

## Mr. SymBioMath

High Performance, Cloud and Symbolic Computing in Big-Data Problems applied to  
 Mathematical Modelling of Comparative Genomics

EU FP7 Industry-Academia Partnerships and Pathways  
 Project Nr. 324554

### Deliverable D5.2 Dissemination Activities

|                           |  |
|---------------------------|--|
| Deliverable Number        | <b>D5.2</b>  |
| Deliverable Title         | <b>Dissemination Activities</b>  |
| Type of Document          | <b>Report</b>  |
| Dissemination Level       | <b>Public</b>  |
| Workpackage               | <b>WP5: Dissemination and Business Plan</b>  |
| Lead Beneficiary          | <b>RISC</b>  |
| Contractual Delivery Date | <b>30.11.2016</b>  |
| Actual Delivery Date      | 30.11.2016   |
| Editor(s)                 | Oscar Torreno  |
| Author(s)                 | Oscar Torreno, Lina Mayorga, Andreas Mitterecker, Johan Karlsson, Ruben Garcia, Birgit Hauer |

### Document Log

| Version | Authors(s)                           | Date       | Modifications  |
|---------|--------------------------------------|------------|--|
| 0.1     | Oscar Torreno                        | 11.11.2016 | Initial Version  |
| 1.0     | Oscar Torreno                        | 14.11.2016 | Sketching the sections                                   |
| 1.1     | Lina Mayorga                         | 14.11.2016 | SAS publications   |
| 1.2     | Ruben García                         | 15.11.2016 | LRZ publications   |
| 1.3     | Johan Karlsson & Andreas Mitterecker | 22.11.2016 | ITG publications   |
| 1.4     | Birgit Hauer                         | 23.11.2016 | JKU publications   |
| 1.5     | Oscar Torreno                        | 23.11.2016 | UMA and RISC publications                                |
| 1.6     | Oscar Torreno                        | 28.11.2016 | Adding dissemination activities from the project website |
| 2.0     | Oscar Torreno                        | 29.11.2016 | Merging and proof reading                                |
| 2.1     | Oscar Torreno                        | 30.11.2016 | Final minor changes                                      |

## Contents

|  |           |
|--|-----------|
| <b>1 Publications</b>  | <b>5</b>  |
| 1.1 ITG-JKU-RISC-SAS-UMA   | 5         |
| 1.2 ITG-RISC-UMA   | 5         |
| 1.3 ITG-UMA  | 5         |
| 1.4 JKU  | 6         |
| 1.5 LRZ  | 6         |
| 1.6 LRZ-RISC-UMA   | 7         |
| 1.7 RISC-UMA   | 7         |
| 1.8 SAS  | 9         |
| 1.9 SAS-UMA  | 9         |
| 1.10 UMA   | 10        |
| <b>2 Project summer schools</b>  | <b>10</b> |
| 2.1 Summer School on Bioinformatics, Biomedicine, and Cloud Computing  | 11        |
| 2.2 Machine Learning and Visualization Summer School   | 11        |
| 2.3 Autumn school on the industrial perspective of bioinformatics, biomedicine and visualization                                       | 11        |
| <b>3 Workshops and seminars</b>  | <b>11</b> |
| 3.1 Galaxy tutorial in the ECCB conference   | 11        |
| 3.2 Galaxy workshop in the SoiBio conference   | 12        |
| 3.3 Long Night of Research in Hagenberg 2016   | 12        |
| 3.4 Presentation of Mr. SymBioMath Visualizations to LMU students  | 12        |
| 3.5 3DScover at LRZ Virtual Reality Open Lab Day   | 12        |
| 3.6 Mr. SymBioMath Presentation at RISC Forum  | 13        |
| 3.7 Jornadas de formación en bioinformática  | 13        |
| 3.8 Meeting on Spotfire Galaxy Integration   | 13        |
| 3.9 Presentation at the Spanish National Biotechnology Centre (CNB)  | 13        |
| 3.10 Mr. SymBioMath Presentation at PRACE Spring School  | 13        |
| 3.11 Mr. SymBioMath at the Long Night of Science   | 13        |
| 3.12 Meeting FreeBIT   | 14        |
| 3.13 Talk on GlobusOnline in the Mr.SymBioMath project   | 14        |
| 3.14 Encounter with Science  | 14        |
| 3.15 Mr. SymBioMath researchers participate at the Andalucia researchers night   | 14        |
| 3.16 Presentation on Mr. SymBioMath for a Romanian company delegation  | 14        |
| 3.17 Bioinformatics presentation for a group of Czech high school children   | 15        |
| <b>4 Press releases</b>  | <b>15</b> |
| 4.1 2013-02-01: Mr. SymBioMath project started   | 15        |
| 4.2 2013-02-11: Press announcement by UMA on Mr. SymBioMath  | 16        |
| 4.3 2013-02-11: Spanish press article on the start of the Mr. SymBioMath project on <a href="http://ucienca.uma.es">ucienca.uma.es</a> | 16        |
| 4.4 2013-02-26: German online press article on Mr. SymBioMath on <a href="http://derstandard.at">derstandard.at</a>                    | 16        |
| 4.5 2013-03-01: Spanish online article on Mr. SymBioMath   | 16        |
| 4.6 2013-03-13: Spanish online press article on the Mr. SymBioMath project on El Observador  | 16        |
| 4.7 2013-03-14: MrSymBioMath press announcement by ITG   | 16        |

