

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Harvard Medical School, Department of Systems Biology: The Megason Lab -GoFigure Software

RRID:SCR_008037

Type: Tool

Proper Citation

Harvard Medical School, Department of Systems Biology: The Megason Lab -GoFigure Software (RRID:SCR_008037)

Resource Information

URL: <https://wiki.med.harvard.edu/SysBio/Megason/GoFigure>

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Description: GoFigure is a software platform for quantitating complex 4d in vivo microscopy based data in high-throughput at the level of the cell. A prime goal of GoFigure is the automatic segmentation of nuclei and cell membranes and in temporally tracking them across cell migration and division to create cell lineages. GoFigure v2.0 is a major new release of our software package for quantitative analysis of image data. The research focuses on analyzing cells in intact, whole zebrafish embryos using 4d (xyzt) imaging which tends to make automatic segmentation more difficult than with 2d or 2d+time imaging of cells in culture. This resource has developed an automatic segmentation pipeline that includes ICA based channel unmixing, membrane nuclear channel subtraction, Gaussian correlation, shape models, and level set based variational active contours. GoFigure was designed to meet the challenging requirements of in toto imaging. In toto imaging is a technology that we are developing in which we seek to track all the cell movements and divisions that form structures during embryonic development of zebrafish and to quantitate protein expression and localization on top of this digital lineage. For in toto imaging, GoFigure uses zebrafish embryos in which the nuclei and cell membranes have been marked with 2 different color fluorescent proteins to allow cells to be segmented and tracked. A transgenic line in a third color can be used to mark protein expression and localization using a genetic approach that this resource developed called FlipTraps or using traditional transgenic approaches. Embryos are imaged using confocal or 2-photon microscopy to capture high-resolution xyzt image sets used for cell tracking. The GoFigure GUI will provide many tools for visualization and analysis of bioimages. Since fully automatic segmentation of cells is never perfect, GoFigure will provide easy to use tools for semi-automatically and manually adding, deleting, and editing traces in 2d (figures-xy, xz, or yz), 3d (meshes- xyz), 4d (tracks- xyzt) and 4d+cell division (lineages).

GoFigure will also provide a number of views into complex image data sets including 3d XYZ and XYT image views, tabular list views of traces, histograms, and scattergrams. Importantly, all these views will be linked together to allow the user to explore their data from multiple angles. Data will be easily sorted and color-coded in many ways to explore correlations in higher dimensional data. The GoFigure architecture is designed to allow additional segmentation, visualization, and analysis filters to be plugged in. Sponsors: GoFigure is developed by Harvard University., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Synonyms: GoFigure

Resource Type: data or information resource, data processing software, data visualization software, portal, software application, software resource, topical portal

Keywords: embryo, expression, fluorescent, gaussian, genetic, 2d, 2-photon, 4d, analysis, bioimage, cell, cell membrane, cell movement, channel, confocal, contour, culture, data, dimensional, high-resolution, histogram, in vivo, localization, microscopy, model, nuclear, nucleus, protein, scattergram, segmentation, shape, software, technology, toto imaging, tracking, transgenic, visualization, zebrafish, image

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Harvard Medical School, Department of Systems Biology: The Megason Lab -GoFigure Software

Resource ID: SCR_008037

Alternate IDs: nif-0000-10243

Record Creation Time: 20220129T080245+0000

Record Last Update: 20260905T132617+0000

Ratings and Alerts

No rating or validation information has been found for Harvard Medical School, Department of Systems Biology: The Megason Lab -GoFigure Software.

No alerts have been found for Harvard Medical School, Department of Systems Biology: The Megason Lab -GoFigure Software.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Zhou J, et al. (2024) Integrative analysis of the methylome and transcriptome of tomato fruit (*Solanum lycopersicum* L.) induced by postharvest handling. *Horticulture research*, 11(6), uhae095.

Green AA, et al. (2017) Recovery of shape and size in a developing organ pair. *Developmental dynamics : an official publication of the American Association of Anatomists*, 246(6), 451.

Giovannone D, et al. (2012) Slits affect the timely migration of neural crest cells via Robo receptor. *Developmental dynamics : an official publication of the American Association of Anatomists*, 241(8), 1274.

Clarke J, et al. (2009) Live imaging of development in fish embryos. *Seminars in cell & developmental biology*, 20(8), 942.

Ursic-Bedoya RJ, et al. (2007) *Rhodnius prolixus*: identification of immune-related genes up-regulated in response to pathogens and parasites using suppressive subtractive hybridization. *Developmental and comparative immunology*, 31(2), 109.