# Mikel Egaña Aranguren, Ph.D.

## Background

Research statement:   My research area is Bioinformatics. I am interested in the exploitation of Semantic Web technology (RDF, OWL, automated reasoning, *etc.*) to improve knowledge management in Life Sciences. The realisation of this interest involves the development of semantic resources (Ontologies, Knowledge Bases, Linked Data datasets, Semantic Web Services, *etc.*) and the creation of tools for exploiting such resources.

Research keywords:   Bioinformatics, Life Sciences Semantic Web, Linked Data, Biomedical ontologies, (Meta) Genomics, Open Data, Identifiers, Beyond PDF, Beyond Impact Factor, Open Access, Free Software.

## Placements (Including funding) and education

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| 4/2014-4/2015 | Post-doc at the University of Basque Country (UPV-EHU), as a member of the Functional Genomics Group of the Department of Genetics, Physical Anthropology and Animal Physiology. |
| 2/2011-2/2014 | Post-doc at UPM (Spain) funded by Marie Curie Cofund (EU). Biological Informatics Group, Centre for Plant Biotechnology and Genomics (CBGP); Ontology Engineering Group, Computer Science Department. |
| 11/2009-12/2009 | Researcher in the OGO project at UM, Spain. Funded by the project "Web platform for ontology-guided knowledge management in functional genomics" (11/01/2007 to 10/01/2010), Autonomous Community of the Region of Murcia (BIO-TEC 06/01-0005). |
| 5/2006-10/2006 | Researcher at Flanders Institute for Biotechnology (VIB), Belgium, funded by Marie Curie Early Stage Training (EST) by the EU. Member of the Computational Biology group of the Department of Plant Systems Biology. |
| 9/2005 | Research visit to the European Bionformatics Institute (EBI), UK, to work with the Gene Ontology editors. Funded by the Network of Excellence on Semantic Interoperability and Data Mining in Biomedicine (EU). |
| 1/2005-7/2009 | Ph.D. in Computer Science at University of Manchester, UK, as a member of the Bio-Health Informatics Group, |

thesis title: "Role and Application of Ontology Design Patterns (ODPs) in Bio-ontologies". External examiner: Michel Dumontier (Carleton University, Canada); Supervisor: Robert Stevens; Advisor: Alan Rector. Fees allowance by Engineering and Physical Sciences Research Council (EPSRC) and maintenance allowance by University of Manchester.

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| 10/2003-9/2004 | M.Sc. in Bioinformatics at University of Manchester (UK). Distinction award for the thesis entitled "Improving the structure of the Gene Ontology". |
| 6/2002 | Evolutionary Ecology field course at Cardiff University, organised by Canterbury Christ Church University College (UK). |
| 9/2001-3/2002 | Environmental Biology at Canterbury Christ Church University College (UK) as Erasmus student. |
| 10/1997-9/2003 | B.Sc. in Biology at University of Basque Country (EHU). |

## Journal publications

- Mikel Egaña Aranguren, Jesualdo Tomás Fernández-Breis, Michel Dumontier. Special issue on Linked Data for Health Care and the Life Sciences (Editorial). *Semantic Web Journal* 2014, 5(2): 99-100.

- José Antonio Miñarro-Giménez, Mikel Egaña Aranguren, Boris Villazón-Terrazas, Jesualdo Tomás Fernández-Breis. Translational research combining orthologous genes and human diseases with the OGOLOD dataset. *Semantic Web Journal* 2014, 5(2): 145-149.

- Mikel Egaña Aranguren, Jesualdo Tomás Fernández-Breis, Erick Antezana, Chris Mungall, Alejandro Rodríguez González, Mark D. Wilkinson. OPPL-Galaxy, a Galaxy tool for enhancing ontology exploitation as part of bioinformatics workflows. *Journal of Biomedical Semantics* 2013, 4(1): 2.

