Towards appropriate environmental assessment of DNA technologies: from abstract comparisons to life-cycle approach

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Abstract

The interest of DNA-mediated technologies for information technologies is often justified by their potential environmental advantages compared to silicon-based computing, based on higher operating energy efficiency (10^9 vs. $2 \cdot 10^{19}$ operations per Joule), information storage density (10^3 vs. 10^{-9} µm^3 required per bit), and long-term expected stability (Liao et al. 2020, Shu et al. 2023, Xu et al. 2025). However, there is currently no proper environmental assessment of DNA computing in the literature, apart from a conference paper with little transparency (Nguyen et al. 2020).

The CalcADN project aims to design the first fully DNA-mediated computer capable of large-scale computations within a generic framework, mobilizing enzyme reactions (CNRS, 2025). One part of the project is to provide the first rigorous and transparent environmental assessment of this technology, using a life-cycle approach. Environmental life-cycle assessment (LCA) is a quantitative method to assess the environmental impacts of any system/product/service. It is multi-criteria (climate change, mineral resources and water use, toxicity and ecotoxicity, etc.) and encompasses all life-cycle stages (from raw materials extraction to end-of-life), preventing both burden shifting and blind spots. Even though it is more adequately applied to established technologies, for which data is more reliable, prospective LCA for emerging technologies is particularly insightful to guide technological developments (Caldeira et al. 2024, Woods-Robinson et al. 2025). This strategy is thus explicitly recommended by the Safe & Sustainable by Design (SSbD) framework, pushed by the European Commission (EU, 2022).

Here, we present first results regarding life-cycle environmental impacts representative of typical DNA computations, like resolving a space partitioning problem or an arborescence querying (Okumura et al. 2022). At the scale of a droplet containing one computation, relative contributions of DNA, dNTP, buffer, reagents and salts are elucidated, hinting at optimization targets regarding dNTP concentration and buffer choice. A preliminary model at the scale of a microfluidic system allows to investigate the role of droplet size and parallelization, computation time, and the associated heat and electricity required.

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