|          |  |           |
|----------|--|-----------|
| 4.8      | 2013-03-20: English online article on Mr. SymBioMath on andaluciabioregion.es                        | 17        |
| 4.9      | 2013-03-26: German online press article on Mr. SymBioMath on derstandard.at                          | 17        |
| 4.10     | 2013-04-09: German newspaper article on MrSymBioMath in OOEN . . . . .                               | 17        |
| 4.11     | 2013-10-31: Spanish press article on the Mr. SymBioMath project on SaberUn-<br>versidad.es . . . . . | 17        |
| 4.12     | 2016-11-18: Spanish press article on the Mr. SymBioMath project . . . . .                            | 17        |
| <b>5</b> | <b>Social networks</b>   | <b>17</b> |
| 5.1      | Facebook . . . . .   | 17        |

## Executive Summary

In accordance with the technical Mr. SymBioMath Annex [AnnexI] the deliverable D5.2 is focused on reporting the dissemination activities performed within the project, including scientific publications in journals and congresses, summer schools, workshops and press releases. The Mr. SymBioMath project either appears in the acknowledgements or as funding source (thanks to the European Commission). The deliverable has been split into several sections corresponding with the previously mentioned types of dissemination activities. Given the static nature of this document, a dynamically-updated list of dissemination activities can be found at the project website (<http://www.mrsymbiomath.eu/events> and <http://www.mrsymbiomath.eu/bioinformatics-resources>)

## 1 Publications

This section contains the publications of the project consortia related to the project. The naming convention of the subsections indicate the acronym of the project partner(s) involved in each publication.

### 1.1 ITG-JKU-RISC-SAS-UMA

- A Cloud-based GWAS Analysis Pipeline for Clinical Researchers.  
P. Heinzlreiter, J.R. Perkins, O. Torreño, J. Karlsson, J.A. Ranea, A. Mitterecker, M. Blanca, and O. Trelles.  
Proc. of the 4th International Conference on Cloud Computing and Services Science (CLOSER 2014), ISBN 978-989-758-019-2, Barcelona, Spain, pp. 387-394, April 2014, doi:10.5220/0004802103870394

### 1.2 ITG-RISC-UMA

- Running workflows in the cloud.  
Oscar Torreno, Johan Karlsson, Paul Heinzlreiter and Oswaldo Trelles.  
XXV Jornadas de paralelismo.
- Bioinformatics with mobile devices.  
S. Díaz del pino, O. Torreño, J. Karlsson, O.Trelles, J. Falgueras.  
Jornadas de Bioinformatica (JBI), 2014.
- Integrating Galaxy in the Mr.SymBioMath Cloud Infrastructure.  
Oscar Torreno; Johan Karlsson; Alex Upton; Michael Krieger and Oswaldo Trelles.  
Galaxy Community Conference (GCC2015).