- Astrid Duque-Ramos, Jesualdo Tomás Fernández-Breis, Miguela Iniesta, Michel Dumontier, Mikel Egaña Aranguren, Stefan Schulz, Nathalie Aussenac-Gilles, Robert Stevens. Evaluation of the OQuaRE framework for ontology quality. *Expert Systems with Applications* 2013, 40(7): 2696-2703.

- José Antonio Miñarro-Giménez, Mikel Egaña Aranguren, Boris Villazón-Terrazas, Jesualdo Tomás Fernández-Breis. Publishing Orthology and Diseases Information in the Linked Open Data cloud. *Current Bioinformatics* 2012, 7(3): 255-266.

- Vladimir Mironov, Erick Antezana, Mikel Egaña Aranguren, Ward Blondé, Bernard De Baets, Robert Stevens, Martin Kuiper. Flexibility and utility of the cell cycle ontology. *Applied Ontology* 2011, 6(3): 247-261.

- Jose Antonio Miñarro-Gimenez, Mikel Egaña Aranguren, Rodrigo Martínez Béjar, Jesualdo Tomás Fernández-Breis, Marisa Madrid. Semantic integration of information about orthologs and diseases: The OGO system. *Journal of Biomedical Informatics* 2011, 44: 1020-1031.

- Erick Antezana, Ward Blondé, Mikel Egaña Aranguren, Alistair Rutherford, Robert Stevens, Bernard De Baets, Vladimir Mironov, Martin Kuiper. BioGateway: a semantic systems biology tool for the life sciences. *BMC bioinformatics* 2009, 10(Suppl 10): S11.

- Erick Antezana, Mikel Egaña Aranguren, Ward Blondé, Aitzol Illarramendi, Iñaki Bilbao, Bernard De Baets, Robert Stevens, Vladimir Mironov, Martin Kuiper. The Cell Cycle Ontology: An application ontology for the representation and integrated analysis of the cell cycle process. *Genome Biology* 2009, 10: R58.

- Mikel Egaña Aranguren, Erick Antezana, Martin Kuiper, Robert Stevens. ODPs for bio-ontologies: a case study on the Cell Cycle Ontology. *BMC bioinformatics* 2008, 9(Suppl 5): S1.

- Mikel Egaña Aranguren, Chris Wroe, Carole Goble, Robert Stevens. *In situ* migration of handcrafted ontologies to Reason-able Forms. *Data & Knowledge Engineering* 2008, 66: 147-162.

- Erick Antezana, Mikel Egaña Aranguren, Bernard De Baets, Martin Kuiper, Vladimir Mironov. ONTO-PERL: An API supporting the development and analysis of bio-ontologies. *Bioinformatics* 2008, 24(6): 885-887.

- Mikel Egaña Aranguren, Sean Bechoffer, Phillip Lord, Ulrike Sattler, Robert Stevens. Understanding and using the meaning of statements in a bio-ontology: recasting the Gene Ontology in OWL. *BMC Bioinformatics* 2007, 8: 57.

- Robert Stevens, Mikel Egaña Aranguren, Katy Wolstencroft, Ulrike Sattler, Nick Drummond, Mathew Horridge. Using OWL to Model Biological Knowledge. *International Journal of Human Computer Studies* 2006, 65(7): 583-594.

## Conference proceedings

- Alejandro Rodríguez Iglesias, Marcos Martinez Romero, Mikel Egaña Aranguren, Mark D. Wilkinson. Nanopublishing clinical diagnoses: tracking diagnostic knowledge base content and utilization. 27th IEEE International Symposium on Computer-Based Medical Systems (CBMS 2014): 335-340.

- Alejandro Rodríguez Iglesias, Mikel Egaña Aranguren, Alejandro Rodríguez González, Mark D. Wilkinson. Plant-Pathogen Interactions Ontology (PPIO). IWBBIO 2013: 695-702.

