Project Eden — Reproduction, Neural Development and Evolution of C. elegans inside NEEUMAN

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Project Eden turns NEEUMAN's simulated C. elegans into a population that reproduces, inherits, mutates and builds a new brain in every generation. Four founder worms, three hermaphrodites and one male, grew to 257 individuals over 12 generations. Every brain is wired from its own genome along the measured developmental connectomes, from 222 neurons at hatching to 302 in the adult.

- **Faithful:** a batch of simulated worms reproduces the original single-worm model to machine precision. A wild-type genome builds exactly the 3,709-connection Cook 2019 brain.
- **Measured inheritance:** offspring brains differ from their mothers' in about 900 connections. That is mostly developmental chance, as in real isogenic worms. On top of it sits an inherited component that scales with genetic distance (Spearman $\rho = 0.34$, $p \approx 10^{-84}$).
- **Evolution, not yet adaptation:** five 16-generation lines show founder strains fixing and mutations accumulating. One line gained about 170 new synapses per worm. But evolved worms do not out-compete their ancestors (48.7 % of offspring, $p = 0.62$), so longer and larger runs are the next step.
- **Honest limits:** life-history time runs 3,600× faster than behaviour, broods are scaled, males use the hermaphrodite connectome, and the base worm steers weakly toward food.

A 54-second vertical reel with no on-screen text was rendered on the GPU from the recorded simulation, with a timed voice-over script below.

Research foundation

Every rule in Eden comes from a measured fact about C. elegans, or is marked as an assumption. These are the facts the model is built on.

Topic	What is known	Source	How Eden uses it
Sexes and reproduction	Mostly self-fertilising XX hermaphrodites; XO males arise at under 0.2 %	Corsi et al. 2015, Genetics primer	Hermaphrodites self; males come from X non-disjunction ("him" gene, 0.15 % baseline)
Brood size	About 300 self-sperm limit selfing; a mated hermaphrodite can produce over 1,000 progeny	Cox, Molecular Biology, Cutter et al.	300 self-sperm and 1,000 per mating, scaled down 30× (or 10× in evolution cycles)
Male sperm	Male sperm are used before self-sperm; cross-progeny are about half male	WormBook, NCBI	Mated hermaphrodites use male sperm first; a male's sperm carry an X or none, 1:1
Life cycle	14 h embryo, then four larval stages L1 to L4 over about 36 h at 25 °C	WormBook, NCBI	14 h embryos; Witvliet timeline (adult at 45 h after hatching)
Neurons at hatching	222 neurons at hatching (202 somatic + 20 pharyngeal); 80 more are born after hatching, mostly ventral-cord motor neurons, each at a known stage	WormAtlas postembryonic neurons	All 80 join the network at their recorded birth stage

Topic	What is known	Source	How Eden uses it
Brain wiring across development	Eight brains from birth to adult: synapses rise about 6-fold (≈1,300 to ≈8,000), connections 2.4-fold; the decision-making core stays stable while sensory and motor pathways remodel	Witvliet et al. 2021, Nature	Every brain connection follows its measured trajectory through ages 0, 5, 8, 16, 23, 27 and 45 h
Individuality	About 43 % of adult connections differ between genetically identical worms; they are mostly weak (1.4 ± 1.0 synapses vs 6.6 ± 5.8 for stable ones)	Witvliet et al. 2021	Weak connections form by chance at birth with the probability Witvliet observed: not inherited
Where new synapses form	New connections form preferentially between neurons that already touch over large areas	Witvliet et al. 2021; contact areas from Brittin et al. 2021	Mutations can only add synapses between brain neurons that touch, in proportion to contact area
Adult wiring	Whole-animal connectomes of both sexes: 302 neurons in the hermaphrodite, 385 in the male	Cook et al. 2019, Nature	The adult hermaphrodite wiring (3,709 chemical connections, 1,105 gap junctions) is the wild-type target

