

Theodor Spiro

Independent Researcher — cellular perception, aging biomarkers, and the comparative biology of learning systems

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Emergent Ventures grant recipient (2026)

PROFILE

Independent computational researcher; biophysics training (Lomonosov Moscow State University). Current result: the malignant cells of **25 cancers, from every major lineage, converge on one normal human cell type** — the placental cytotrophoblast — a state that malignancy deepens about sixfold inside a patient's own tissue (Zenodo [10.5281/zenodo.20542130](https://doi.org/10.5281/zenodo.20542130) (<https://doi.org/10.5281/zenodo.20542130>)). Alongside: aging biomarkers replicated across unrelated substrates (412,730 ECG recordings; 823 EEG subjects across two cohorts; 263 GTEx donors plus four species) and the statistical structure of trained transformers (arXiv:2604.10571; 1,584 controlled ablations on Pythia 410M). Author and maintainer of two released, DOI-archived open-source research tools: **perceptome** (cellular perception analysis; 74/74 tests) and **metric-autopsy** (red-teaming a computed single-cell metric against QC and technical artifacts; 35 tests). 2026 Emergent Ventures recipient. Methodology inherited from experimental physics: predictions locked before the data are seen, bitwise-reproducible pipelines, bootstrap uncertainty quantification, and negative results published in full.

SOFTWARE & TOOLS

perceptome (2026) — Python toolkit for cellular perception analysis. 44 signaling modules; 9-PC eigenspace built from 154 Human Protein Atlas cell types; capacity-floor predictor; validity scorecard with three null controls; and the cancer-convergence reference anchored on the placental cytotrophoblast. Zenodo [10.5281/zenodo.20113468](https://doi.org/10.5281/zenodo.20113468) (<https://doi.org/10.5281/zenodo.20113468>) · 74/74 tests passing.

metric-autopsy (2026) — metric-agnostic gate system for separating biological signal from QC and technical artifacts in single-cell metrics. Eight gates (mathematical independence under simulated dropout, factorial QC parity, `n_genes` matching, stratified controls, cross-dataset replication, plus two judgment gates the tool elicits) probe a black-box `metric(data) -> float` and stop at the first blocking failure. Ships as a pip package, a Claude Code skill, and an MCP server. Zenodo [10.5281/zenodo.21195679](https://doi.org/10.5281/zenodo.21195679) (<https://doi.org/10.5281/zenodo.21195679>) · 35 tests passing.

PUBLICATIONS & PREPRINTS

Preprints (public — arXiv, or self-archived on Zenodo; not peer reviewed):

- **Cancers of all lineages converge on the placental cytotrophoblast, a normal invasive cell state that malignancy deepens.** Zenodo preprint, 2026. 25 cancers projected into a 44-module eigenspace built from normal cells only; program space contracts 6.3-fold, and within matched tumour–normal pairs malignancy deepens the state $\sim 6\times$ (colorectal 43/46, paired $P < 10^{-12}$). Zenodo [10.5281/zenodo.20542130](https://doi.org/10.5281/zenodo.20542130).
- **Universal statistical signatures of evolution in artificial intelligence architectures.** arXiv:2604.10571, 2026. 935 ablation experiments across 161 publications; substrate-independent heavy-tailed DFE.
- **Spectral exponents of the twelve-lead ECG reveal the anatomy of cardiac conduction disorders and a bifurcation between aging and disease.** Zenodo preprint, 2026 (submitted to bioRxiv). 412,730 recordings across three continents; CLBBB vs CRBBB AUC ≈ 0.98 cross-population. Zenodo [10.5281/zenodo.19945065](https://doi.org/10.5281/zenodo.19945065).
- **Transcriptomic noise accumulates within tissue identity across human aging.** Zenodo preprint (post-review v4), 2026. GTEx v8 + Tabula Muris Senis + Calico rat + macaque atlas; aging as systemic noise, not selective accumulation. Zenodo [10.5281/zenodo.19944444](https://doi.org/10.5281/zenodo.19944444).

Under review:

- **Waveform asymmetry as a biomarker of neural aging.** *Frontiers in Aging Neuroscience*, 2026. LEMON (N=215) + Dortmund Vital Study (N=608) + 208-subject 5-year longitudinal. Zenodo [10.5281/zenodo.19912202](https://doi.org/10.5281/zenodo.19912202).

Manuscripts (submission-ready / in preparation):

- **Cellular proteostasis modules causally enable memory consolidation through region-specific architectures.** Submission-ready. 26 predictions pre-registered across seven transcriptomic datasets; TLR9 knockout selectively blunts ER-chaperone induction by 60–75% and impairs contextual fear memory; 28 of 32 published proteostasis perturbations predicted, zero contradictions. [Summary \(https://mool32.github.io/memory-consolidation/\)](https://mool32.github.io/memory-consolidation/).
- **Functional differentiation generates universal fitness-effect distributions in neural networks.** Submission-ready. Pythia 410M, 1,584 controlled ablations across 8 checkpoints.
- **Clonal crystallization as a shared signature of bone-marrow aging and neural-network training.** Cross-substrate (Gini, eff_N) framework; caloric restriction rescues 64% of the aging drift in rat bone marrow.
- **Temporal architecture of signaling oscillations predicts cancer gene function across pathways.** Rise/recovery temporal classification; OR = 27.5, $p = 3.6 \times 10^{-9}$ across 14 pathways.
- **Negative feedback loop architecture as a modular predictor of cancer vulnerability.** 128 NFLs from KEGG; 59-fold CGC enrichment ($p = 9 \times 10^{-44}$); Irreversible Authority metric ($\rho = 0.83$).
- **The Oracle's Fingerprint: correlated AI forecasting errors and the limits of bias transmission.** GPT-4o / Claude / Gemini error correlation $r = 0.78$ on 568 Metaculus forecasts.
- **21,000 attempts to think differently: a Russian adaptation of the Divergent Association Task.** N = 21,159; Cronbach's $\alpha = 0.899$; live instrument deployed.