- Mikel Egaña Aranguren, Jesualdo Tomás Fernández-Breis, Erick Antezana. OPPL-Galaxy: Enhancing ontology exploitation in Galaxy with OPPL. SWAT4LS 2011, ACM 2012: 12-19.

- José Antonio Miñarro-Giménez, Mikel Egaña Aranguren, Francisco García-Sánchez, Jesualdo Tomás Fernández-Breis. A Semantic Query Interface for the OGO Platform. ITBAM (DEXA) 2010, LNCS 6266: 128-142.

- Mikel Egaña Aranguren, Alan Rector, Robert Stevens, Erick Antezana. Applying ODPs in bio-ontologies. EKAW 2008, LNCS 5268: 7-16.

## Books and chapters in books

- Mikel Egaña Aranguren, Robert Stevens, Erick Antezana, Jesualdo Tomás Fernández-Breis, Martin Kuiper, Vladimir Mironov. Technologies and best practices for building bio-ontologies. In Alterovitz, G. and Ramoni, M., eds., *Knowledge-based Bioinformatics: From Analysis to Interpretation*, 67-86. Wiley-VCH 2010, ISBN: 978-0-470-74831-2.

- Role and application of ODPs in bio-ontologies. Lambert Academic Publishing 2010, ISBN 978-3-8433-7661-7. (Ph.D. thesis).

## Publications in workshops and other publications

- Matthew Horridge, Mikel Egaña Aranguren, Jonathan Mortensen, Mark Musen, Natalya Noy. ODP language expressivity requirements. WOP 2012 (co-located with ISWC), Boston, USA.

- M. Scott Marshall, Richard Boyce, Helena F. Deus, Jun Zhao, Egon L Willighagen, Matthias Samwald, Elgar Pichler, Janos Hajagos, Mikel Egaña Aranguren, Eric Prud'hommeaux, Susie Stephens. Health Care and Life Science (HCLS) Linked Data Guide. W3C note 2012.

- Jose Antonio Miñarro Giménez, Mikel Egaña Aranguren, Jesualdo Tomás Fernández-Breis, Erick Antezana. NCBO-Galaxy: bridging the BioPortal web services and the Galaxy platform. Software demo at ICBO 2012, Graz, Austria.

- Publishing information in the LOD cloud. Bioinformatics Knowledge-Blog post.

- "Automatic maintenance of multiple inheritance ontologies"; Review of "Componetns of an Ontology"; Review of "Reference and Application Ontologies". Ontogenesis KnowledgeBlog posts 2011.

- Jesualdo Tomás Fernández-Breis, Mikel Egaña Aranguren, Robert Stevens. A Quality Evaluation Framework for Bio-Ontologies. ICBO 2009, Buffalo, USA.

- Luigi Iannone, Mikel Egaña Aranguren, Alan Rector, Robert Stevens. Augmenting the expressivity of the Ontology Pre-Processor Language. OWLed 2008 Eu (co-located with ISWC), Karlsruhe, Germany.

- Mikel Egaña Aranguren, Robert Stevens, Erick Antezana. Transforming the Axiomisation of Ontologies: The Ontology Pre-Processor Language. OWLed 2008, Washington DC, USA.

- Antezana E, Blondé W, Mikel Egaña Aranguren, Rutherford A, Stevens R, De Baets B, Mironov V, Kuiper M: Structuring the life science resourceome for Semantic Systems Biology: lessons from the BioGateway project. SWAT4LS 2008, Edinburgh, Scotland, UK.

- ¿Qué puede hacer la web semántica por la biología? BioGaia 7, 2007.

- Software libre (GNU/linux) para biólogos. BioGaia 3, 2003.

- Crítica a Linked Data en Open Data Euskadi (I y II). Trabajo realizado en Open Data Day Deusto 2014 y citado en blog Open Data Euskadi.