### 1.3 ITG-UMA

- A Framework for Accessible Cluster-enabled Epistatic Analysis.  
Alex Upton, Johan Karlsson, Oswaldo Trelles, Miguel Hernandez, Juan Elvira  
Proceedings of the PBio 2016 Workshop (part of EuroPar 2016), 2016.
- jORCA: Jumping to the Cloud (Poster).  
Johan Karlsson, Óscar Torreño Tirado, Oswaldo Trelles.  
European Conference on Computational Biology (ECCB) 2014.
- MAPI: a software framework for distributed biomedical applications (Poster).  
Johan Karlsson, Oswaldo Trelles.

Spanish Bioinformatics Conference (JBI) 2014.

- Usability tests on bioinformatics mobile applications.  
Noura Chelbat, Sergio Díaz, Johan Karlsson, Oswaldo Trelles, Juan Falgueras.  
XII Jornadas de Bioinformatica. (2014)
- Mobile Access to On-line Analytic Bioinformatics Tools.  
Sergio Díaz Del Pino, Tor Johan Mikael Karlsson, Juan Falgueras Cano, and Oswaldo Trelles.  
IWBBIO 2015. 3rd International Work-Conference on Bioinformatics and Biomedical Engineering). IWBBIO 2015, Part II, LNCS 9044:555–565 (2015).

#### 1.4 JKU

- HapFABIA: Identification of very short segments of identity by descent characterized by rare variants in large sequencing data.  
S. Hochreiter.  
Nucl. Acids Res., 41(22):e202, 2013 doi:10.1093/nar/gkt1013
- Aiding Drug Design with Deep Neural Networks.  
T. Unterthiner, A. Mayr, G. Klambauer, M. Steijaert, J. Wegner, H. Ceulemans, and S. Hochreiter.  
Conference Neural Information Processing Systems Foundation (NIPS 2014)  
Workshop on Machine Learning in Computational Biology, Montreal, Canada, December 8-13, 2014
- Furby: fuzzy force-directed bicluster visualization.  
M. Streit, S. Gratzl, M. Gillhofer, A. Mayr, A. Mitterecker, and S. Hochreiter.  
BMC Bioinformatics, 15(Suppl 6):S4, 2014 doi:10.1186/1471-2105-15-S6-S4
- DeepTox: Toxicity Prediction using Deep Learning.  
A. Mayr, G. Klambauer, T. Unterthiner, and S. Hochreiter  
Front. Environ. Sci. 3:80., 2016 doi:10.3389/fenvs.2015.00080

#### 1.5 LRZ

- Benefits of Tablet Interfaces for Immersive Visualization in Information Visualization.  
Luisa Wurm, Rubén García, Christoph Anthes, Dieter Kranzlmüller, Wolfgang Höhl.  
International Conference in Central Europe on Computer Graphics, Visualization and Computer Vision (WSCG 2016). 30 May - 3 June 2016. Plzen, Czech Republic.  
POSTER papers proceedings, Computer Science Research Notes [CSRN] 2603, pp 1-4, ISSN 2464-4617, ISBN 978-80-86943-59-6

- Perspectives for Using Virtual Reality to Extend Visual Data Mining in Information Visualization.  
R. García-Hernández, C. Anthes, M. Wiedemann, D. Kranzlmüller.  
2016 IEEE Aerospace Conference. 5-12 March 2016. Yellowstone Conference Center. Big Sky, Montana (Estados Unidos). Electronic ISBN: 978-1-4673-7676-1. DOI: 10.1109/AERO.2016.7500608
- State of the Art of Virtual Reality Technology.  
C. Anthes, R. García-Hernández, M. Wiedemann, D. Kranzlmüller.  
2016 IEEE Aerospace Conference. 5-12 March 2016. Yellowstone Conference Center. Big Sky, Montana (Estados Unidos). Electronic ISBN: 978-1-4673-7676-1. DOI: 10.1109/AERO.2016.7500674
- Large-scale Dynamic Visualization of Multiple Comparative Genomic Data.  
Tukora B., C. Anthes, P. Heinzlreiter, D. Kranzlmüller. Poster in: Proceedings of the IEEE Information Visualization Conference (InfoVis '14), Paris, France, November 2014