Topic	What is known	Source	How Eden uses it
How genes wire a brain	The Genetic Connectome Model predicts wiring from which recognition genes each neuron expresses and which pairs of gene products bind; it was validated on the C. elegans gap-junction connectome	Barabási et al., PMC	Genome = gene expression per neuron class + binding rules; one mutation rewires many synapses at once
Genomic bottleneck	The genome is far too small to list every synapse, so it encodes compact wiring rules	Shuvaev et al. 2024, PNAS	Eden's genome is compressed: 1,645 loci shape 8,483 possible connections
Mutation rate	Base substitutions about 1.8×10^{-9} per site per generation; mildly deleterious mutations about 0.03 per genome per generation, about 0.1 % fitness decline per generation	Konrad et al., Vassilieva et al. 2000	Mutator-strain rate: 0.6 mutations per gamete, so change shows within tens of generations
Experimental evolution	Lab populations adapt measurably within 100 generations; outcrossing is favoured under high mutation load or a new environment	Teotónio et al. 2014, Morran et al. 2009	Discrete-generation lines with embryo transfer, plus mutation-accumulation controls
Natural behavioural variation	One amino acid in the neuropeptide receptor NPR-1 switches solitary vs social foraging	de Bono & Bargmann via Portman 2020	A foraging-state gene (npr1) that changes how long worms dwell on food

Topic	What is known	Source	How Eden uses it
Male behaviour	Males leave food to search for mates unless they meet hermaphrodites	Lipton et al. 2004	Males roam off food until they touch a hermaphrodite
Simulated evolution of worm circuits	Evolutionary algorithms have found connectome-constrained circuits for salt chemotaxis	Izquierdo & Lockery 2010, Izquierdo & Beer 2013	Earlier work optimised a circuit against a fitness function; in Eden, worms live and reproduce, and fitness is just who leaves descendants

The last row is the key difference. Earlier studies evolved parameters toward a goal the programmer chose. In Eden nothing is scored: worms that eat, grow and lay eggs faster simply leave more offspring.

The developmental connectomes, contact areas and birth times were extracted from the OpenWorm connectome toolbox `cect` (MIT licence) into `data/celegans/development.json` by `scripts/build_eden_development_data.py`.

The model

Each Eden worm is the full NEEUMAN nematode from the earlier project, run as one batch. It has a 302-neuron connectome brain (exact NEMA port), a proprioceptive cord circuit and a viscoelastic body with 95 muscles in agar. On top of that, every worm now has its own genome, grows its own brain, and lives a life.

1. Genome (`eden_genome.py`). The genome is diploid, with 1,645 loci on six chromosomes (I–V and X).

- *Wiring genes.* 118 neuron classes each express 12 cell-recognition genes, and a 12 × 12 binding matrix O sets how strongly each gene pair attracts (plus a symmetric one for gap junctions). The wiring compatibility of two neurons is $x_i^T O x_j$. Founders carry O = 0, so they build the measured wild-type brain exactly.
- *Physiology genes.* Seven named loci: npr1 (dwelling on food), chemosensory gain, spontaneous reversal rate, pirouette gain, self-sperm number (more sperm delays maturity), egg-laying drive, and him (male production).

- *Meiosis.* Exactly one crossover per chromosome pair, as C. elegans has complete crossover interference. Males (XO) pass an X or no X with 1:1 odds.
- *Mutation.* Each gamete carries Poisson(0.6) new mutations with Gaussian effects. This is a mutator-strain rate, chosen so change is visible in tens of generations.

2. Development (`eden_development.py`). A worm's connection strength at age t is:

```
w_{ij}(t) = w^{\mathrm{Cook}}_{ij}\; d_{ij}(t)\; e^{\,x_i^\top O\, x_j}\;
\pi_{ij} \;+\; \kappa\, \lambda\, \max\!\left(0,\; x_i^\top O\, x_j -
\theta\right) \sqrt{A_{ij}/\tilde A}\; d(t)
```

- w^{cook} is the adult synapse count (Cook 2019).
- $d_{ij}(t)$ is the measured Witvliet trajectory for brain connections, or body-length growth for cord and tail.
- π_{ij} is the developmental coin-flip for weak, variable connections.
- The last term is new synapses between touching neurons (A_{ij} is their Brittin contact area).
- Neurons born after hatching are absent from the network until their recorded birth stage. Hatchlings have 222 neurons and adults 302.
- The brain is rebuilt from the genome every 2 s of life as the worm ages.

3. Body growth. Length goes from 0.25 mm at hatching to about 1 mm as a young adult, following WormAtlas stage lengths. Radius, bending stiffness ($\propto R^3$), muscle curvature range ($\propto 1/L$) and proprioceptive thresholds scale with size, so a larva behaves as a small worm.