Technical reports:

- **EEG-based comprehension detection: a multi-dataset non-replication.** Honest negative result; 18 metrics, 5 datasets, 126 subjects.

ONGOING PILOTS

- **Self-specific representations localize in emergent attention heads.** Pilot study (Pythia 410M): 29 active meta-heads, all $\Delta_{\text{self}} > \Delta_{\text{cross}}$ (binomial $p < 10^{-8}$). Scaling and cross-model replication in progress before write-up.
- **Epistasis mapping in transformer attention heads.** Cross-model pairwise head-ablation interactions (Pythia 410M, OLMo-2 1B); pre-registered, multi-phase.
- **Developmental epistasis in single-cell RNA-seq.** Biology-side test of the ML epistasis signature on Schiebinger 2019 reprogramming; pilot calibration.
- **Epistemic Fitness Pilot.** Pre-registered (hash-locked) test of whether an LLM can discriminate scientific ideas by future impact.

RESEARCH EXPERIENCE

Independent computational researcher · 2020 – present Independent research program across cellular perception, aging biomarkers, comparative biology of neural networks, and research-validation methodology. Recent concentration on the perceptome framework and single-cell / transcriptomic analysis; earlier work in computational neuroscience (EEG) and systems biology. All inferential projects preregistered; full code and data released on GitHub and Zenodo.

Affiliated with Vaika Inc. · 2024 – present Vaika Inc. is a not-for-profit aging-research organization associated with the laboratory of Andrei Gudkov (Roswell Park Comprehensive Cancer Center). Aging manuscripts developed in this affiliation (e.g. pi-tissue-aging) were revised under Gudkov review.

Computational Biology Intern — BostonGene · 2022 Computational analysis in immuno-oncology: molecular tumor profiling and multi-omics data in a clinical-genomics setting.

B.Sc. / M.Sc. research — Moscow State University, Faculty of Physics · 2018 – 2022 Supervisor: Prof. L. Yakovenko. Agent-based / cellular-automata modeling of the cellular response to pro-inflammatory stimuli (TLR4/TLR6 → NF- κ B → TNF → apoptosis), identifying key parameters of the innate-immunity signaling pathway.

RESEARCH METHODOLOGY

Author of the validation framework applied across the portfolio (mool32.github.io/methodology (<https://mool32.github.io/methodology/>)) — hash-locked pre-registration, sign-convention locks, locked-vs-working artifacts, reproducibility standards, negative results published in full, and machine-readable publishing. Includes explicit disclosure of how AI systems are used as research instruments and what they are deliberately not trusted with.

EDUCATION

M.Sc. Biophysics (coursework completed) — Lomonosov Moscow State University, Faculty of Physics · 2021 – 2022 Computer simulation in biology; physics of biopolymers; physicochemical kinetics; magnetic radio-spectroscopy in biology and medicine. Thesis defense not completed due to relocation from Russia in 2022.

B.Sc. Biophysics — Lomonosov Moscow State University, Faculty of Physics · 2014 – 2021 Completed over an extended period: taught mathematics and physics throughout the degree (see Teaching) and became a parent during it.

Lyceum 1525, Physics & Mathematics — Moscow · 2010 – 2014

TEACHING

Eleven years teaching mathematics and physics (ages 11–25), including curriculum design at Le Sallay Academy (selective international gifted program, 2025–2026), co-founder and lead teacher of BrainyBara (Israel, 2022–present), and prior roles at Foxford Online School (Moscow, 2015–2018) and Moscow State University (Instructor, Advanced Mathematics, 2018–2020). Full teaching record available on request.

PROFESSIONAL DEVELOPMENT

- Evidence-Based Teaching Practices — Harvard University BOK Center · 2022 – 2024
- Psychology of Development and Learning — MSUPE, Moscow · 2020
- Learning to Teach Online — University of New South Wales · 2020

GRANTS & HONORS

- **Emergent Ventures grant** — Mercatus Center · 2026
- **Lomonosov Scientific Conference** — presentation, Moscow · 2021

TECHNICAL SKILLS

- **Programming:** Python (NumPy, Pandas, SciPy, scikit-learn, matplotlib, PyTorch), Git, Bash, LaTeX, SQL basics
- **Methods:** preregistered experimental design, bootstrap uncertainty quantification, distribution fitting with AIC comparison, dimensionality reduction, time-series and signal analysis, agent-based modeling
- **Bioinformatics:** single-cell RNA-seq pipelines (scanpy / AnnData), quality control and batch/confound diagnostics, gene-set and pathway module scoring, differential expression, PCA and eigenspace construction, cross-dataset replication
- **Data domains:** single-cell & bulk RNA-seq, GTEx / Tabula Muris Senis / Human Protein Atlas, EEG / ECG signals, neural-network interpretability, large-scale forecasting data
- **Software engineering:** installable Python packages (`pyproject.toml`), pytest suites, GitHub Actions CI, MCP servers, containerless reproducible pipelines with pinned environments
- **AI-assisted research:** LLM-integrated analysis pipelines under an explicit preregistration / reproducibility framework

LANGUAGES

Russian (native) · English (C1; all research published in English) · Hebrew (beginner)