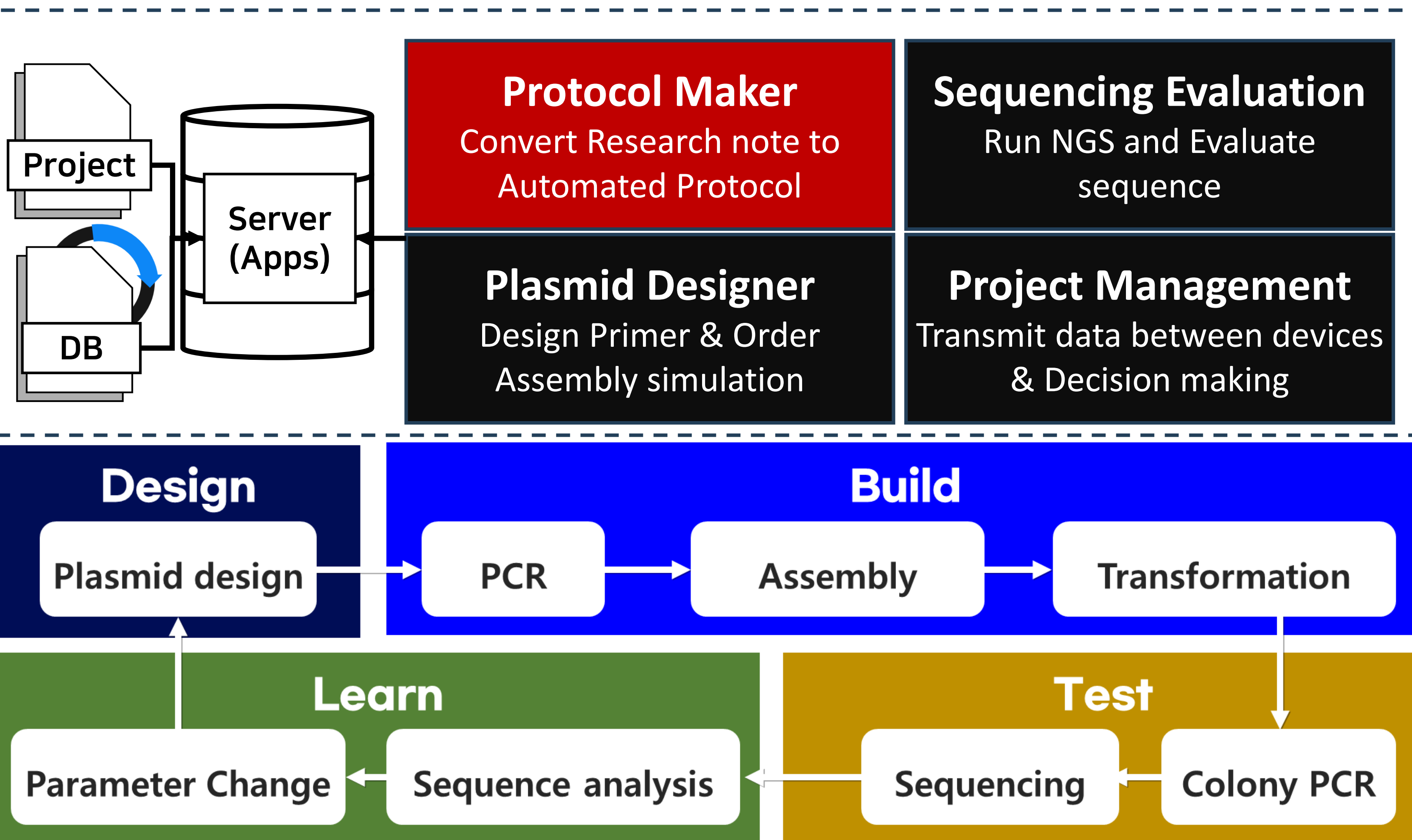# Toward Automated workflows in synthetic biology

Seong-Kun Bak[1,2], Wonjae Seong[1], Aporva Gupta[1], Seung-Goo Lee[1], Haseong Kim[1,2]*