## Posters

- Sushil Tripathi, Aravind Venkatesan, Mikel Egaña Aranguren, Zahra Zavareh, Konika Chawla, Finn Drabløs, Liv Thommesen, Torunn Bruland, Vladimir Mironov, Martin Kuiper, and Astrid Lægreid. Automated Assessment of High Throughput Hypotheses on Gene Regulatory Mechanisms Involved in the Gastrin Response. The 14th Annual Bio-Ontologies Meeting 2011, Vienna, Austria.

- J.T. Fernández-Breis, M.Madrid, J.A. Miñarro-Giménez, M.C. Legaz-García, M. Egaña Aranguren, R. Stevens. Exploitation of Semantic

Gene Ontology Annotations for Schizosaccharomyces Pombe. 6th International Fission Yeast Meeting 2011.

- Antezana, E., Blondé, W., Egaña M., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. The Cell Cycle Ontology: an application ontology supporting the study of cell cycle control. ICBO (International Conference on Biomedical Ontology) 2009, University at Buffalo, NY, US.

- Antezana, E., Blondé, W., Egaña M., Rutherford, A., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. BioGateway: an integrated RDF store to enable Semantic System Biology. ICBO (International Conference on Biomedical Ontology) 2009, University at Buffalo, NY, US.

- Antezana, E., Blondé, W., Egaña M., Rutherford, A., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. BioGateway: integrated RDF for life science queries. SWAT4LS - Semantic Web Applications and Tools for Life Sciences 2008, e-Science Institute, Edinburgh, Scotland, UK.

- Antezana, E., Egaña M., Blondé, W., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. The Cell Cycle Ontology: an application ontology supporting the Life Sciences. SWAT4LS - Semantic Web Applications and Tools for Life Sciences 2008, e-Science Institute, Edinburgh, Scotland, UK.

- Antezana, E., Egaña M., Blondé, W., Mironov, V., Stevens, R., De Baets, B., Kuiper, M. The Cell Cycle Ontology: a step towards Semantic Systems Biology. EKAW 2008 - The 16th International Conference on Knowledge Engineering and Knowledge Management Knowledge Patterns. Acitrezza, Catania, Italy.

- Antezana, E., Blondé, W., Egaña M., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. BioGateway: enabling Semantic Systems Biology. MLSB08 - The 2nd International Workshop on Machine Learning in Systems Biology. Brussels, Belgium.

- Antezana, E., Blondé, W., Egaña M., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. Semantic Systems Biology: enabling integrative biology by semantic web technologies. The 9th International Conference on Systems Biology 2008. Gothenburg, Sweden.

- Antezana, E., Egaña M., Stevens, R., De Baets, B., Mironov, V., Kuiper, M. The Cell Cycle Ontology: an application ontology for data integration. The 9th International Conference on Systems Biology 2008. Gothenburg, Sweden.

- Antezana, E., Egaña M., Mironov, V., Kuiper, M. Ontology driven data integration for enabling systems biology. The 8th International Conference on Systems Biology 2007. Long Beach, California, US.

- Antezana, E., Mironov, V., Egaña, M., and Kuiper, M. Ontology-driven Data Integration for Enabling Systems Biology: Cell-Cycle Ontology. The 4th Annual Integrative Bioinformatics Meeting 2007, Ghent, Belgium.

- Antezana, E., Egaña, M., Mironov, V., and Kuiper, M. CCO, a paradigm for knowledge integration. The 10th Annual Bio-Ontologies Meeting 2007, Vienna, Austria.

## Editor

Semantic Web Journal (SWJ), special issue on Linked Data for Health Care and the Life Sciences. Editors: Mikel Egaña Aranguren, Michel Dumontier, and Jesualdo Tomás Fernández-Breis.

## Referee

PeerJ (2013), Data and Knowledge Engineering (DKE) (2013), BMC Bioinformatics (2012), Journal of Biomedical Informatics (JBI) (2012), Computational and Mathematical Methods in Medicine (CMMM) (2012), Journal of Medical Systems (JOMS) (2012), Journal of Biomedical Semantics (JBS) (2012), Semantic Web Journal (SWJ) (2011), Journal of Research and Practice in Information Technology (JRPIT) (2011).