4. Behaviour added for life on a plate. These additions are documented in the code, and each is a known worm behaviour:

- slowing down on bacteria (Sawin et al. 2000);
- backing up and turning when the nose leaves a lawn (Shtonda & Avery 2006);
- pirouettes driven by the ON- and OFF-cell contrast in the connectome's own activity;
- males leaving food to search for mates (Lipton et al. 2004);
- local-search reversal rates of about 3 per minute (Gray et al. 2005).

5. Ecology and life history (`eden_world.py`). The plate has bacterial lawns on a 160 × 160 grid, eaten at the pharynx, regrowing slowly and exhausting over time, with new lawns appearing. Each worm has an energy reserve (intake minus maintenance $\propto$ size^2) that sets:

- larval development speed (starved L1s arrest);
- egg laying;
- death by starvation, plus Gompertz ageing with a median adult life of about 8 days.

A male's tail held on an adult hermaphrodite for 3 s inseminates her. Eggs hatch after 14 h. On a full plate, new larvae enter a bounded dauer pool and return when there is room.

6. Time. Neurons, muscles and bodies run in real time at 5 ms steps. The life-history clock runs 3,600× faster (1 h of life per second), so a generation takes about 70 s instead of about 3 days. Brood sizes are scaled down. Selection only depends on differences between worms, and those are preserved.

Part	Measured data	Assumption or tuned
Adult wiring, neuromuscular junctions	Cook 2019	—
Synapse growth L1 → adult	Witvliet 2021, 8 animals	Interpolated between ages; cord/tail scaled with length
Neuron birth times	WormAtlas	Stage names mapped to hours
Individual variability	Witvliet presence frequencies	Weak cord connections: 60 % presence
Genome → wiring	Genetic Connectome Model form	12 genes, effect sizes, new-synapse threshold
Brain dynamics, body mechanics	NEMA; Boyle 2012; Cohen & Ranner 2017	Unchanged from the earlier worm
Feeding, energy, egg rate	Brood sizes, egg-laying rates	Energy units, intake and maintenance constants
Time scale	—	3,600× life-history acceleration

Validation

Eden's population engine reproduces the original single-worm NEEUMAN model to machine precision. Its development, genetics and life cycle pass 11 automated tests (`tests/test_eden.py`).

Check	Result	Expected
One-worm batch vs original single worm, 800 steps (4 s), tail touch	Brain differs by 8.8×10^{-15}, body by 2.4×10^{-10} mm	Identical up to rounding
Neurons at hatching / in the adult	222 / 302	222 / 302 (WormAtlas)
Neurons at 8 h, 16 h, 24 h	230, 293, 301	Births at mid L1, late L1, L2 and L3
Adult chemical connections, wild-type genome	3,709	3,709 (Cook 2019)
Brain synapses at birth, as a fraction of adult	0.17	≈1,300 / 8,000 (Witvliet 2021)
Whole-animal synapse units, hatchling → adult	3,525 → 20,965 (5.9×)	About 6×
A wild-type genome builds the reference brain	Compatibility exactly 0 for every pair	No change
One wiring mutation (one binding rule)	Changes more than 20 synapses	Pleiotropic rewiring
Crossovers per chromosome per meiosis	At most 1 in every test	Exactly 1 (C. elegans)
Males among self-progeny / cross-progeny	Under 1.5 % / 40–60 %	0.1–0.2 % / about 50 %
New mutations per zygote	1.0–1.4	2 × 0.6
Life cycle on a plate	Founders feed, lay eggs; eggs hatch into L1 larvae with fewer than 302 neurons	—

Locomotion holds across growth. In 20 s on agar, an L1 (0.26 mm) crawled at 33 µm/s and a 10-h L1 at 85 µm/s. An L3 crawled at 142 µm/s and a young adult at 215 µm/s, about 0.23 body lengths per second. Real adults crawl at 0.1–0.3 mm/s.

The batched engine runs 40 worms at about 9 ms per 5-ms step on one CPU core, against 1.2 ms for one worm alone. That is 5× cheaper per worm, and it is what makes a living population affordable.

