

RELICT BRINGS ORDER TO THE MULTIVERSE OF BIOLOGICAL DATA

The Reproducible, Open-Source Environmental DNA Platform.

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Environmental DNA Platform.



From raw sequencing reads to a
cryptographically proven
biodiversity inventory in minutes.

ONE PLATFORM ELIMINATES THE EIGHT-STEP GAUNTLET

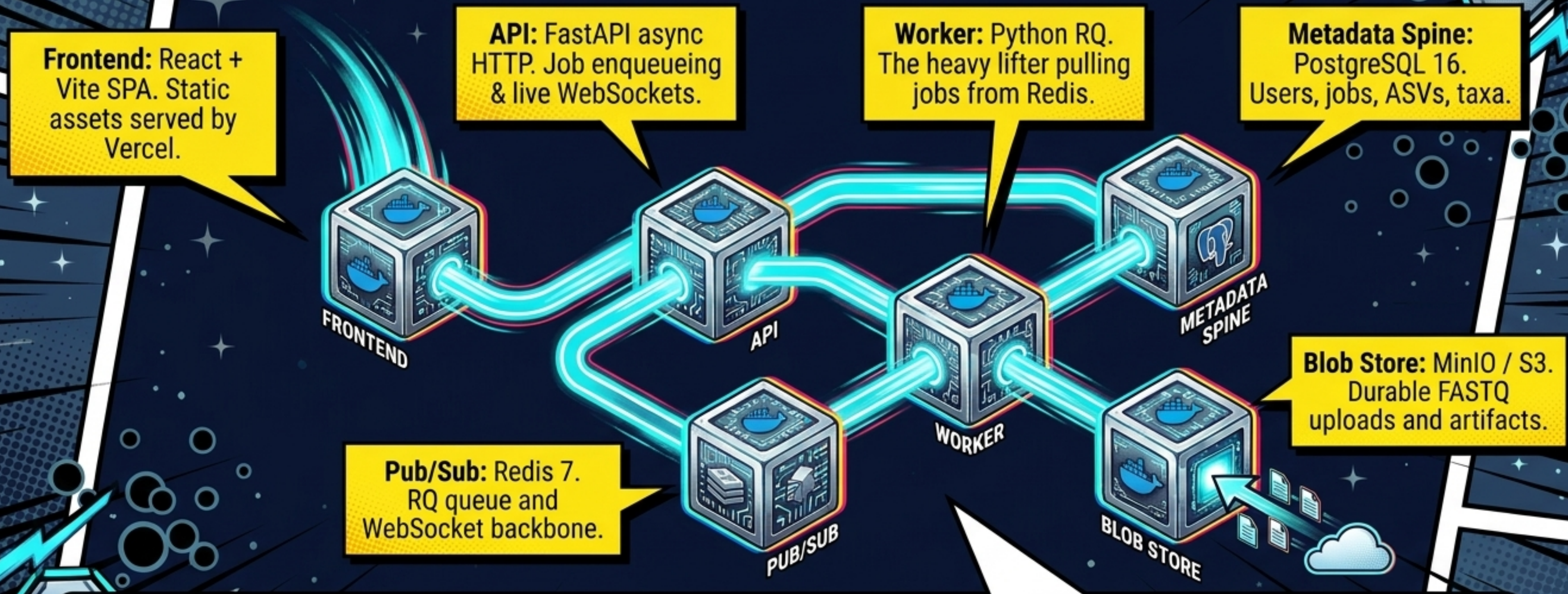
Upload a FASTQ. Pick a marker. Relict handles the rest. Built for the field ecologist and the citizen-science club alike.

FULL PIPELINE.
Quality control to ordination in minutes.

CONSERVATION INTEL.
Automated cross-referencing against GBIF and IUCN Red List.

GLOBAL RECORDS.
Automatically generates GBIF-ready Darwin Core Archives.

SIX SYNCHRONIZED SERVICES WIRED OVER A PRIVATE NETWORK



API and Worker never talk directly—only through Postgres and Redis. Infinite horizontal scaling with zero code changes.

A SCIENTIFIC INSTRUMENT RENDERED AT SIXTY FRAMES PER SECOND

THE TECH

React 18.3, TypeScript 5.8 strict, Vite 5.4. 66 components spread across 9 pages. 426 KB gzipped.