[1] Synthetic Biology and Bioengineering Research Center, Korea Research Institute of Bioscience and Biotechnology (KRIBB), Daejeon 34141, Republic of Korea

[2] Graduate School of Engineering Biology, Korea Advanced Institute of Science and Technology (KAIST), Daejeon 34141, Republic of Korea

Software Structure for Cloning Project

Protocol Maker — Convert Research note to Automated Protocol

Sequencing Evaluation — Run NGS and Evaluate sequence

Plasmid Designer — Design Primer & Order Assembly simulation

Project Management — Transmit data between devices & Decision making

Design: Plasmid design

Build: PCR → Assembly → Transformation

Learn: Parameter Change ← Sequence analysis

Test: Sequencing ← Colony PCR

Abstract

In **biofoundry** construction, people generally concern about automated equipment and its throughput. However, to achieve the ultimate goal of automated and high-throughput biofoundry, digital-based experiment design and integrated data management among the automated devices are essential for prerequisites. Recently reported automation techniques are limited to a specific experiment and lab environment due to the nature of complicated biological experiments.

In this study, we develop a flexible system that **can automatically perform cloning tasks** and introduce how we approached the problems mentioned above.

The system is **modularized with workflows** which are basic experimental protocols such as PCR, Golden gate assembly, Gibson assembly, and transformation. A task can be conducted by combinatorial linking the workflows.

Sample information and the output of each workflow with corresponding equipment are collected into one integrated server so that appropriate parameter values from a workflow are automatically passed to the next step.

Our system provides a web-based tool and a research note format familiar to biologist is available as input. All data is converted to a machine-readable format for the further extension with IT technologies such as large-language models.

Software development pipeline for Biofoundry

Scenarios for Cloning task

(A) Plasmid design → PCR → Assembly → Transformation → Sequencing

(B) UnitProcess / Workflow / Task

(C) Cloning Scenarios → Accepted Scenarios → Variables, Parameters
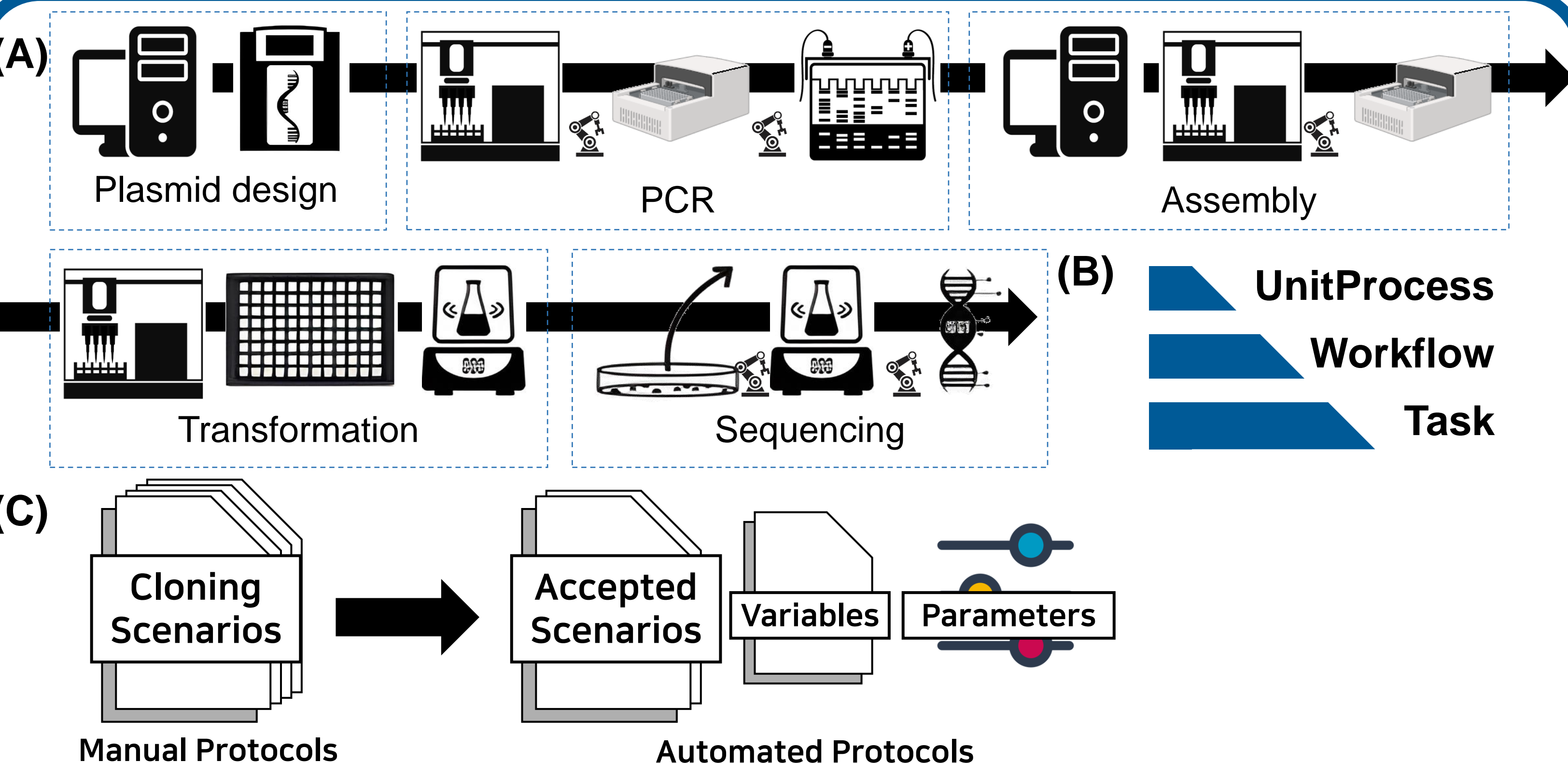
Manual Protocols → Automated Protocols

