

# Giuseppe-Antonio Saldi Sato

Computational Biologist & Programmer

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## Education

Aug 2015 – July 2021	<b>New York University, Graduate School of Arts and Science, New York, NY</b> <i>PhD in Computational Biology</i> Thesis: "Cell fate and function during brain development revealed by systems biology methods" under the supervision of Prof. Richard Bonneau and Prof. Gordon Fishell GPA: 3.75
Sep 1998 – Jun 2003	<b>Haute École de la Province de Liège Rennequin Sualem, Liège, Belgium</b> <i>Bachelor in Industrial Informatics and Real time computing</i> Internship : "A study of genetic linkage related to animal genomics" under the supervision of Prof. Michel Georges

## Work Experience

Jun 2017 - Present	<b>Broad Institute of MIT and Harvard, Stanley center – Cambridge MA Associate Member</b> <ul style="list-style-type: none"><li>Developed and applied computational methods to investigate neuron progenitor priming, and derive critical insight of microglia synapse pruning.</li></ul>
Jan 2013 - Aug 2015	<b>New York University Abu Dhabi, Center for Genomics and Systems Biology (CGSB) – Abu Dhabi UAE Full Stack Developer &amp; Research Assistant</b> <ul style="list-style-type: none"><li>Provided support for the analysis of a variety of large datasets obtained by next generation DNA and RNA sequencing.</li><li>Conceptualized, implemented and deployed a Laboratory Information Management System (LIMS) for the Core Sequencing Facilities using Django, AJAX, REST, service redundancy, automated database backup, Shibboleth Single Sign-on architecture, Apache2 setup) The LIMS is currently in production at NYU.</li></ul>
Jul 2010 - Dec 2012	<b>EGOWEB – Belgium Web developer</b> <ul style="list-style-type: none"><li>Converted graphic designs into working websites using PHP, AJAX, CSS, HTML5, JavaScript, wordpress and FLASK.</li></ul>
Mar 2007 - Dec 2012	<b>GIGA University of Liège (ULG) – Belgium System Administrator</b> <ul style="list-style-type: none"><li>Complete setup and management of high performance computing (HPC) related to bioinformatics analysis</li><li>IT support hardware and software, including network management and security, data backup and recovery, OS (Linux, MacOS, Windows )</li></ul>
Jul 2006 - Feb 2007	<b>Synerglass Soft S.A. – Belgium Analyst Programmer</b> <ul style="list-style-type: none"><li>Implemented various Synerglass functions using Windev</li></ul>
Oct 2005 - Jul 2006	<b>LabSET IFRES University of Liège – Belgium Web developer</b> <ul style="list-style-type: none"><li>PHP portal development and administration</li></ul>
Feb 2005 - Oct 2005	<b>Sony Service Center Europe – Belgium Customer Support Analyst</b> <ul style="list-style-type: none"><li>Provided IT and network support in French, English and Italian.</li></ul>
Jun 2003 - Dec 2004	<b>Faculty of Veterinary Medicine University of Liège – Belgium Programmer</b> <ul style="list-style-type: none"><li>Database and Software development applied to data collection and curation for genomic analysis. PERL, bash, JAVA, MySQL.</li></ul>

## Skills

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- Language: English (fluent); French (native); Italian (Fluent).
- Programming: Python, R, C/C++ , Java, Javascript, Django, HTML, CSS, PHP, REST, PERL, AJAX, SQL, bash, MATLAB, FLASK.
- Software: Illustrator, Photoshop, Linux, MacOS, Windows, Jupyter.
- Domain Expertise: Machine Learning, Neuroscience, Gene regulation, Single Cell Genomics data analysis and integration, Server administration, Web development, High Performance Computing, Kubernetes, Dask.

## Publications

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| 2021 | <ol style="list-style-type: none"><li>1. Favuzzi, E., Huang, S., <b>Saldi, G.-A.</b>, Binan, L., Ibrahim, L. A., Fernández-Otero, M., Cao, Y., Zeine, A., Sefah, A., Zheng, K., <i>et al.</i> GABA-receptive microglia selectively sculpt developing inhibitory circuits. <i>Cell</i> <b>184</b>, 4048–4063 (2021).</li><li>2. Gibbs, C. S., Jackson, C. A., <b>Saldi, G.-A.</b>, Shah, A., Tjärnberg, A., Watters, A., De Veaux, N., Tchourine, K., Yi, R., Hamamsy, T., <i>et al.</i> Single-cell gene regulatory network inference at scale: The Inferelator 3.0. <i>bioRxiv</i> (2021).</li><li>3. Tjärnberg, A., Mahmood, O., Jackson, C. A., <b>Saldi, G.-A.</b>, Cho, K., Christiaen, L. A. &amp; Bonneau, R. A. Optimal tuning of weighted kNN-and diffusion-based methods for denoising single cell genomics data. <i>PLoS computational biology</i> <b>17</b>, e1008569 (2021).</li></ol>  |
| 2020 | <ol style="list-style-type: none"><li>4. Jackson, C. A., Castro, D. M., <b>Saldi, G.-A.</b>, Bonneau, R. &amp; Gresham, D. Gene regulatory network reconstruction using single-cell RNA sequencing of barcoded genotypes in diverse environments. <i>Elife</i> <b>9</b>, e51254 (2020).</li><li>5. Vormstein-Schneider, D., D Lin, J., Pelkey, K. A., Chittajallu, R., Guo, B., Arias-Garcia, M. A., Allaway, K., Sakopoulos, S., Schneider, G., Stevenson, O., Vergara, J., Sharma, J., Zhang, Q., Franken, T. P., Smith, J., Ibrahim, L. A., Kevin, J., Sabri, E., Huang, S., Favuzzi, E., Burbridge, T., <b>Saldi, G.-A.</b>, Gorissen, B. L., Yuan, X., Zaghloul, K. A., Devinsky, O., Sabatini, B. L., Batista-Brito, R., Reynolds, J., Feng, G., Fu, Z., McBain, C. J., Fishell, G. &amp; Dimidschstein, J. Viral manipulation of functionally distinct interneurons in mice, non-human primates and humans. <i>Nature neuroscience</i> <b>23</b>, 1629–1636 (2020).</li></ol> |
| 2016 | <ol style="list-style-type: none"><li>6. Dimidschstein, J., Chen, Q., Tremblay, R., Rogers, S. L., <b>Saldi, G.-A.</b>, Guo, L., Xu, Q., Liu, R., Lu, C., Chu, J., <i>et al.</i> A viral strategy for targeting and manipulating interneurons across vertebrate species. <i>Nature neuroscience</i> <b>19</b>, 1743–1749 (2016).</li><li>7. Perry, M., Kinoshita, M., <b>Saldi, G.-A.</b>, Huo, L., Arikawa, K. &amp; Desplan, C. Molecular logic behind the three-way stochastic choices that expand butterfly colour vision. <i>Nature</i> <b>535</b>, 280–284 (2016).</li></ol>   |