THE TELEMETRY

Live WebSocket streaming. Real-time ordination rendered directly in the browser via UMAP + HDBSCAN.

THE VISUALS

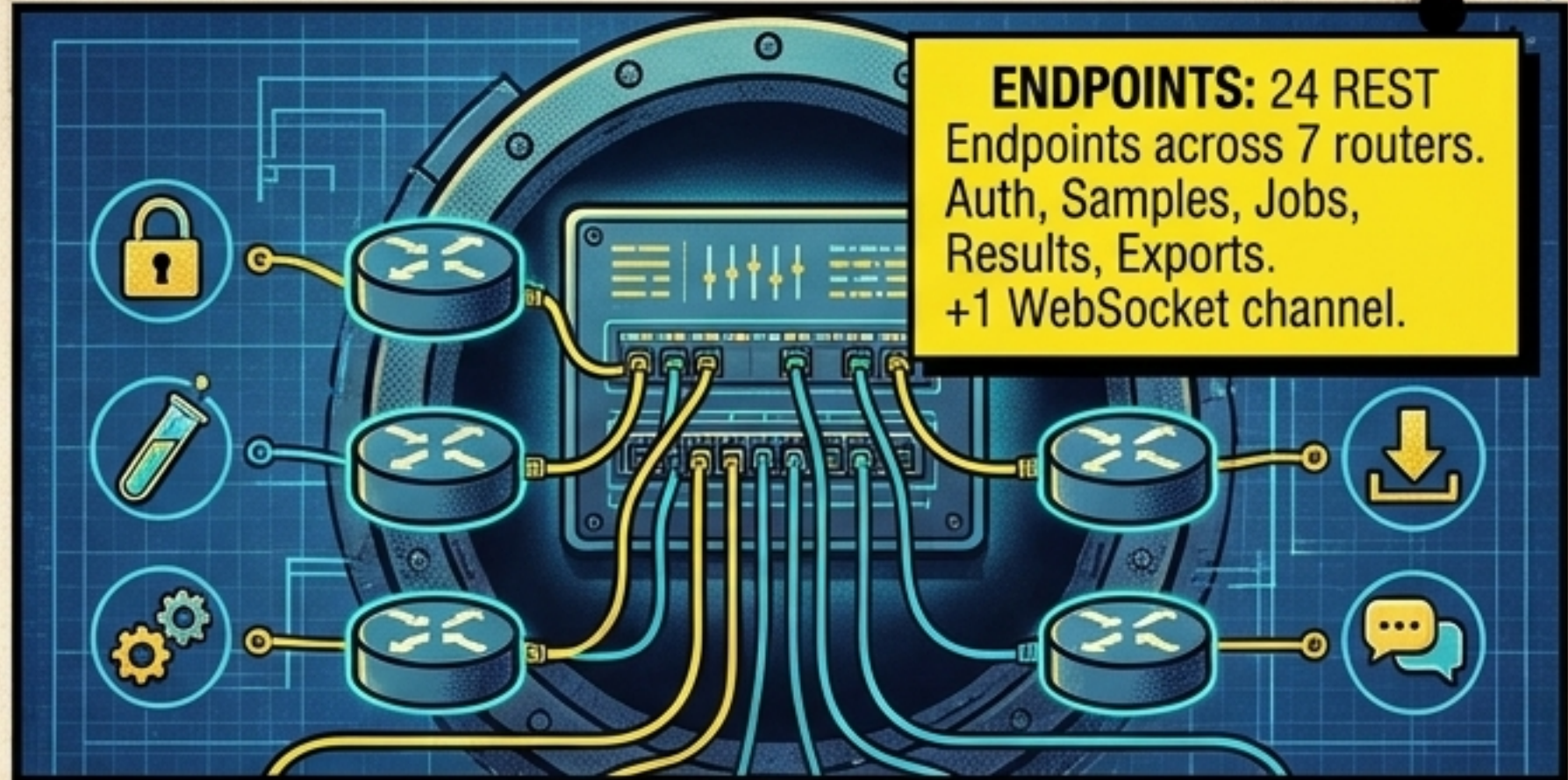
Three.js physics engine. 1,200 instanced particles with Perlin-noise motion. Live ATCG base-pair terminal streams.