## Member of scientific committee

- Managing Interoperability and compleXity in Health Systems (MIX-HS 2012). In conjunction with the ACM International Conference on Information and Knowledge Management.

- Joint Workshop on Semantic Technologies Applied to Biomedical Informatics and Individualized Medicine (SATBI + SWIM 2012). In conjunction with International Semantic Web Conference (ISWC).

- Managing Interoperability and compleXity in Health Systems (MIX-HS 2011). In conjunction with the ACM International Conference on Information and Knowledge Management.

- Additional reviewer in K-CAP (Knowledge Capture 2011).

- Semantic Applied Technologies on Biomedical Informatics (SATBI 2011). In conjunction with the ACM International Conference on Bioinformatics and Computational Biology.

- ONTORACT 2008.

**Talks**

- Building reasonable biomedical ontologies for a Life Sciences Semantic Web. 3S (Systems, Synthetic, and Semantic) Biology summer school. CIBIO (Centre for Integrative Biology), University of Trento, Italy, 2014. Invited talk.

- OPPL-Galaxy: Enhancing ontology exploitation in Galaxy with OPPL. SWAT4LS, London, UK, 2011.

- Linked Data for Functional Genomics. NTNU, Trondheim, Norway, 2011. Invited talk.

- Publicar datos de manera inteligente en la Web: la filosofía y la práctica de los datos enlazados (Linked Data). Reunión de la Red de Observatorios de Sostenibilidad. Évora, Portugal, 2011.

- A Semantic Query Interface for the OGO Platform. ITBAM (DEXA), Bilbo, Spain, 2010.

- Aplicación de la Web Semántica en Biología Molecular. Universidad de Deusto, Facultad de Ingeniería, Spain, 2010. Invited talk.

- Applying ODPs in bio-ontologies. EKAW, Catania, Italy, 2008.

- Transforming the Axiomisation of Ontologies: The Ontology Pre-Processor Language. OWLed, Washington DC, USA, 2008.

- Aplicación de la Web Semántica en Bioinformática. UM, Facultad de Informática, Spain, 2008. Invited talk.

- ODPs for bio-ontologies. Bio-ontologies SIG at ISMB, Vienna, Austria, 2007.

- Métodos y resultados actuales en Bioinformática: know-how y know-what de las redes tecnocientíficas en Bioin-formática. EHU, Facultad de Filosofía, Spain, 2004. Invited talk.

**Technical skills**

- Semantic Web and Linked Data (Advanced): RDF, RDFS, SPARQL, OWL, SWRL, JSON-LD, OWL API, RDFLib, ONTO-PERL, Jena, Sesame, Stardog, Pubby, Protégé 4, TopBraid composer.

- Programming languages (Medium): Java, Perl, Python, Sed, Bash, JavaScript.

- UNIX systems (Medium): GNU/Linux (Debian, Ubuntu, CentOS, Red Hat).

- Markup languages (Medium): XML, HTML 5, $\LaTeX\,2_\varepsilon$.

- Web Services (Basic): SADI framework, NCBO services.

- Web (Basic): Galaxy, Apache, Nginx, Tomcat, Jetty, lighttp, Solr/Lucene, Wordpress, Drupal, MarkDown, Jekyll.

- Software development (Basic): Maven, Ant, SCons, Eclipse, Subversion, Mercurial, Git, Trac.

- Teaching systems (Basic): Moodle.

- Relational Databases (Basic): MySQL, PostgreSQL.

- File based data storage (Basic): HDF5, YAML, JSON.

- Statistical analysis (Basic): R.

- Cloud computing (Basic): Amazon EC2.

