# Amit R. Indap

Specialties: Bioinformatics, Human Genetics, Python

## Experience

Since December 2013

*Research Fellow for* [*Reproductive Endocrine Unit, Massacusetts General Hospital*](http://www.massgeneral.org/reproductiveendocrine//) (Boston, Massachusetts).

Investigating the genetic basis of reproductive endocrine disorders using whole exome and genome sequencing

January 2009 - October 2013

*PhD in Bioinformatics with* [*Gabor T. Marth*](http://bioinformatics.bc.edu/marthlab/wiki/index.php/Main_Page) (Boston College Chestnut Hill, Massachusetts).

Utilized existing and wrote novel software to analye data from population scale and family based whole genome and whole exome re-sequencing studies to characterize the contribution of rare variants to human genetic diversity and disease risk.

August 2005 - December 2008

*Bioinformatics Programmer* [*Cornell University*](http://www.cornell.edu/) (Ithaca, NY).

Implemented bioinformatic data analysis pipelines for DNA re-sequencing and genotyping datasets for research projects in population and evolutionary genomics which helped facilitate the publication of over 10 papers in leading scientific journals.

February 2001 - July 2002

*Bioinformatics Programmer at* [*Stanford University*](http://www.stanford.edu) (Stanford, CA).

Implemented informatics pipeline for sequencing and genotyping of candidate genes involved in complex diseases.

## Selected Publications

[Variant discovery in targeted resequencing using whole genome amplified DNA](http://www.ncbi.nlm.nih.gov/pubmed/23837845)

[The functional spectrum of low-frequency coding variation](http://www.ncbi.nlm.nih.gov/pubmed/21917140)

[A map of human genome variation from population-scale sequencing](http://www.ncbi.nlm.nih.gov/pubmed/20981092)

[Assessing the evolutionary impact of amino acid mutations in the human genome](http://www.ncbi.nlm.nih.gov/pubmed/18516229)

[Proportionally more deleterious genetic variation in European than in African populations](http://www.ncbi.nlm.nih.gov/pubmed/18288194)

[Analysis of concordance of different haplotype block partitioning algorithms](http://www.ncbi.nlm.nih.gov/pubmed/16356172)

## Education

2009-2013

*PhD in Bioinformatics at Boston College* Chestnut Hill , Massachusetts.

Title: Discovering rare variants from populations to families. Advisor: [Gabor T. Marth](http://bioinformatics.bc.edu/marthlab/wiki/index.php/Main_Page) Defended in October 2013.

2003-2005

*MS in Bioinformatics at Medical College of Wisconsin and Marquette University* Milwaukee, Wisconsin.

Title: Analysis of concordance of haplotype block partitional algorithms. Advisor: Michael Olivier

1996-2000

*BS in Molecular and Cellularl Biology, minor Computer Science University of Arizona* Tucson, Arizona.

Selected as Outstanding Graduating Senior in Department of Molecular and Cellular Biology.

## Skills

Bioinformatics : GATK, MOSAIK, Freebayes, PLINK, samtools, Picard.

Programming : Python, R, Perl, familiar with Java and C++, [GitHub repo](https://github.com)

Molecular Biology : PCR, gel electrophoresis.

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