THE SYNAPSE NETWORK SECURES EVERY BYTE OF DATA



```
1 import python
2 from typing import Dict
3
4 def __soux(froult):
5     data = - fillere
6     data_s filteref
7     data_co = 8suen
8     try:
9         deta = d546
10        if date.teb
11            dicoecta,
12            ooos,8osffrom deta.pett(€)
13        ):
14            exittee, e (aroad/hac;B...
15        }
16        else:
17            éaved_packet:atne(s,pactt).
18        }
19    }
20    def __sancioablee):
21        data = moos3stn(7k0217?;Tppatinc) (,3")
22        return deta.ooof6)
```

SCALE: 4,255 lines of strict Python. Zero raw dictionaries cross the wire.



ENDPOINTS: 24 REST Endpoints across 7 routers. Auth, Samples, Jobs, Results, Exports. +1 WebSocket channel.



BOUNDARIES: Strict Pydantic v2 double validation. Checked at ingress, checked at egress.

BRIEE: Strict Pydantic v2 double validation.



SECURITY: Argon2id password hashing (OWASP-compliant). Short 15-min JWT access tokens + 14-day refresh tokens.

ADDING INTELLIGENCE AND LOCKING THE CRYPTOGRAPHIC CHAIN

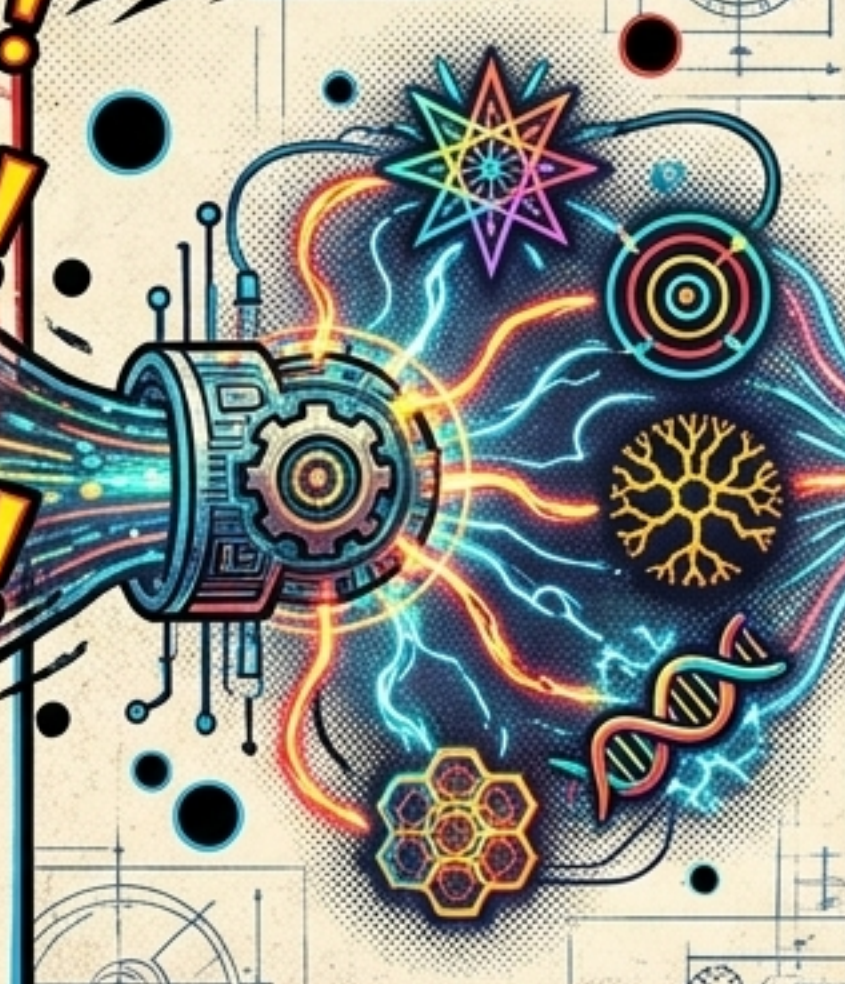
STAGE 4B: CONSERVATION.
Queries GBIF and IUCN Red List. Triggers red alert badges for threatened species.



GBIF & IUCN
QUERIES

STAGE 4B: CONSERVATION.
Queries GBIF and IUCN Red List. Triggers red alert badges for threatened species.

ZAPP!



STAGE 5: DIVERSITY.
Computes 5 alpha indices (Shannon, Simpson, Chao1) via scikit-bio 0.6.2.

ZAPP!