## 1.6 LRZ-RISC-UMA

- Building an open source cloud environment with auto-scaling resources for executing bioinformatics and biomedical workflows.  
Michael T. Krieger, Oscar Torreno, Oswaldo Trelles and Dieter Kranzlmüller.  
Future Generation Computer Systems, Volume 67, February 2017, Pages 329-340, ISSN 0167-739X, <http://dx.doi.org/10.1016/j.future.2016.02.008>.

## 1.7 RISC-UMA

- Easily registering bioinformatics services metadata.  
Óscar Torreño and Oswaldo Trelles  
ECCB'14, the 13th European Conference on Computational Biology. Methods and technologies for computational biology.
- Software for featuring genome evolution.  
Jose Arjona-Medina, Óscar Torreño Tirado and Oswaldo Trelles.  
ECCB'14, the 13th European Conference on Computational Biology. Methods and technologies for computational biology.
- Intuitive library for efficient access of compressed genome sequences.  
Iris Leitner and Oswaldo Trelles.  
ECCB'14, the 13th European Conference on Computational Biology. Methods and technologies for computational biology.

- Experimental Study of Local Alignment Distributions in the Comparison of Large Genomic Sequences.  
Jose A. Arjona-Medina, Oscar Torreño, Noura Chelbat and Oswaldo Trelles  
ISCB-Latin America x-Meeting on Bioinformatics with BSB & SoiBio (2014).
- Pairwise genome comparison workflow in the Cloud using Galaxy.  
O. Torreño, M. Krieger, P. Heinzlreiter, O. Trelles.  
International conference on Computer Science (ICCS), 2015.
- Auto-scaling strategy for OpenStack cloud resources managed by TORQUE.  
Oscar Torreño and Oswaldo Trelles.  
XXVI Jornadas de Paralelismo (2015).
- Breaking computational barriers in pairwise genome comparison.  
Óscar Torreño and Oswaldo Trelles  
BMC Bioinformatics 16:250 (2015).
- SwiftGECKO: a provenance-enabled parallel comparative genomics workflow.  
Maria Luiza Mondelli, Oscar Torreño, Kary A. C. S. Ocaña, Marta Mattoso, Michael Wilde, Ana T. Vasconcellos, Oswaldo Trelles, Luiz M. R. Gadelha Jr.  
X-Meeting 2015 - 11th International Conference of th AB3C + Brazilian Symposium of Bioinformatics.
- Computational Synteny Block: A Framework to Identify Evolutionary Events.  
J. Arjona-Medina, O. Trelles.  
IEEE transactions on nanobioscience Apr 20 (2016).
- GECKO-MGV: Evolution Events driven tool for enhanced visual analysis of multi-genome comparisons.  
S. Diaz-del-Pino, J. Arjona, O. Torreno, S. Benavides, and O. Trelles.  
International Work-conference on Bioinformatics and Biomedica Engineering (IWBBIO2016).
- Computational workflow for the fine-grained analysis of metagenomic samples.  
Esteban Pérez-Wohlfeil, José Arjona-Medina, Óscar Torreño-Tirado, Eugenia Ulzurrun, Oswaldo Trelles  
BMC Genomics 17(Suppl 8):802 (2016).
- Refining borders of Computational Synteny Blocks using repetitions.  
J. Arjona-Medina, O. Trelles.  
BMC Genomics 17(Suppl 8):804. (2016).