Two findings from validation shaped the design:

- **Lawn retention was too low at first.** Wild-type worms kept only 24 % of their time on a lawn. Adding the known slowing on food and edge reversals raised this to 71 %, close enough for larvae to grow, with room for evolution to improve it.
- **Food-directed steering is weak in the base worm.** Even an oracle that reversed exactly when the worm moved away from food did not steer it to food. Its turns do not reliably reorient it, so selection in Eden acts mainly on search, dwelling and life history, not on chemotaxis. The result is reported as is, not tuned away.

Experiments

After 16 generations, no line, selected or control, out-competes its ancestors. Evolved worms leave 48.7 % of the offspring in head-to-head competition (n = 36, p = 0.62 against 50 %). Genomes and brains did change, most of all in one selection line.

Design. The protocol is classic experimental evolution, as in the Teotónio and Morran labs:

- Each generation, 32 worms hatch together as L1s on a fresh plate with six randomly placed bacterial lawns. They grow, feed, mate and lay eggs for 72 h of life.
- Embryos are then collected ("bleaching"), and 32 drawn at random found the next generation. A worm's share of the next generation therefore equals its share of the eggs, which is selection by reproductive success.
- The founders are four strains, each carrying ten random variants. One strain contributes males.
- **Selection lines (3):** mutation rate 0.6 per gamete.
- **Mutation-accumulation controls (2), the same founders as selection lines 1 and 2:** every hermaphrodite parent contributes equally, so mutations accumulate without selection.
- **Fitness test:** 16 evolved and 16 ancestral hermaphrodites share each plate, 12 replicate plates per line, and the evolved share of the eggs is counted. A share of 0.5 means equal fitness.

A first version of the fitness test was flawed: its ancestor side included males, which lay no eggs, and that inflated every line's score. It was corrected, and all results below are from the corrected test.

Line	Treatment	Evolved share of eggs (12 plates)	t-test vs 0.5	Wiring divergence from founders, gen 0 → 15	Chemical connections per worm, gen 0 → 15	New contact synapses per worm (gen 15)	Connections changed ≥ 2-fold
Selection 1	selection + mutation	0.448	p = 0.15	2.17 → 4.41	2,708 → 2,880	170.6	503
Selection 2	selection + mutation	0.540	p = 0.49	1.38 → 2.46	2,711 → 2,724	14.3	165
Selection 3	selection + mutation	0.472	p = 0.58	1.44 → 1.72	2,694 → 2,712	0.0	132
Control 1 (founders of line 1)	mutation only	0.527	p = 0.36	2.17 → 3.37	2,708 → 2,710	0.6	128
Control 2 (founders of line 2)	mutation only	0.499	p = 0.98	1.38 → 2.89	2,711 → 2,711	5.4	121

Statistics

Comparison	Result
Selection lines vs ancestors, all plates	mean share 0.487, n = 36, t = −0.50, p = 0.62
Selection vs control lines, competition shares	0.487 vs 0.513, Mann–Whitney p = 0.83
Same loci changing in independent selection lines (parallel evolution)	correlation of allele-frequency change ≈ 0 (−0.0002 to 0.010)
Founder-strain composition at generation 15	lines 1 and 2: one strain fixed (100 %); line 3: 72 % / 28 %
Eggs per hermaphrodite over generations	line 1 rising (+0.08 per generation, p = 0.03); lines 2–3 and controls flat; fresh random lawns each generation make this noisy

Reading the results

- Evolution as genetic change clearly happened. Founder strains went to fixation, new mutations accumulated, and wiring genomes diverged.
- Adaptation, meaning a heritable rise in fitness, was not detected. With 32 worms per generation, mostly selfing and 16 generations, drift dominates. Line 1's large brain change (more synapses, 170 new contact synapses per worm) was not followed by higher fitness, so it is most likely hitchhiking or drift, not adaptation.
- No parallel evolution across lines is the pattern expected without strong selection.

Raw data, per line: `eden_runs/evo_*/evolve.json`, `gen_*.npz`, `brains_gen_*.npy`, `compete_*.json` and `analysis.json`. Reproduce with the commands under *How to run it in NEEUMAN*.

Neural changes in offspring

Every offspring grew a brain that differs from its mother's by about 900 connections. Most of that difference is developmental chance, as in real worms. A smaller inherited part grows with how far the genomes have drifted apart.

These numbers come from the recorded Eden plate: 1,200 s of behaviour, about 50 days of worm life, 257 individuals, 248 with adult brains, up to generation 12, 244 mother–offspring pairs.