Fig 1. Software development pipeline for Automated protocols
(A) Diagram of general Cloning task.
(B) Legend of (A). They define the level of behavior the lowest level (single action) is unitprocess, abstracted conceptual behavior is workflow, one experiment for a project is task.
(C) The way to make protocol. Collect all scenarios, select the acceptable scenarios and confirm variables and parameters.

Abstraction & Data Structure

(A) Source (Template) → Destination / Source (Primer I) → Destination / Source (Primer II) → Destination — PCR

(B) **Embodied form (Machine)**

Source	Name	Destination
A1	Template I	D1
A2	Primer I	D1
A3	Primer II	D1
A4	Template II	D2
A5	Primer III	D2
A6	Primer IV	D2

Abstracted form (Human)

Name	Template	Primer F	Primer R
Fragment I	Template I	Primer I	Primer II
Fragment II	Template II	Primer III	Primer IV

The software receives the research note format(abstracted) as input and convert it to machine-readable format internally.
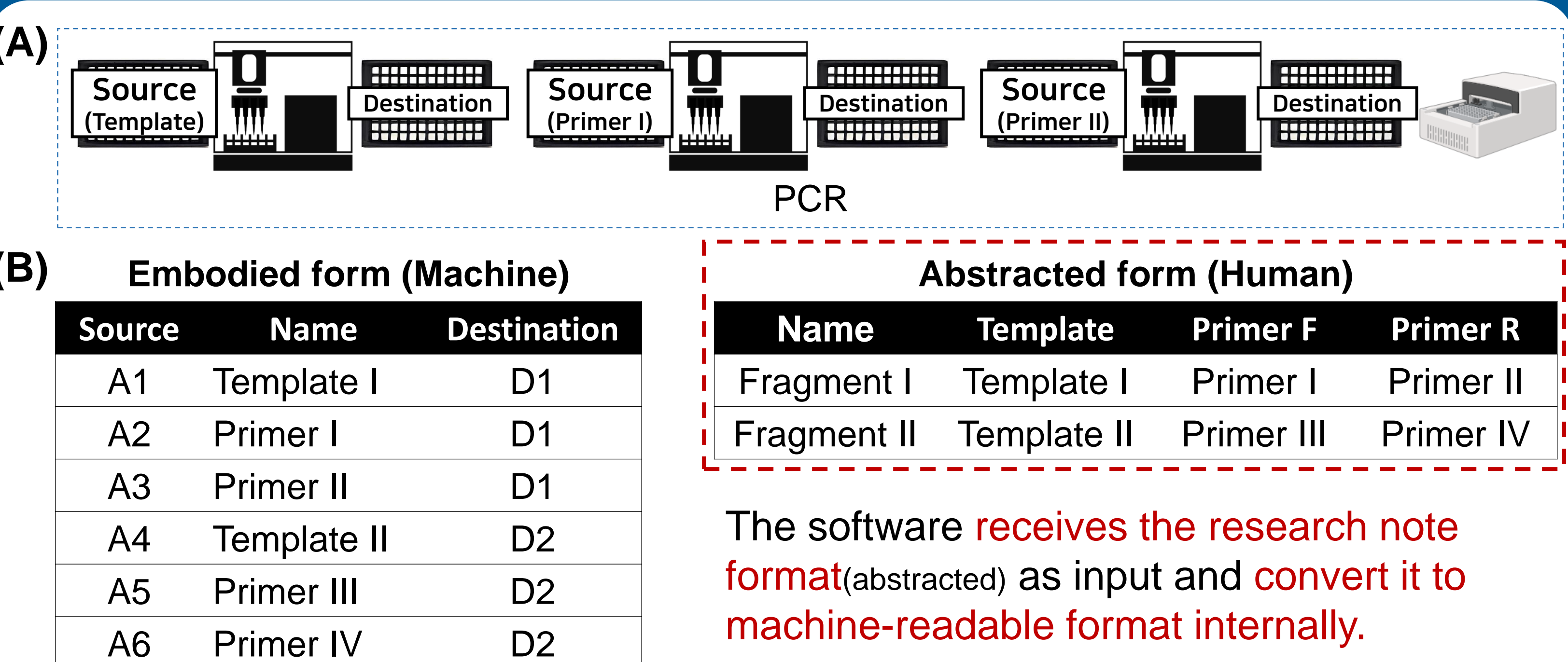
Fig 2. Software Abstraction and Input data structure
(A) Diagram of embodied PCR workflow.
(B) Liquid handler order sheet for machine (Long-form, machine readable). (C) Abstracted PCR order sheet.

Protocol Maker (Result)