STAGE 6: ORDINATION.
5-mer frequency matrix. Projects into 2D with UMAP and clusters with HDBSCAN.

ZAPP!



STAGE 7: PROVENANCE.
Canonical JSON manifest recording SHA-256 hashes of inputs, tools, and DBs.

THE ARSENAL: TWO POINT FOUR MILLION PINNED SEQUENCES

A version-pinned, SHA-verified downloader caches 20GB of persistent reference data. If an upstream file changes, the pipeline logs and halts. Silent failures are impossible.

SILVA 138.1: 436,680
curated rRNA sequences.
Covers Bacteria, Archaea,
and Eukaryotes.

MIDORI2 COI: 1,801,886
invertebrate
sequences.

MIDORI2 12S + MitoFish: 193,724
fish and
vertebrate sequences.

VAULT 1:
SILVA 138.1

VAULT 2:
MIDORI2 COI

VAULT 3:
MIDORI2 12S + MitoFish

VAULT 1: SILVA 138.1

VAULT 2: MIDORI2 COI

VAULT 3: MIDORI2 12S + MitoFish

AUTO-ROUTING SIX TARGET MARKERS TO THE CORRECT WEAPON

TARGET PROFILE



WEAPON:
SILVA

TARGET: 16S V4 (Bacteria/Archaea)

TARGET PROFILE



WEAPON:
MIDORI2
+ MitoFish

TARGET: 12S MiFish (Fish)

TARGET PROFILE



WEAPON:
MIDORI2

TARGET: COI Leray (Invertebrates)

TARGET PROFILE



WEAPON:
SILVA

TARGET: 18S V9 (Eukaryotes)

TARGET PROFILE



WEAPON:
SILVA

TARGET: rbcL (Plants)

TARGET PROFILE



WEAPON:
SILVA

TARGET: ITS2 (Fungi)

The amplicon is a first-class enum. Relict automatically deploys the precise reference database for the job.

SEAMLESS TRANSLATION TO EVERY MAJOR GLOBAL STANDARD

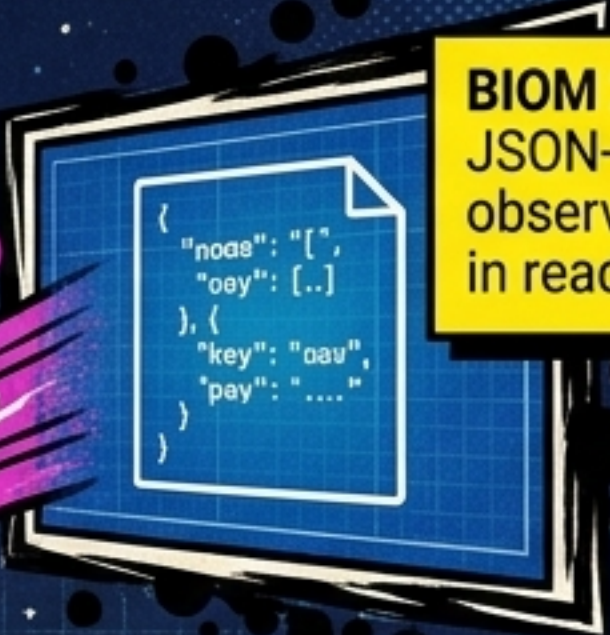
WHOOSH!



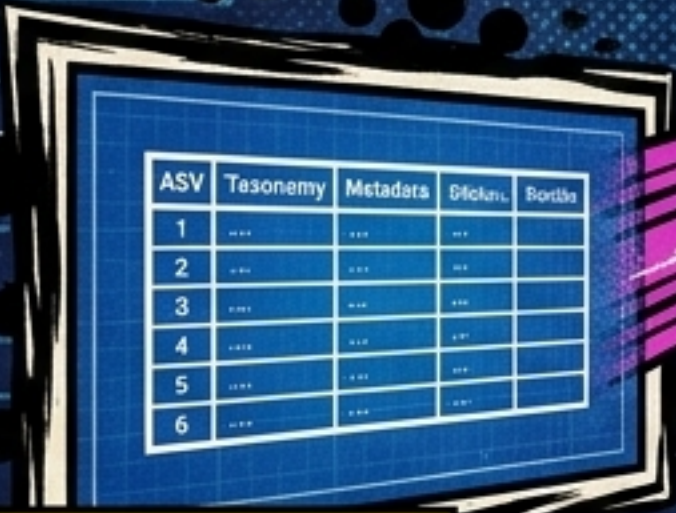
Darwin Core Archive (DwC-A).
A ZIP conforming to GBIF standards. Ready to publish.



