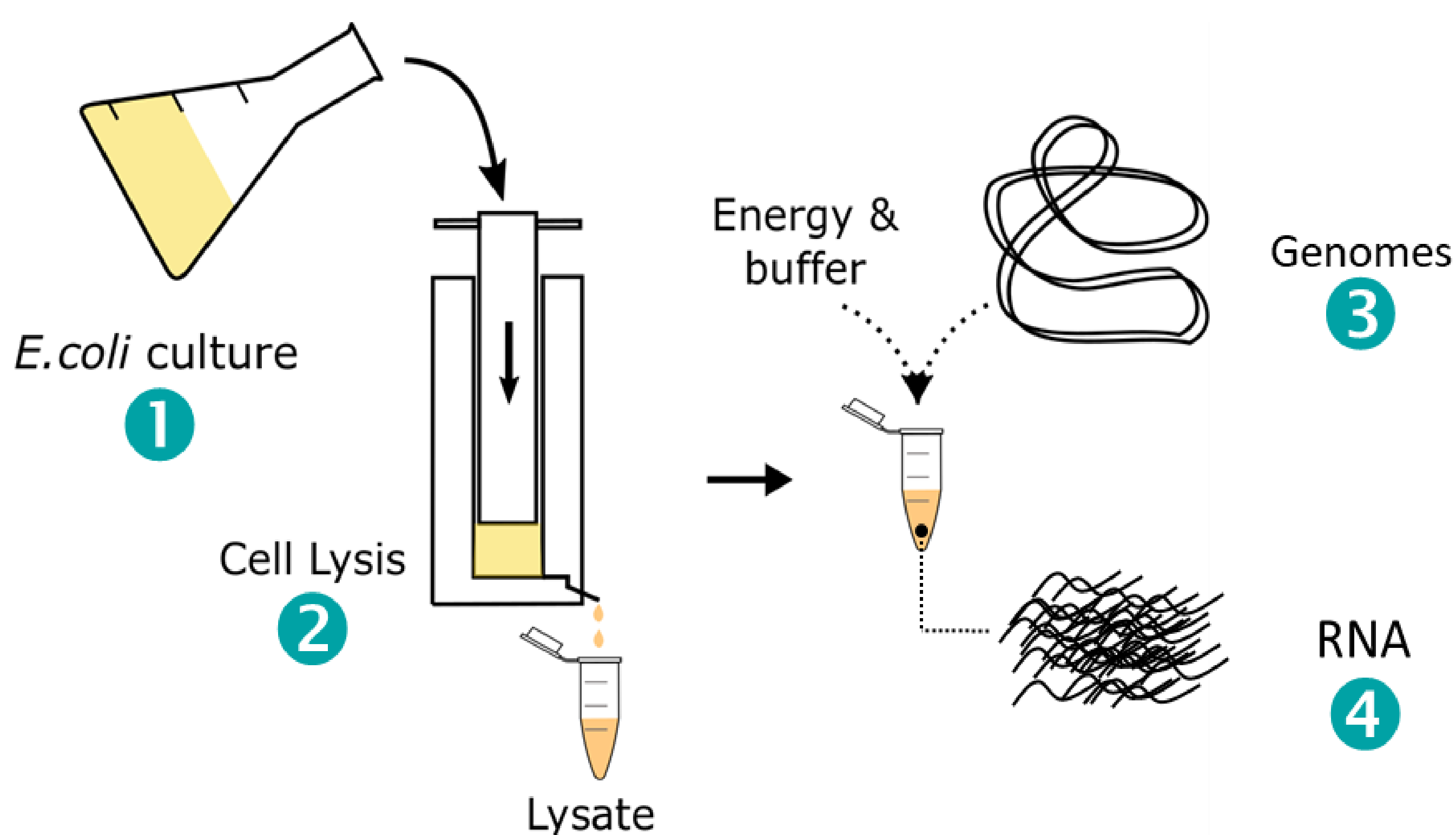


Active learning for cell-free optimization

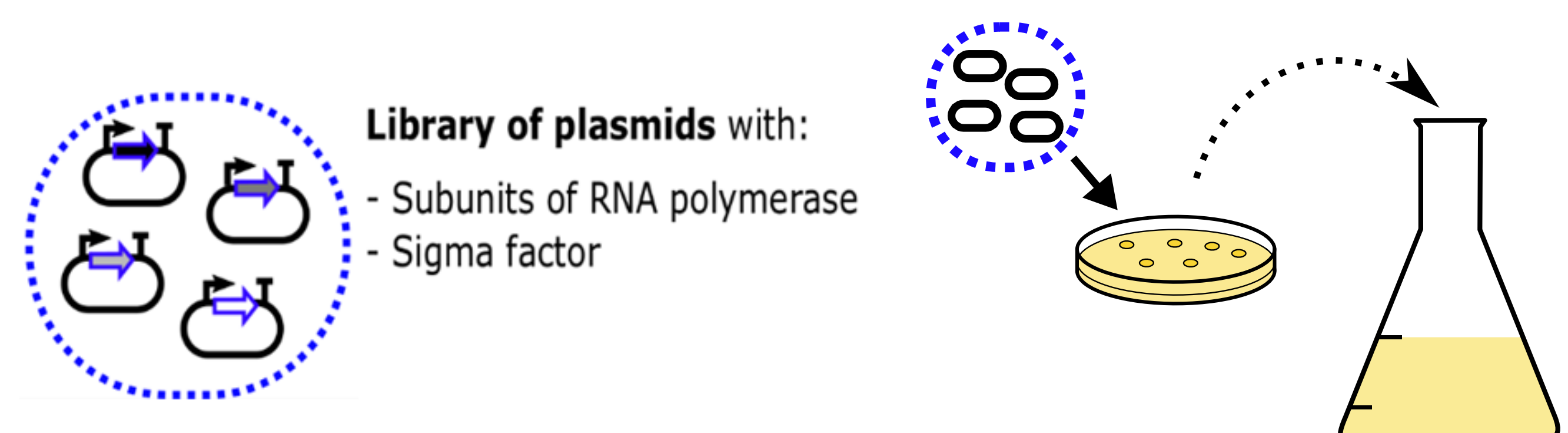


- A machine learning approach coupled with a liquid-handling robot has been used to maximize protein production in cell-free [4].
- RNA production can also be maximized by exploring a combinatorial space of ~1,000,000 cell-free compositions.

