

Resource Summary Report

Generated by [ASWG](#) on Aug 5, 2026

GEMS

RRID:SCR_009188

Type: Tool

Proper Citation

GEMS (RRID:SCR_009188)

Resource Information

URL: <http://www.angelfire.com/mn2/nath/gems.html>

Proper Citation: GEMS (RRID:SCR_009188)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented September 22, 2016. Software application for fitting Genetic Epidemiology Models by running stochastic simulation in relation to disease dynamics.

Abbreviations: GEMS

Synonyms: Genetic Epidemiology Models

Resource Type: software application, software resource

Keywords: gene, genetic, genomic, unix, (dec-alpha), linux

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: GEMS

Resource ID: SCR_009188

Alternate IDs: nlx_154327

Old URLs: <http://statgen.genomecenter.howard.edu/gems.htm>

Record Creation Time: 20220129T080251+0000

Record Last Update: 20260805T044219+0000

Ratings and Alerts

No rating or validation information has been found for GEMS.

No alerts have been found for GEMS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 463 mentions in open access literature.

Listed below are recent publications. The full list is available at [ASWG](#).

Raposo CJ, et al. (2025) Functional memory T cells are derived from exhausted clones and expanded by checkpoint blockade. *bioRxiv : the preprint server for biology*.

Liu C, et al. (2025) Integrative single-cell and spatial transcriptome analysis reveals heterogeneity of human liver progenitor cells. *Hepatology communications*, 9(3).

van Hijfte L, et al. (2025) Gemistocytic tumor cells programmed for glial scarring characterize T cell confinement in IDH-mutant astrocytoma. *Nature communications*, 16(1), 1156.

Ding X, et al. (2025) Giant KASH proteins and ribosomes synergistically establish cytoplasmic biophysical properties in vivo. *bioRxiv : the preprint server for biology*.

Amisaki M, et al. (2025) IL-33-activated ILC2s induce tertiary lymphoid structures in pancreatic cancer. *Nature*, 638(8052), 1076.

Li X, et al. (2025) Immunoregulatory programs in anti-N-methyl-D-aspartate receptor encephalitis identified by single-cell multi-omics analysis. *Clinical and translational medicine*, 15(1), e70173.

Munke K, et al. (2025) In vivo regulation of the monocyte phenotype by *Mycobacterium marinum* and the ESX-1 type VII secretion system. *Scientific reports*, 15(1), 4545.

Li X, et al. (2025) Single-Cell RNA sequencing reveals mitochondrial dysfunction in microtia chondrocytes. *Scientific reports*, 15(1), 1021.

Xu J, et al. (2025) Personalized Human Astrocyte-Derived Region-Specific Forebrain Organoids Recapitulate Endogenous Pathological Features of Focal Cortical Dysplasia. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(8), e2409774.

Perez JM, et al. (2025) Investigating proteogenomic divergence in patient-derived xenograft models of ovarian cancer. *Scientific reports*, 15(1), 813.

Shen Y, et al. (2025) Therapeutic potential and mechanisms of umbilical cord mesenchymal stem cells differentiating into tendon cells and promotion of rotator cuff tendon-bone healing. *Journal of tissue engineering*, 16, 20417314251315185.

Oudbier SJ, et al. (2025) Patients' Experienced Usability and Satisfaction With Digital Health Solutions in a Home Setting: Instrument Validation Study. *JMIR medical*

informatics, 13, e63703.

McCreery CV, et al. (2025) Investigating intestinal epithelium metabolic dysfunction in celiac disease using personalized genome-scale models. *BMC medicine*, 23(1), 95.

Tatsumi N, et al. (2025) CD301b+ dendritic cell-derived IL-2 dictates CD4+ T helper cell differentiation. *Nature communications*, 16(1), 2002.

Beura S, et al. (2024) Genome-scale community modelling elucidates the metabolic interaction in Indian type-2 diabetic gut microbiota. *Scientific reports*, 14(1), 17259.

Chang LY, et al. (2024) Inference of single-cell network using mutual information for scRNA-seq data analysis. *BMC bioinformatics*, 25(Suppl 2), 292.

Nev OA, et al. (2024) Metabolic modelling as a powerful tool to identify critical components of *Pneumocystis* growth medium. *PLoS computational biology*, 20(10), e1012545.

De Bernardini N, et al. (2024) pan-Draft: automated reconstruction of species-representative metabolic models from multiple genomes. *Genome biology*, 25(1), 280.

Ye J, et al. (2024) Single cell-spatial transcriptomics and bulk multi-omics analysis of heterogeneity and ecosystems in hepatocellular carcinoma. *NPJ precision oncology*, 8(1), 262.

Zhang X, et al. (2024) Single-cell expression and immune infiltration analysis of polyamine metabolism in breast cancer. *Discover oncology*, 15(1), 666.