BIOM 2.1.0.
JSON-format observation matrix. in ready for QIIME2.



CSV.
Flat ASV x metadata table for Excel/R/Pandas. All 7 taxonomic ranks.



Signed JSON.
The cryptographic chain of custody.



HTML Report.
Self-contained, single-file interactive dashboard.



BATTLE TESTED: SYNTHETIC PERFECTION AND REAL-WORLD SPEED

SYNTHETIC SANDBOX

Input: 5 known species, 100 reads.

Results: 10/10 Score. Recovers exactly 5 ASVs.

Metrics: Perfect Shannon (1.6094), Simpson (0.8000), Evenness (1.0).



THE REAL WORLD

Input: SRA ERR2283086. 45,204 reads.

Results: 51 ASVs. 100% taxonomy assigned at 100% SILVA identity. Shannon 2.585.

Runtime: 215.4 Seconds (3m 36s on a single worker instance).

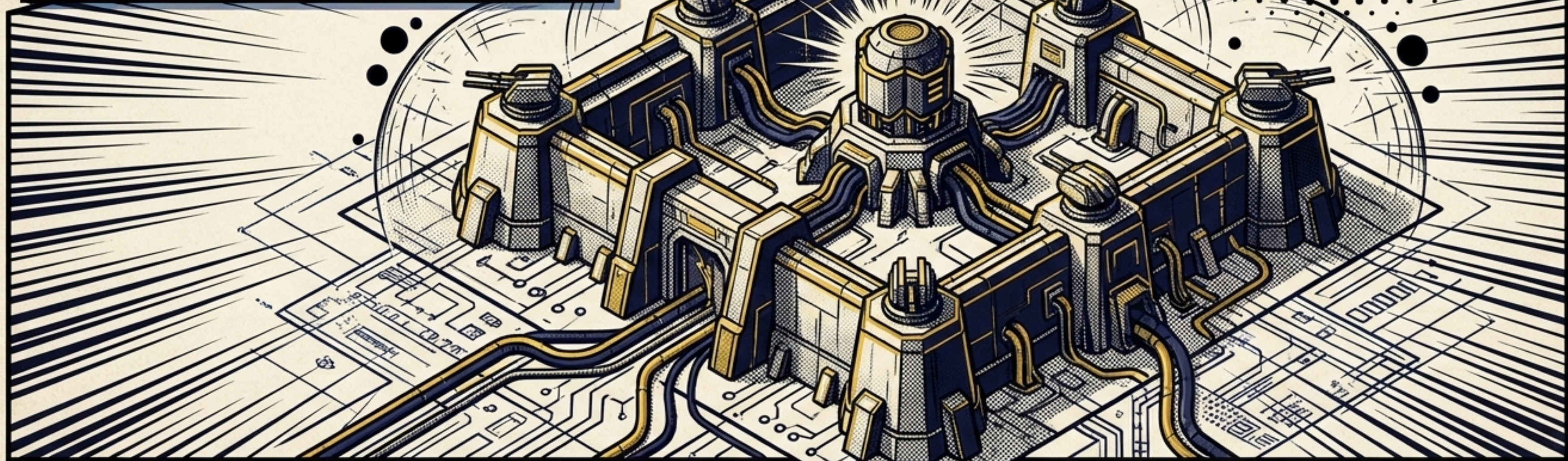


HARDENED INFRASTRUCTURE WITH ZERO HARDCODED PATHS

DEPLOYMENT: Environment-driven infrastructure. Docker Compose for local dev. Vercel for Frontend. Render Blueprint for the Backend. Cloudflare R2 for object storage.

DATA MODEL: 9 Alembic-managed tables (users, jobs, samples, taxa, diversity_metrics, conservation_cache). ~110 columns total.

Every deployment-critical path is env-driven. Bring the whole stack up with one "docker compose up".