Measure	Value
Neurons at hatching → adult	222 → 302; the 80 newcomers join at their recorded birth stages
Adult chemical connections per worm	2,709 ± 27 of the 3,709 possible; the weak variable ones form by chance, about 27 % absent in any one worm
Synapse growth from first record to adult	3.1× per worm (records start at hatching or at dauer exit)
Connections present in one but not the other, mother vs offspring	897 (median 896)
Same measure, two worms with identical genomes	889
Large synaptic changes (≥ 3 synapses, ≥ 2-fold), mother vs offspring	123 on average, 90th percentile 147, maximum 185

Measure	Value
Same measure, identical genomes	131
Inherited signal: large changes vs genetic distance (3,000 random pairs)	Spearman $\rho = 0.34$, $p \approx 2 \times 10^{-84}$; +2.8 large changes per unit of wiring-genome distance, on a baseline of 114
Offspring with new synapses between touching neurons	1.6 %

Three things follow from this.

- **Every brain is unique, even without mutation.** Identical genomes produced brains differing in about 890 connections. That matches what Witvliet et al. measured in isogenic worms, and it is the reason Eden has a developmental-noise layer.
- **Mutations leave a measurable, heritable mark on the wiring.** Each unit of wiring-genome change adds about 2.8 large synaptic changes. The correlation is unmistakable over thousands of pairs, though in any single family it is hidden by noise.
- **New wiring is rare.** New synapses need a binding rule mutated past its threshold, and only 1.6 % of offspring got one in 12 generations. Most heritable change re-weights existing connections.

The connections that differed most between the four founders and the last generations (9 worms) are listed below. With 9 late worms these are illustrations, not established trends.

Connection	Founders (mean synapses)	Generations 10–12
CEPVR → RMHR	0.0	6.7
AWCR → ASEL	6.0	0.0
RIMR → AVAL	0.0	5.8
RIS → AVL	6.8	1.0
AWAR → ADFR	2.3	7.0
RICL → ADAR	1.8	6.2
DVA → SMBVR	3.8	0.0
ADAR → AVAR	9.1	5.5

The reel's offspring-vs-mother shot draws exactly this comparison for one family. Connections the offspring gained glow gold, and connections it lost glow blue.

What this proves, and what it does not

Eden shows that NEEUMAN can run every ingredient of Darwinian evolution together, mechanistically, inside one simulation:

- reproduction;
- inheritance through real meiosis;
- mutation;
- development of a unique brain in every individual;
- competition for food that decides who leaves descendants.

It does not yet show adaptation: after 16 generations, evolved worms do not out-compete their ancestors.

Supported by the runs

- Populations sustain themselves for many generations. The recorded plate reached generation 12 with 257 individuals over about 50 days of worm life.
- Genetic change accumulates and spreads. Wiring-genome divergence from the founders rose 1.3–2× in every line. In two of three selection lines, one founder strain's genome took over the whole population.

- Every offspring builds its own brain from its genome and grows from 222 to 302 neurons along the measured developmental trajectories. Inherited wiring changes are measurable (Spearman $\rho = 0.34$ between genetic and synaptic difference, $p \approx 10^{-84}$).
- One selection line changed its brain far more than its matched control from the same founders: about 170 new synapses per worm and 503 connections changed two-fold, against 128 in the control.

Not supported (yet)

- **Adaptation.** In head-to-head competition, evolved worms are statistically indistinguishable from their ancestors (see Experiments). With 32 worms per generation and mostly selfing, random drift is strong. Real C. elegans experiments needed around 100 generations and hundreds of worms to detect fitness gains.
- **Evolved behaviour.** Because the base worm steers poorly toward food, the strongest route to better foraging is weak. Selection acts on noisier traits: search, dwelling and development speed.
- **Real-time life history.** Life runs 3,600× faster than behaviour, and brood sizes are scaled. Males use the hermaphrodite connectome, and mating is a contact rule.
- **"Life".** This is a mechanistic model of a living worm, built from measured data, not life. The right claim is that NEEUMAN simulates the processes that drive evolution, at the level of neurons and synapses.