## Participation in development of resources and tools

OpenLifeData2SADI:  This a set of SADI services that wraps the Linked Data resources from Open Life Data (formerly known as Bio2RDF). [http://github.com/wilkinsonlab/OpenLifeData2SADI]

DDx2NP:  This programme can be used to add Nanopublications to a given medical Knowledge Base. [http://github.com/wilkinsonlab/DDx2NP]

SADI-Galaxy:  SADI-Galaxy is able to install SADI services as regular Galaxy tools, and therefore SADI services can be used as part of any Galaxy workflow. [http://github.com/mikel-egana-aranguren/SADI-Galaxy]

LSLD:  This is a standalone, light-weight, configuration-free bundle to publish Linked Data. It is meant as an educational tool that students can use to become familiar with Linked Data, by publishing their own dataset at localhost with only the necessary hassle, but still being aware of the overal technical setting. It can also be used for rapid prototyping and deployment of a Linked Data system. [http://github.com/mikel-egana-aranguren/LSLD]

Linked Data Open Data Euskadi:  Este proyecto contiene el trabajo realizado en el Open Data Day Deusto 2014 por el grupo de trabajo "Tutorial de Linked Data con ejemplo real de Open Data Euskadi". Es un "pack", basado en LSLD,

que puede ser desplegado en cualquier máquina GNU/Linux y una vez funcionando demuestra la estructura y funcionamiento completo de un servidor Linked Data, con un dataset sobre consulados extraído de Open Data Euskadi. [http://github.com/OpenDataDayBilbao/Linked-Data-Open-Data-Euskadi]

PPIO: The Plant-Pathogen Interactions Ontology offers an axiomisation of plant-pathogen interactions in order to annotate, query and reason over such domain of knowledge. [http://github.com/wilkinsonlab/PPIO]

PPIO software: OWLNumericIDGenerator (Generate alphanumeric OWL URIs) and NCBITaxonomy2OWL (Import NCBI taxa from BioPortal Web Service) were written for producing PPIO. [http://github.com/mikel-egana-aranguren/OWLNumericIDGenerator] [http://github.com/mikel-egana-aranguren/NCBITaxonomy2OWL]

NCBO-Galaxy: NCBO-Galaxy provides graphical interfaces for the NCBO web services available at BioPortal, to access and exploit biomedical ontologies as part of Galaxy workflows. [http://toolshed.g2.bx.psu.edu/]

OGO: OGO integrates orthology information with diseases from OMIM, exploiting OWL, SPARQL and OBO ontologies. [http://miuras.inf.um.es:9080/OGO-1.0/]

OGOLOD: OGOLOD is the Linked Open Data version of the OGO system. [http://miuras.inf.um.es/~ogo/ogolod.html]

ODPs catalogue: A repository of ontology engineering best practices, focused on biological knowledge. [http://github.com/mikel-egana-aranguren/ODPs]

BioGateway: An RDF store holding information integrated from different bioinformatics resources, like the OBO ontologies, GOA files and SwissProt. [http://www.semantic-systems-biology.org/biogateway]

CCO: The Cell Cycle Ontology is an application ontology that describes different aspects of the cell cycle, integrating information from UniProt, IntAct, GOA, NCBI taxonomy and GO. [http://cellcycleontology.org]

OPPL: The Ontology Pre-Processor Language is a scripting language for defining and performing axiomatic changes in OWL ontologies, thus offering an abstraction of the OWL API that works directly with axioms instead of programmatic procedures. [http://oppl.sourceforge.net/]

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| OPPL-Galaxy: | OPPL-Galaxy is an OPPL wrapper to execute workflows that combine OPPL and other Galaxy tools to enhance the exploitation of biomedical ontologies in bioinformatics. [http://github.com/mikel-egana-aranguren/OPPL-Galaxy] |
| ONTO-PERL: | A Perl API for manipulating OBO and OWL ontologies. [http://search.cpan.org/dist/ONTO-PERL/] |
| GONG: | Gene Ontology Next Generation is a methodology for enriching OBO ontologies by adding OWL axioms based on dissecting the structure of the term names with regular expressions. |

## Collaboration with research groups in publications

- Biological Informatics Group. CBGP (UPM), Spain (2014).