## 1.8 SAS

- The study of severe cutaneous drug hypersensitivity reactions from a systems biology perspective.  
Perkins, J. R., Ayuso, P., Cornejo-García, J. A., & Ranea, J. A. (2014).  
Current opinion in allergy and clinical immunology, 14(4), 301-306.
- Systems biology approaches to enhance our understanding of drug hypersensitivity reactions.  
Perkins, J. R., Barrionuevo, E., Ranea, J. A., Blanca, M., & Cornejo-Garcia, J. A. (2014).  
Clinical & Experimental Allergy, 44(12), 1461-1472.
- Hypersensitivity to Nonsteroidal Anti-inflammatory Drugs in Children and Adolescents: Cross-Intolerance Reactions.  
Blanca-Lopez, N., Cornejo-Garcia, J. A., Plaza-Seron, M. C., Doña, I., Torres-Jaén, M. J., Padilla-España, L., ... & Blanca, M. (2014).  
Journal of investigational allergology & clinical immunology, 25(4), 259-269.
- Genetic Variants in Arachidonic Acid Pathway Genes Associated with Nsaids-Exacerbated Respiratory Disease.  
Ayuso, P., del Carmen Plaza-Serón, M., Blanca-López, N., Doña, I., Campo, P., Laguna, J. J., ... & Cornejo-Garcia, J. A. (2015).  
Journal of Allergy and Clinical Immunology, 135(2), AB114.
- Unravelling adverse reactions to NSAIDs using systems biology.  
Perkins, J. R., Sanak, M., Canto, G., Blanca, M., & Cornejo-García, J. A. (2015).  
Trends in pharmacological sciences, 36(3), 172-180.

## 1.9 SAS-UMA

- Graph theoretical analysis of Clarkson disease GWAS epistatic interactions.  
Alex Upton, Oswaldo Trelles and James R.Perkins.  
International conference on Computer Science (ICCS), 2015.
- Epistatic analysis of Clarkson disease.  
Alex Upton, Oswaldo Trelles and James R.Perkins.  
International conference on Computer Science (ICCS), 2015.
- High Performance Computing to Detect Epistasis in Genome Scale Datasets.  
Alex Upton, Oswaldo Trelles, José Antonio Cornejo-Garcia, James Richard Perkins.  
Briefings in bioinformatics 17(3):368-379 (2016)

- Epistatic Analysis of NSAIDs Hypersensitivity using High Performance Computing.  
Alex Upton, Oswaldo Trelles, Ming Ta Michael Lee, Lieh-Bang Liou, Miguel Blanca, Jose Antonio Cornejo-Garcia, James Perkins.  
Immunoinformatics & Immune-computation - ICSI32015.
- Epistasis Approaches to Identify Novel Genes Potentially Involved In NSAIDs Hypersensitivity.  
James Richard Perkins, Jose Antonio Cornejo García<sup>1</sup>, Oswaldo Trelles, Inmaculada Doña, Esther Barrionuevo, María Salas, María Auxiliadora, Guerrero, Miguel Blanca, Alex Upton.  
7th Drug Hypersensitivity Meeting (2016).

### 1.10 UMA

- Accelerating GWAS Epistatic interaction analysis methods.  
Alex Upton, Priscill Orue and Oswaldo Trelles.  
Jornadas de Bioinformatica (JBI), 2014
- Adapting GECKO for metagenomics studies.  
Fernando Moreno, Oscar Torreno, and Oswaldo Trelles  
International Work-conference on Bioinformatics and Biomedica Engineering (IWBBIO2016).
- Two-level parallelism to accelerate multiple genome comparisons.  
Oscar Torreño, Oswaldo Trelles.  
4th International Workshop on Parallelism in Bioinformatics (2016).
- High resolution refinement of Large Scale Genomic Rearrangements using repetitions: A case study.  
J. Arjona Medina, G. Thode, O. Trelles.  
European Conference on Computational Biography (ECCB2016).
- New-Venues for the visual analysis of multiple genome comparison S. Díaz-Del-Pino, J. Arjona-Medina, O. Torreño, S. Benavides, O. Trelles  
European Conference on Computational Biography (ECCB2016).

## 2 Project summer schools

This section describes the three summer schools organised by the project consortia.

## 2.1 Summer School on Bioinformatics, Biomedicine, and Cloud Computing

This summer school<sup>1</sup> organized from the 10th to the 12th of September 2013 in Málaga was aimed at providing an overview on the three main fields that converge in the project: bioinformatics, biomedicine and cloud computing.

