

Project Title:

Uncovering human origins and millennia of genome evolution through whole-genome genealogies

Name:

○Leo Speidel (1)

Laboratory at RIKEN:

(1) RIKEN, iTHEMS

(2) RIKEN, Mathematical Genomics ECL Research Unit

	FY 2025.
<p>1. Background and purpose of the project, relationship of the project with other projects</p> <p>We will develop and apply new statistical techniques that leverage large-scale modern and ancient genomic datasets to understand the key drivers of evolution.</p>	
<p>2. Specific usage status of the system and calculation method</p> <p>I joined RIKEN in November 2024. Since then, I have used 31681.6 CPU hours (according to the HOKUSAI webpage).</p>	
<p>3. Result</p> <p>I have set up the key infrastructure to start projects and will be utilizing HOKUSAI more intensively in future.</p>	
<p>4. Conclusion</p> <p>HOKUSAI will be essential for my group to leverage large-scale genomic datasets going forward.</p>	
<p>5. Schedule and prospect for the future</p> <p>We will expand our usage of HOKUSAI, likely requesting more storage space and compute hours in</p>	