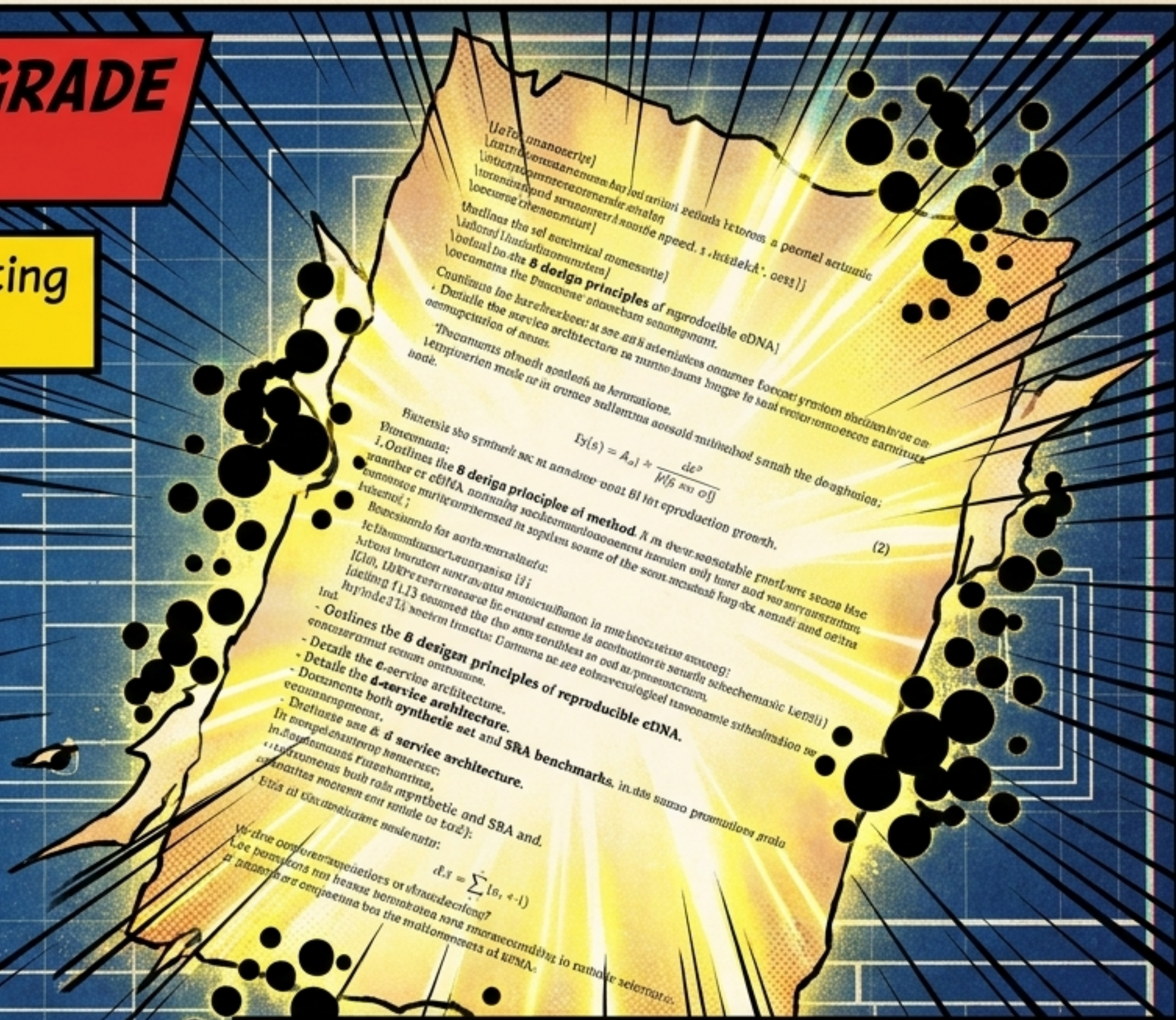


BACKED BY PEER-REVIEW-GRADE SCIENTIFIC LITERATURE

A 3,187-word LaTeX manuscript targeting Methods in Ecology and Evolution.

- Outlines the 8 design principles of reproducible eDNA.
- Details the 6-service architecture.
- Documents both synthetic and SRA benchmarks.

Relict bridges the gap between software engineering and peer-reviewed ecology.



A FULLY-BUILT, OPEN-SOURCE PIPELINE READY FOR DEPLOYMENT **GROUND ZERO TO TODAY.**



10,299 lines of strict, fully-tested code.

Conservation-annotated and cryptographically reproducible.

A Darwin Core Archive export, ready for the global record.

The wait for reproducible environmental DNA is over.