## 2.2 Machine Learning and Visualization Summer School

This summer school<sup>2</sup> organized from the 15th to the 16th of September 2014 in Munich focused on a general introduction into Machine Learning on the first day as well as visualization specifically in the field of Comparative Genomics during the second day.

It showcased the achievements of the Mr. SymBioMath project and gave the attendees an opportunity to work with the Mr. SymBioMath visualization software as well as receiving a hands-on training on how to extend the software to fit their own visualization needs within the domain of comparative genomics.

## 2.3 Autumn school on the industrial perspective of bioinformatics, biomedicine and visualization

This autumn school<sup>3</sup> took place from the 19th to the 21st of October 2015 in Linz. The school was aimed to provide the industrial perspective of research projects, showing use case scenarios coming from project.

## 3 Workshops and seminars

This section contains the events in which project partners disseminated the work being performed within the project.

### 3.1 Galaxy tutorial in the ECCB conference

On 3rd of September 2016 Oscar Torreno and Michael Krieger instructed a Galaxy tutorial entitled “Scientific workflows under Galaxy. Use case: multiple genome comparison” in the 15th European Conference on Computational Biology. In the tutorial, Galaxy was presented as the workflow manager of the project and in addition project software for multiple genome comparisons was presented.

---

<sup>1</sup><http://mrsymbiomath.eu/events/46-summer-school-on-bioinformatics-biomedicine-and-cloud-computing>

<sup>2</sup><http://mrsymbiomath.eu/events/81-machine-learning-and-visualization-summer-school-munich>

<sup>3</sup><http://as15.mrsymbiomath.eu/>

### **3.2 Galaxy workshop in the SoiBio conference**

On 22nd of April 2016 Oswaldo Trelles, Jose Arjona and Oscar Torreno instructed a Galaxy workshop in the SoiBio International Conference 2016 on “Bioinformatics & Computational Biology for Innovative Genomics”<sup>4</sup>. Galaxy was presented as the workflow management system used in the project.

### **3.3 Long Night of Research in Hagenberg 2016**

The Mr. SymBioMath project has been presented at the Long Night of Research 2016 in Hagenberg. The event took place on the 22nd of April 2016 with 1400 people attending. Multiple elements of Mr. SymBioMath research were shown and attracted significant attention from a particularly young audience like for example school children.

### **3.4 Presentation of Mr. SymBioMath Visualizations to LMU students**

Twice, in 2016 and 2015.

On 28.4.2016 a presentation on Mr. SymBioMath was given at LRZ to a group of around 80 students. The presentation took place as part of the lecture on Virtual Reality at LMU Munich and - after giving a general presentation of the project - focused on the different visualization approaches being developed at LRZ for Mr. SymBioMath. The presentation also included live demonstrations of the software being developed, such as the multiple genome comparison visualization application 3D-Scover (desktop and immersive variants) and the tree visualization software which currently being developed at LRZ. The presentation was given by Ruben Garcia Hernandez.

On 23.4.2015 a presentation on Mr. SymBioMath was given at LRZ to a group of around 80 students. The presentation took place as part of the lecture on Virtual Reality at LMU Munich and - after giving a general presentation of the project - focused on the different visualization approaches being developed at LRZ for Mr. SymBioMath. The presentation also included live demonstrations of the software being developed, such as the multiple genome comparison visualization application 3D-Scover (desktop and immersive variants) and the tree visualization software which currently being developed at LRZ. The presentation was given by Ruben Garcia Hernandez and Paul Heinzlreiter.

### **3.5 3DScover at LRZ Virtual Reality Open Lab Day**

A poster and a video on the Multiple Genome Visualization Application 3D-Scover has been presented at the Virtual Reality Open Lab Day at LRZ on the 16.12.2014.

---

<sup>4</sup><http://icmexico2016.soibio.org/>

### **3.6 Mr. SymBioMath Presentation at RISC Forum**

At the 18.5.2015 Oswaldo Trelles and Paul Heinzlreiter gave a presentation on the work done within Mr. SymBioMath at the RISC Forum held at the RISC Institute in Hagenberg, Austria. A special focus was being put on the project infrastructure as well as comparative genomics. The audience consisted of the faculty and the PhD students of the Research Institute for Symbolic Computation.

