Loupe · 2026-11-14

Pathology Research Workspace

Loupe is a workspace for **pathology research**: organize materials, draft grant proposals, and run **reproducible computation**. Start with a research goal, keep sources, versions and task history, and review the facts and conclusions yourself.



Real product interface with synthetic materials and projects.

Materials & evidence

Batch materials, retrieve passages and locate sources; choose cross-project reuse explicitly.

Sections & versions

Edit and rewrite a section with sources and revisions; keep missing facts marked as missing.

Compute & reproduce

Fixed CPU statistics retain inputs, scripts, metrics and figures.

Progress & control

Inspect tasks, budgets and artifacts; stopping retains data and cleanup starts with a preview.

Set a goal, organize materials, freeze the method, draft or compute, then review and save artifacts.

Shared skills, separate model adapters

Evidence review, reproducible analysis and grant drafting are frozen into tasks. Codex receives standard SKILL.md bundles, rather than direct Codex execution. Kimi and DeepSeek have adapters and offline continuation checks; online matched-task quality comparisons remain outstanding.

Three pathology directions

Breast cancer TROP2	Study-plan draft · pairing and agreement rules · missing materials
Colorectal tumor budding	Evidence table · spatial-study plan · external-validation rules
Chronic glomerular injury	Quantification draft · denominator and failure rules · multicenter validation

These are synthetic examples and study plans, not completed clinical studies.

Current verification

14 November 2026: 2056 backend checks passed, with 11 skipped for optional environments; 278 frontend checks passed. The 12 public synthetic rows give AUC 2/3, Brier 0.245, and false positives DEMO-04, DEMO-05 and DEMO-06.

Software and synthetic-data checks do not establish clinical validity. Researchers still review provenance, applicant facts and scientific interpretation.

From walkthrough to local trial

The public site provides trilingual tours, a usage guide and synthetic CSV, without model calls or file uploads. Trial packages are arranged separately with the maintainer. A prebuilt package requires Python 3.11 or 3.12 and initial network access for dependencies, without Node.js.

Keep the pathology-example window open; Ctrl+C stops it and retains practice data. Reopening creates a new demo. The workspace launcher runs your own research in the background, with stop and cleanup controls. Model writing needs a connection; advanced experiments and EvoScientist are off by default. For research and teaching.

Project maintainer: github.com/Hxitech