Next steps that would make the adaptation result decisive

1. Longer and larger lines: 100 generations at 100 worms per line, 5 selection and 5 control lines. The `evolve` command does this unchanged; on the PC it takes about a day per line.
2. Stronger, measurable selection: a fixed foraging challenge, such as distant lawns, so selection has a clear target.
3. Better steering in the base worm (klinotaxis through the SMD/RIA head circuit), so wiring mutations can improve chemotaxis.
4. The male connectome (Cook 2019, 385 neurons) and the real mating circuit.

The reel and voice-over

The reel is a plain vertical video (1080 × 1920, 30 fps, about 54 s) with no text on screen. Every frame is drawn from the recorded simulation:

- worms by NEEUMAN's implicit-body microscope renderer;

- brains and the family tree by a glow renderer, from each worm's own connectome and its recorded neural activity.

The voice-over below is timed to the shots. Read it at a calm pace; each line fits its shot with a little room.

Time	Shot	Voice-over
0–7 s	Four founder worms crawl on a bacterial lawn, under the microscope	"These four worms don't exist. Every neuron, every muscle, every movement is simulated inside NEEUMAN."
7–12 s	The male finds a hermaphrodite and mates	"One of them is a male. When he finds a mate, their genes mix."
12–19 s	Eggs are laid; embryos develop and hatch into larvae (time-lapse)	"Eggs. Embryos. And then, new life hatches out."
19–28 s	A newborn's brain grows: 222 neurons at hatching, 80 more are born, synapses multiply six-fold	"Each baby builds its own brain from its DNA: 222 neurons at birth, 302 as an adult, wired by the real developmental data of this animal."
28–35 s	The offspring's brain against its mother's: gained connections glow gold, lost ones blue	"And no two brains are the same. Mutation rewired this one: gold is new, blue is lost."
35–43 s	The whole plate across generations, time-lapse	"Generation after generation they compete for food, and the ones that eat, grow and breed faster leave more children."
43–49 s	The family tree grows outward from the four founders	"Four ancestors. Hundreds of descendants. Evolution, running inside a simulation."
49–54 s	A late-generation descendant, live	"This is Project Eden. Life, in NEEUMAN."

A shorter alternative for the first line, if the hook needs to land faster: "I simulated life. Then it started to evolve."

Keep claims in the narration matched to what the simulation shows. Say "simulated", not "alive", and "evolving in simulation", not "proved life". The evidence section shows what was measured.

How to run it in NEEUMAN

All commands run from the repository root with the NEEUMAN Python.

Goal	Command
Watch a living Eden plate, interactive	`python runtime/neeuman_live.py examples/eden-live.neeuman-code`
Record a continuous plate for the film	`python runtime/neeuman_eden.py run --treatment eden --seconds 1200 --seed 1 --out eden_runs/eden_s1 --record`
One evolution line (selection)	`python runtime/neeuman_eden.py evolve --treatment eden --generations 16 --n 32 --seed 1 --out eden_runs/evo_eden_s1`
Control line (mutation accumulation)	`python runtime/neeuman_eden.py evolve --treatment ma --generations 16 --n 32 --seed 1 --out eden_runs/evo_ma_s1`
Fitness: evolved vs ancestors	`python runtime/neeuman_eden.py compete --evolved eden_runs/evo_eden_s1 --reps 4 --out eden_runs/compete_eden_s1.json`
Statistics and neural changes	`python runtime/neeuman_eden.py analyse eden_runs --out eden_runs/analysis.json`
Render the reel (GPU)	`python runtime/eden_film.py eden_runs/eden_s1 --out eden_reel.mp4 --encoder nvenc`
Tests	`python -m pytest tests/test_eden.py`

New files

- `runtime/physics_kernel/domains/biology/substrate/eden_genome.py` : diploid genome, meiosis, sex, mutation.
- `.../substrate/eden_development.py` : connectome growth from genome and age.

- `.../substrate/eden_world.py`: batched living population, ecology, life history.
- `.../substrate/eden_assay.py`: common-garden behavioural assays.
- `.../substrate/eden_render.py`: microscope geometry of the plate.
- `.../aspects/eden.py`: the `Biology.eden` aspect (live window, film scripts, verification cases).
- `.../data/celegans/development.json` and `CECT_LICENSE`: Witvliet and Brittin data, birth times.
- `runtime/neeuman_eden.py`: experiments, competitions, analysis.
- `runtime/eden_film.py`: GPU reel renderer.
- `scripts/build_eden_development_data.py`, `examples/eden-live.neeuman-code`, `tests/test_eden.py`.