### **3.7 Jornadas de formación en bioinformática**

From 16th to 18th of February 2015 the group of UMA presented the Mr. SymBioMath project during a teaching session at the Jornadas de formación en Bioinformática in Malaga, Spain.<sup>5</sup>

### **3.8 Meeting on Spotfire Galaxy Integration**

The 29th of July 2014 at Parque Científico de Madrid (PTM) Johan Karlsson presented the Mr. SymBioMath project to representatives of Perkin Elmer. Together with Integromics the integration possibilities between Spotfire and Galaxy have been discussed.

### **3.9 Presentation at the Spanish National Biotechnology Centre (CNB)**

Johan Karlsson gave a presentation about the approach to cloud computing and data transfer in Mr.SymBioMath for the Spanish National Biotechnology Center (CNB) in Madrid on the 13th of June 2014.

### **3.10 Mr. SymBioMath Presentation at PRACE Spring School**

Oswaldo Trelles has given a presentation at the PRACE Spring School 2014 containing work performed within the Mr. SymBioMath project in Hagenberg, Austria on 27.04.2014. The title of the talk was About the Importance of HPC for Life Sciences.

### **3.11 Mr. SymBioMath at the Long Night of Science**

On the 4th of April 2014 Mr. SymBioMath was presented during the Long Night of Science - an event to present research to the general public. Project partner RISC presented the project among others to around 1500 visitors in the IT Center in Hagenberg, Austria. The general focus of the event was being put on software-related research, and Mr. SymBioMath was presented by RISC Software GmbH.

---

<sup>5</sup><http://www.bitlab-es.com/jfbi/index.html>

### **3.12 Meeting FreeBIT**

In the “4to. Congreso Argentino de Bioinformática y Biología Computacional” held from the 29th - 31th of October 2013 in Rosario (Argentina), Oswaldo Trelles gave a Mr. SymBioMath-related presentation on HPC Computing in Comparative Genomics.

### **3.13 Talk on GlobusOnline in the Mr.SymBioMath project**

On 19th of September 2013 Johan Karlsson gave a speech on GlobusOnline in the Mr.SymBioMath project at the GlobusEUROPE 2013.

The talk was focused on the use of the GlobusOnline data transfer solution within the technical setup of the Mr. SymBioMath infrastructure including its integration into the client software jORCA.

### **3.14 Encounter with Science**

Within the scope of the event Encuentros con la ciencia 2013 (Encounter with science) Oswaldo Trelles gave a talk on the topic “Genomas, mathematicas y supercomputadores” (Genomes, math and supercomputers).

The event took place on the 19th of November 2013 in the Ambito Cultural de El Corte Inglés de Málaga.

### **3.15 Mr. SymBioMath researchers participate at the Andalucia researchers night**

The Mr. SymBioMath researchers Jose Antonio Arjona Medina and Oswaldo Trelles participated in the dissemination event La noche de los investigadores (Andalucia Researchers' Night) and gave a presentation there focusing on the use of supercomputers for Bioinformatics with Mr. SymBioMath being a prominent example.

The presentation on Mr. SymBioMath is named Supercomputadores y ADN: Calculando las bases de la vida.

### **3.16 Presentation on Mr. SymBioMath for a Romanian company delegation**

On 8.7.2013 RISC Software GmbH was invited to give a presentation on the company and its projects to a delegation from the Romanian company Lasting.

Besides a general presentation on RISC Software GmbH, Mr. SymBioMath was presented as an example project including an overview of the project and its goals.

### **3.17 Bioinformatics presentation for a group of Czech high school children**

On 4th of July 2013 Oswaldo Trelles and Paul Heinzlreiter have been invited to give a presentation on Bioinformatics for a group of high school children from the Czech Republic. The event took place in the JKU Softwarepark Hagenberg, Austria.

