



# Ryan J. O'Hara

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## SUMMARY

- Web developer with experience in Python and Django
- Developed a #1 ranked iPad app
- Contributed to multiple open-source projects
- Produced at every stage of the software lifecycle
- Recently learned Backbone, Marionette, and Bootstrap
- Background in Java and object-oriented design
- Co-authored over five biomedical articles
- Began building websites at an underprivileged school
- Committed code thousands of times over the last decade

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## EXPERIENCE

*Analyst/Programmer, Children's Hospital of Philadelphia*  
Philadelphia, PA — 2008-Present

As a software developer in biomedical research, I designed simple and elegant solutions to complex problems to help support researchers, clinicians, and scientists in advancing healthcare. Areas of contribution include genomics, electronic health record, clinical decision support, and mobile and web development.

### Accomplishments

- Contributed to Harvest, a three-layered, open-source toolkit for creating web apps for integrating and reporting data
- Lead development of CBMiSeq, a genome sequence analysis platform built with Django and Bootstrap
- Developed Genome Wowser, a top-ranked, award-winning genome browser iPad application

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## EDUCATION

University of Pennsylvania, PA — BA  
Cognitive Science, 2006

- Concentrated on Computer Science
- Minored in Linguistics
- Wrestled on varsity team

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## SKILLS

Python, Django, Objective C, iOS, Javascript, JQuery, Backbone, Marionette, Bootstrap, HTML5, CSS, Java, PHP, Perl, PostgreSQL, MySQL, SQLite, Ant, Maven, Puppet, Vagrant, Cron, Makefile, CVS, SVN, Mercurial, Git, Github, Emacs, Eclipse, IntelliJIDEA, Linux, UNIX, Apache, Tomcat, Lucene, Berkeley DB, Inkscape, Gimp, FogBugz, Request Tracker, Trello, Wordpress, Scrum, Jenkins, Selenium, Sublime, XCode JSON, XML, Balsamiq, KML



- Owned the process of resolving the findings from quarterly PCI audits of CBMI's externally accessible websites
- Lead development of CBMiApps, a custom Wordpress site leveraging the WooCommerce and ShopDock plug-ins
- Lead development of MyAsthma, a shared decision making portal for pediatric chronic illness built with Django
- Lead development of a Django-driven immunization alert application built with Django and JQuery
- Developed CNV Workshop, an open-source, Java-based web platform for analyzing genome variation
- Lead development of a geographic information system of Autism providers using GeoDjango and Raphael

*Programmer, Children's Hospital of Philadelphia*  
Philadelphia, PA — 2006-2008

#### Accomplishments

- Developed CNV, a Java application to deliver data from the first high resolution CNV map of the human genome
- Lead development of Peaces, a Facebook application to fundraise for ADHD
- Lead a successful pilot of Confluence, a content management system, to enhance collaboration among researchers

*Intern, Children's Hospital of Philadelphia*  
Philadelphia, PA — 2005-2006

#### Accomplishments

- Developed FABLE, a Java web application to search mined biomedical literature and find lists of associated genes

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## PUBLICATIONS

- X Gai, H M Xie, J C Perin, N Takahashi, K Murphy, A S Wenocur, M D'arcy, **R J O'Hara**, E Goldmuntz, D E Grice, T H Shaikh, H Hakonarson, J D Buxbaum, J Elia and P S White. Rare structural variation of synapse and neurotransmission genes in autism. *Molecular Psychiatry*. 2011.  
<http://cnv.sourceforge.net/>
- Shaikh, T.H., Gai, X., Perin, J.C., Glessner, J.T., Xie, H., Murphy, K., **O'Hara, R.**, Casalunovo, T., Conlin, L.K., D'Arcy,

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## AWARDS

Genome Wowser, Best Science App.  
Genetic Engineering & Biotechnology  
News. February 2013. Vol. 33, No.3

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## ACTIVITIES

Volunteered for town newspaper,  
self-employed as software contractor,  
and coached amateur wrestling

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## REFERENCES

Available upon request



M., Frackelton, E.C., Geiger, E.A., Haldeman-Englert, C., Imielinski, M., Kim, C.E., Medne, L., Annaiah, K., Bradfield, J.P., Dabaghyan, E., Eckert, A., Onyiah, C.C., Ostapenko, S., Otieno, F.G., Santa, E., Shaner, J.L., Skraban, R., Smith, R.M., Elia, J., Goldmuntz, E., Spinner, N.B., Zackai, E.H., Chiavacci, R.M., Grundmeier, R., Rappaport, E.F., Grant, S.F., White, P.S., and Hakonarson, H. High-resolution mapping and analysis of copy number variations in the human genome: a data resource for clinical and research applications. *Genome Res* 19(9): 1682-1690. 2009. <http://cnv.chop.edu/> (feature demo on The OpenHelix Blog <http://blog.openhelix.eu/?p=2814>)

- Porter M.W., D. Milley, K. Oliveti, A. Ladd, **R.J. O'Hara**, B.R. Desai and P.S. White Balancing Entrepreneurship and Business Practices for e-Collaboration: Responsible Information Sharing in Academic Research. *AMIA Annu Symp Proc*, 1100. 2009. <https://share.chop.edu>
- Desai B., **O'Hara R.**, White P. "Use of an Enterprise Wiki as a Research Collaboration Tool." *31st Annual American Medical Informatics Association Symposium*. November 2007.
- White P., Murphy P., **O'Hara R.**, D'arcy M., Carroll S., Jin Y., Fang H., Kim J., Mandel M., Liberman M., McDonald R., and Pereira F. "An automated method for extracting normalized mentions of human genes and proteins in biomedical text." *56th Annual Meeting of the American Society of Human Genetics*. October 2006