Genome expression in cell-free

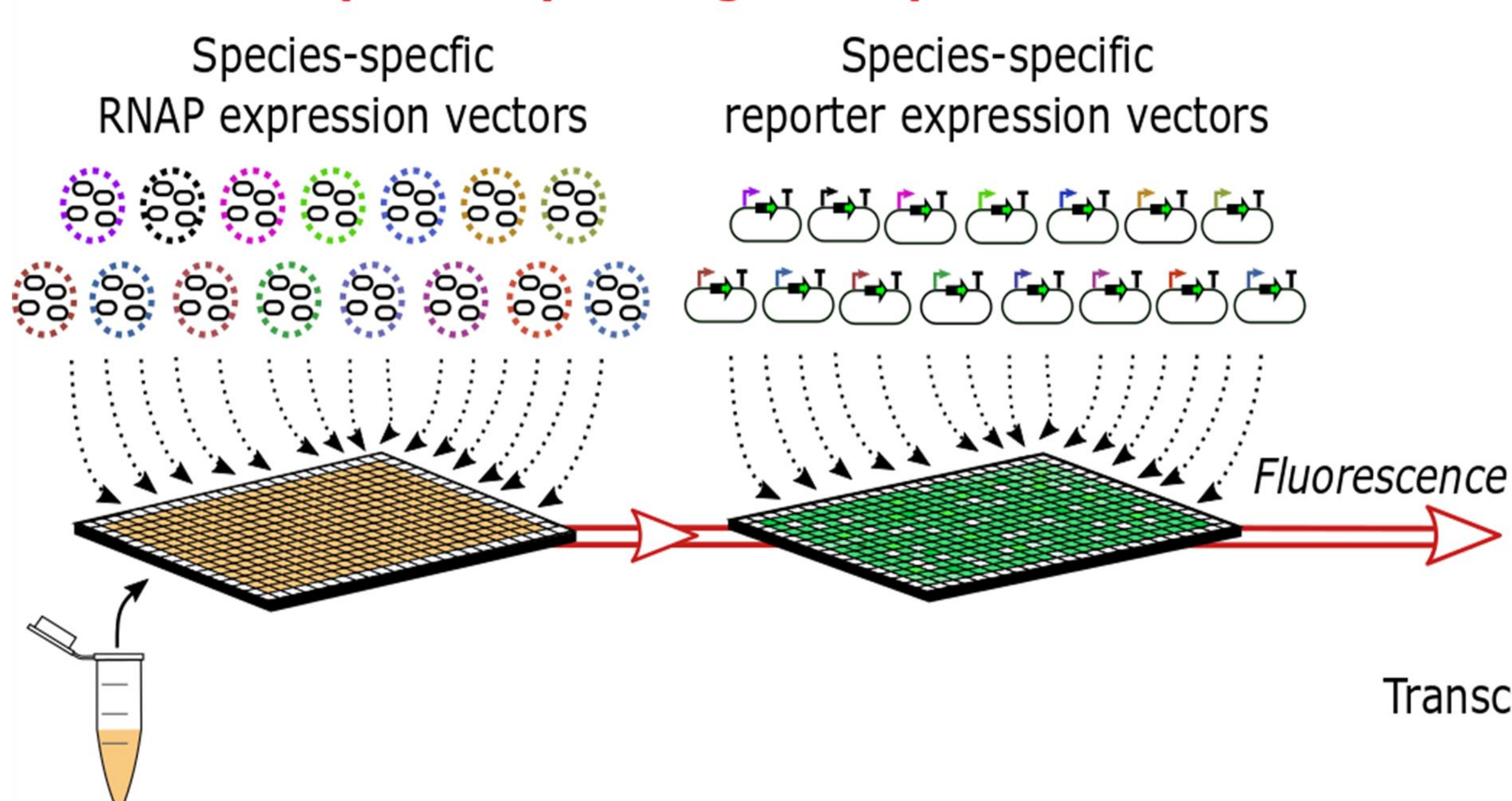


Production of RNAP from nonculturable bacteria

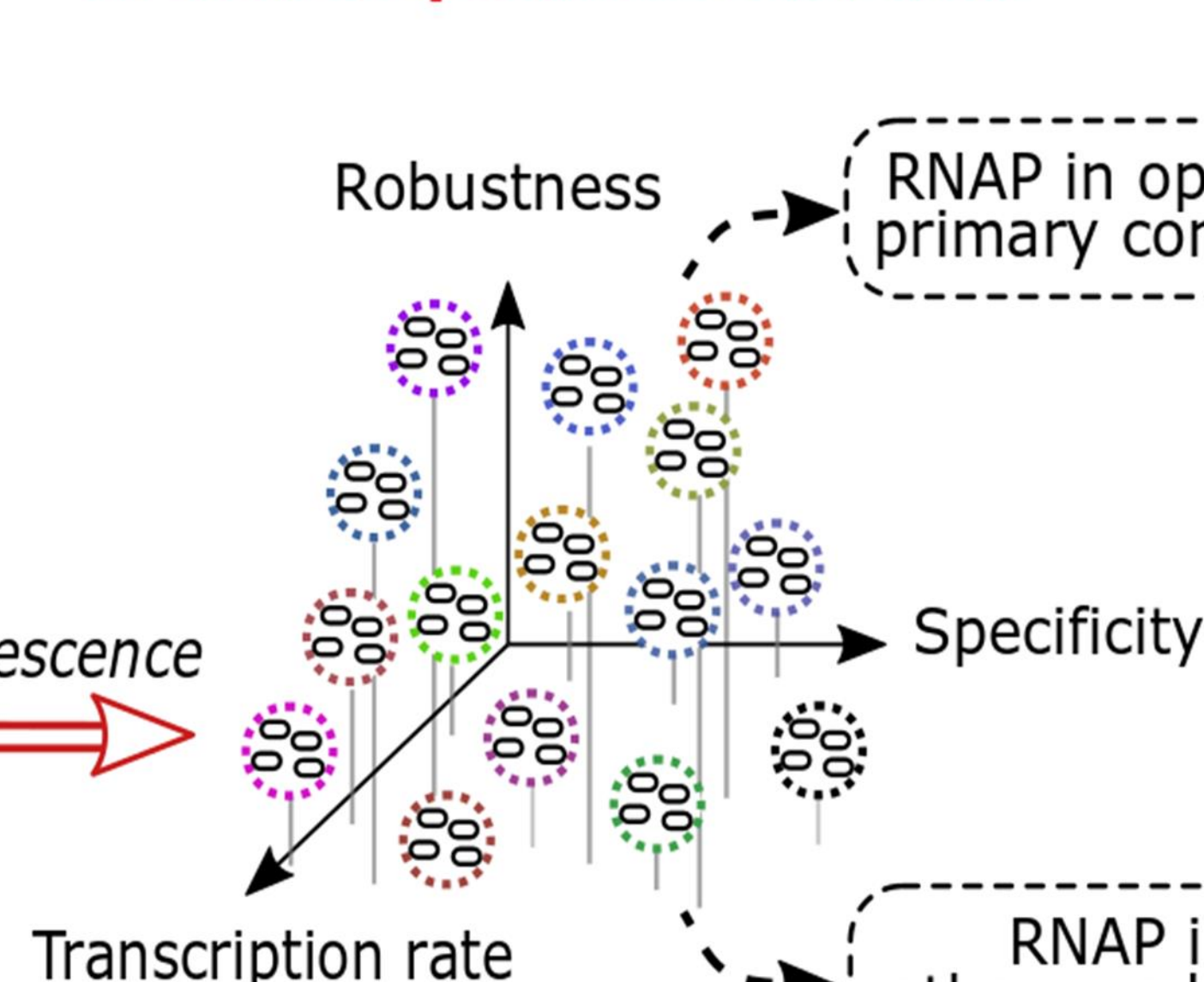