Full APP Open in KMB

A **task** can be conducted by **combinatorial linking the workflows**

Receive **research note format** and implement equipment **operation internally in the software**
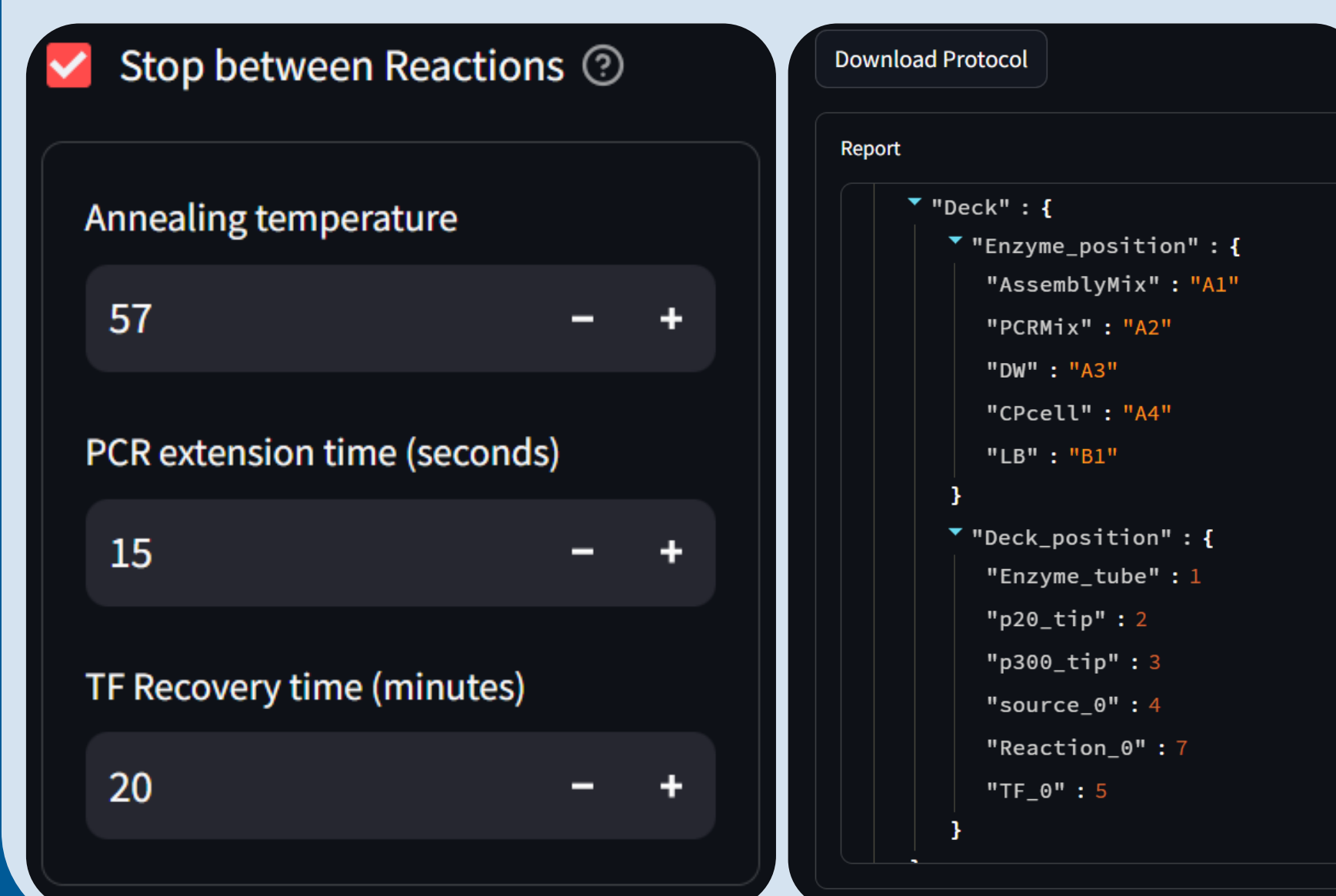
Convert all data to **machine-readable format.**