- Berkeley Bioinformatics Open-source Projects. Lawrence Berkeley National Laboratory, USA (2013).

- Methods and Engineering of Language, Ontology and DIscourse. Toulouse Institute of Computer Science Research, France (2013).

- Institute for Medical Informatics, Statistics and Documentation. Medical university of Graz, Austria (2013).

- Dumontier lab. Carleton University, Canada (2012).

- Bio-Medical Informatics Research Group. Stanford University, USA (2012).

- Isoco Labs. Isoco, Spain (2012).

- Noray bioinformatics, Spain (2009).

- Tecnologías de Modelado, Procesamiento y Gestión del Conocimiento. Universidad de Murcia, Spain (2009).

- Semantic Systems Biology. Trondheim University, Norway (2008).

- KERMIT. Gent University, Belgium (2008).

- Information Management Group. University of Manchester, UK (2005).

- Bio-Health Informatics Group. University of Manchester, UK (2005).

**Teaching**

- Semantic biology tutorial: Use of semantic web resources for knowledge discovery. 3S (Systems, Synthetic, and Semantic) Biology summer school. CIBIO (Centre for Integrative Biology), University of Trento, Italy, 2014. English.

- Galaxy tutorial. Erasmus mundus MSc in Marine Environment and resources, UPV-EHU, 2014. English.

- Life Sciences Semantic Web. MSc Bioinformatics, UM, 2014. Spanish.

- Introductory talk on bioinformatics for high school students visiting the CBGP.

- Galaxy tutorials at CBGP.

- Life Sciences Linked Data. MSc Bioinformatics, UM, 2013. Spanish.

- OWL, as part of ATHENS course (UPM), 2012. English.

- OWL, as part of ATHENS course (UPM), 2012. English.

- Populous tutorial at SWAT4LS (London, UK), 2011. English.

- OWL, as part of ATHENS course (UPM), 2011. English.

- Web Ontology Language (OWL), as part of Artificial Intelligence MSc (UPM), 2011. English.

- OWL/Description Logics, as part of the Artificial Intelligence course (UPM), 2011. Spanish.

- OWL tutorials for biologists (University of Manchester, UK), 2005-2008. English.

**Ph.D. Panels**

- Meifania Monica Chen, "Lipoprotein Ontology: A Formal Representation of Lipoproteins", Curtin University, Australia, 2013.

- Jose Antonio Miñarro-Giménez, "Entorno para la gestión semántica de información biomédica en investigación traslacional", UM, Spain, 2012.

- Doris Mejía Ávila, "Estrategia de interoperabilidad semántica en el contexto de integración de conocimiento geográfico y ambiental. Caso de aplicación: Biodiversity Ontology", UPM, Spain, 2011.

## Memberships

W3C Semantic Web Health Care and Life Sciences Interest Group, Spanish Association of Linked Data, Biologists Association of Basque Country.

## Languages

Fluent in english (IELTS 7.5/9), basque (EGA, HABE 3), and spanish.

## Scholar metrics

Author ID Scopus: 16038705500.

Google Scholar profile: JsMMKnoAAAAJ.

H-Index: 7 (Scopus), 12 (Google Scholar).

Total Number of indexed publications: 15 (Scopus), 35 (Google Scholar).

## Personal data

- Born 1979/8/26, in Bilbo (Basque Country, Spain).

- Web: http://mikeleganaaranguren.com[1].

- Email: mikel.egana.aranguren@gmail.com / mikel.egana@ehu.es.

- Skype: mikel_egana.

Bilbo, 2014/08/27

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[1]Up-to-date CV, pointers to profiles (CiteUlike, GitHub, LinkedIn, *etc.*), links to publications, and other works (slides, theses, teaching materials, videos, *etc.*).