Research objectives of the project

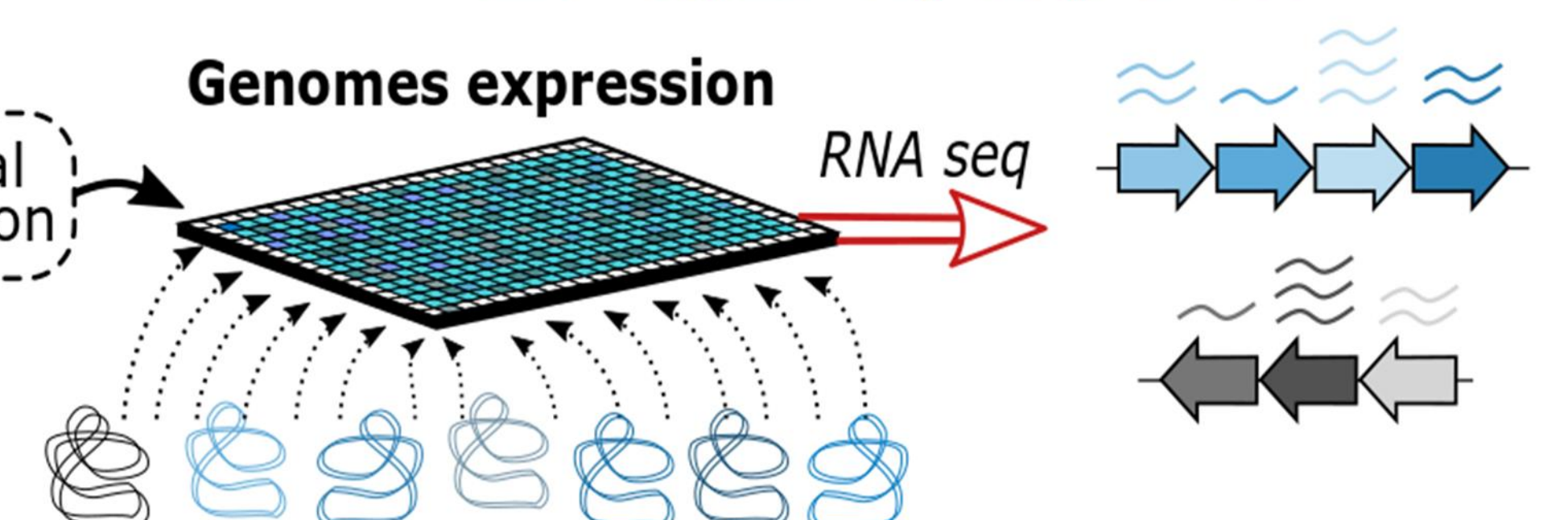
RO1. Development of an *in vitro* platform for species-specific gene expression



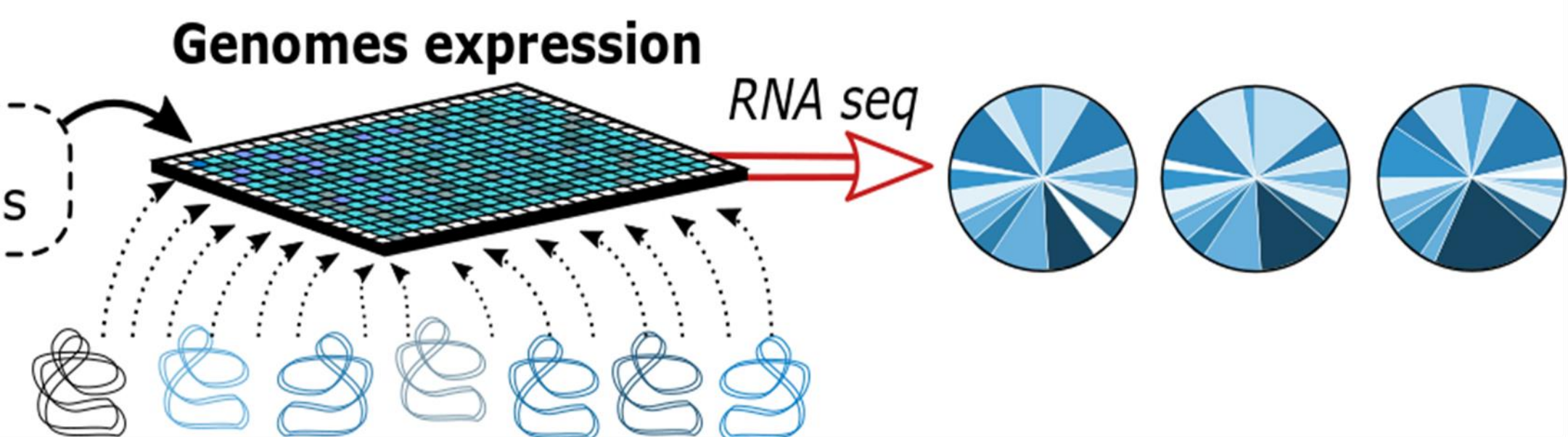
RO2. Characterization of transcription machineries



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

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