It used for **transmission between devices and connection with IT technology**

Discussion

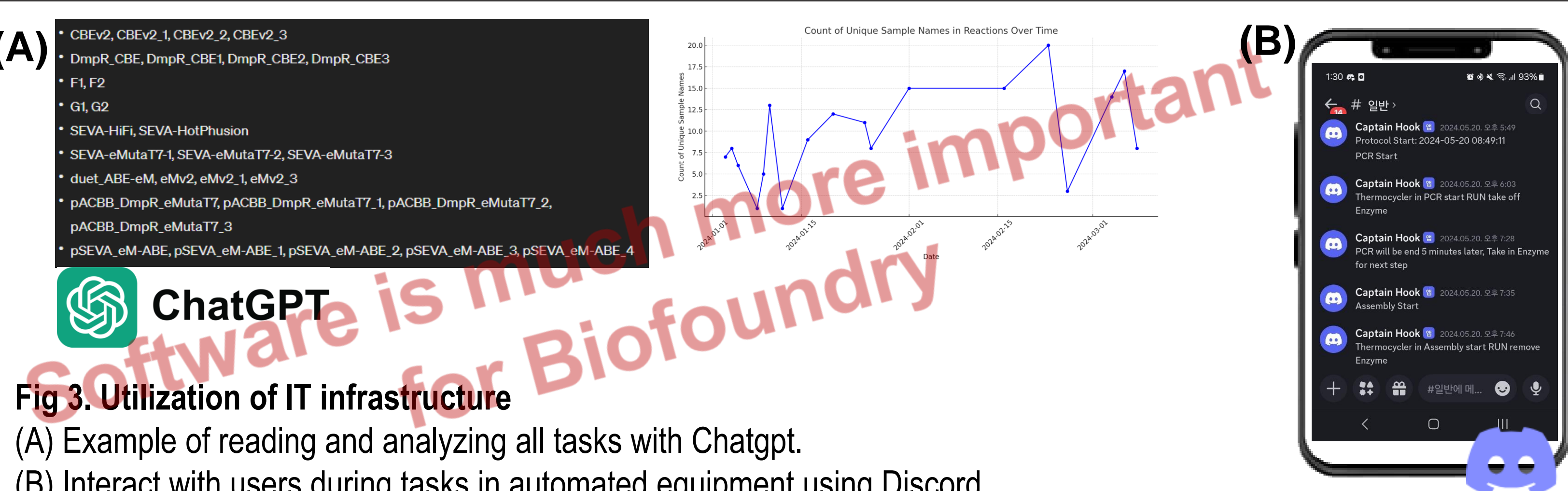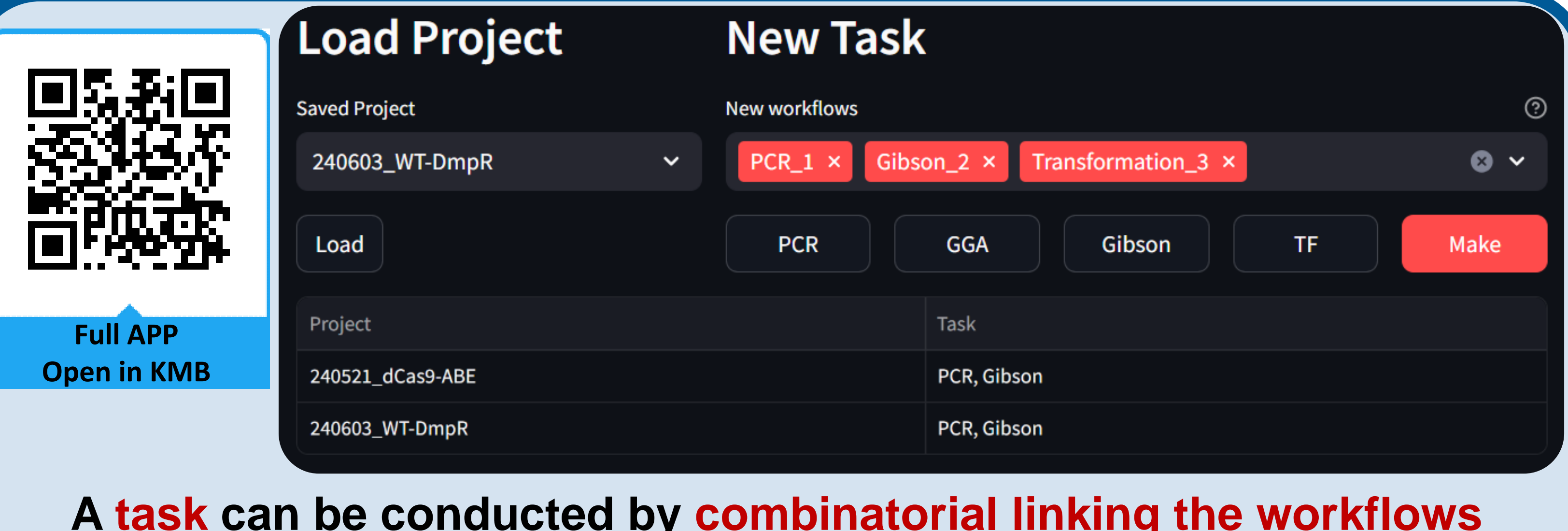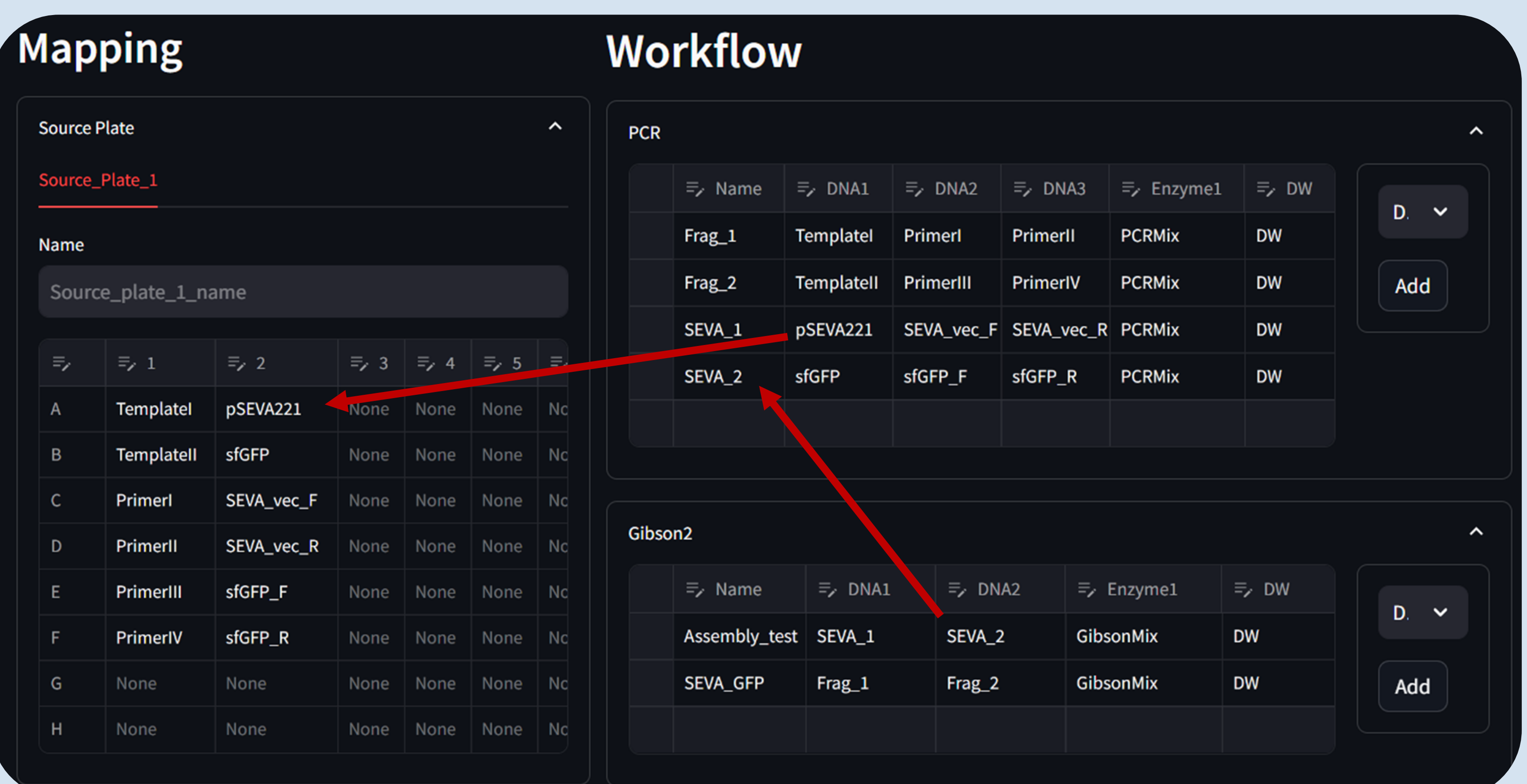

Software is much more important for Biofoundry

Fig 3. Utilization of IT infrastructure
(A) Example of reading and analyzing all tasks with Chatgpt.
(B) Interact with users during tasks in automated equipment using Discord.

Acknowledgements

References

1. Alberto A. Nava et al. (2023). *ACS Synthetic Biology*. 12 (12), 3506-3513.
2. Seqviz (https://github.com/Lattice-Automation/seqviz)
3. Created with BioRender.com