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BioSim Talk #6

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2nd October 2026 (Friday)

4.00 – 5.30 pm

Institute for Protein Research
University of Osaka (Suita Campus)
4th floor seminar room

Computational Biology in the LLM era: coding, tools, workflows, and agents

The emergence of LLMs is changing the way research workflows can be built and executed. Tasks that previously required writing scripts and manually operating several tools can increasingly be carried out through a conversation with an agent. With the appropriate tools and context available, natural language can be all the user needs to create and run a modelling workflow, including without previous coding experience. Skills and Model Context Protocol (MCP) servers extend this approach by providing procedural guidance and access to tools and data sources. Coordinating several agents makes it possible to divide a workflow into tasks, with a central orchestrator assigning work to agents with different expertise.

Through our real case demo, we will provide insights into how to work with such a system and the limitations and bottlenecks you may encounter, including LLM choice and token consumption. We will discuss how researchers can guide these workflows through natural language and discuss practical limitations, including LLM choice, token consumption, and errors that may arise during execution. As agents take on more of the work of developing and operating computational workflows, the researcher's role increasingly involves defining objectives, guiding the system, and evaluating its results.

Link for online participation via Zoom:

Meeting ID: 815 7570 0895

Passcode: 984117

Please inform us if you will be participating online or joining our Slack channel

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