Mr. SymBioMath was used as an example to present the role of science and its applications to young people as well as to try to motivate them to possibly pursue related careers. A focus has been put on describing the application area of Mr. SymBioMath together with its impact on society to the young audience:

- The role of genomes for humans and other beings
- Tracing migrations of peoples over history
- Comparing genomes from different species like for example human, chimpanzee, and dog to determine their evolutionary history

## **4 Press releases**

### **4.1 2013-02-01: Mr. SymBioMath project started**

With beginning of February 2013 the EU funded project High Performance, Cloud and Symbolic Computing in Big-Data Problems applied to Mathematical Modeling of Comparative Genomics (Mr. SymBioMath) has started. It runs over 36 months till January 2016 and is funded within the Maria-Curie programme of the EU 7th framework programme as an Industry-Academia Partnerships (IAPP) project under grant agreement number 324554.

The project will mainly target the application area of comparative genomics while building on top of cloud and high-performance computing. The international project consortium an international project consortium consists of the University of Malaga (Spain), RISC Software GmbH (Austria), the Johannes Kepler University Linz (Austria), Integromics (Spain), the Servicio Andaluz de Salud (Spain), and the Leibniz Supercomputing Center (Germany). The project is specifically supporting the cooperation between industry and academia through the exchange of personnel.

Based on its interdisciplinary approach the project interconnects the application domain of life sciences with technologies from bioinformatics as well as Cloud Computing and High Performance Computing, which is required for processing the large amounts of data, which are generated by modern genome sequencing technology. The size of this datasets also poses the main motivation for newly developing applications from the domain of comparative genomics, since the currently available versions are not prepared to handle full genomes.

Core points to be addressed within the project are comparisons and visualizations of sizeable genome sequences up to complete genomes as well as phylogenetic trees. An additional goal is given by the user-friendly presentation of the result data based on visualization techniques for different types of output devices ranging from tablet PCs to Virtual Reality Environments.

Within the project multiple interconnected software components will be developed including support layers for cloud computing and high performance computing, as well as modules for

data access and visualization on different types of output devices. These modules can be interconnected to form complex workflows for processing genomic data.

#### **4.2 2013-02-11: Press announcement by UMA on Mr. SymBioMath**

Project partner UMA has issued a spanish press announcement on the start of Mr. SymBioMath as well as the project kickoff meeting.

#### **4.3 2013-02-11: Spanish press article on the start of the Mr. SymBioMath project on [ucienca.uma.es](http://ucienca.uma.es)**

The kickoff meeting of the Mr. SymBioMath project has been taken as an opportunity to communicate the envisioned role and contributions of the project to a local Spanish newspaper through a press conference including an interview with project coordinator Oswaldo Trelles (UMA), as well as the representatives from the other partner institutions, namely Michael Krieger (RISC), Ulrich Bodenhofer (JKU), Juan Elvira (ITG), Miguel Blanca (SAS), and Christoph Anthes (LRZ).

#### **4.4 2013-02-26: German online press article on Mr. SymBioMath on [derstandard.at](http://derstandard.at)**

An online press article<sup>6</sup> on Mr. SymBioMath was published by the Austrian Newspaper “Der Standard”.

#### **4.5 2013-03-01: Spanish online article on Mr. SymBioMath**

A Spanish online article<sup>7</sup> on Mr. SymBioMath has been published on Lifescienceslab.com.

#### **4.6 2013-03-13: Spanish online press article on the Mr. SymBioMath project on [El Observador](http://ElObservador)**

Spanish online press article<sup>8</sup> from “El Observador”

#### **4.7 2013-03-14: MrSymBioMath press announcement by ITG**

Project partner Integromics has issued a press announcement<sup>9</sup> on its participation in the Mr. SymBioMath project.

---

<sup>6</sup><http://derstandard.at/1361241161499/Wie-man-sequenzierte-Genome-in-Zukunft-effizient-verarbeiten-kann>

<sup>7</sup><http://www.lifescienceslab.com/es/noticias/del-sector/integromics-invierte-en-la-optimizacion-del-rendimien>

<sup>8</sup><http://www.revistaelobservador.com/index.php/suplementos/idi-uma/7357-la-uma-coordina-un-proyecto-internaci>  
html

<sup>9</sup><https://www.integromics.com/integromics-invests-in-the-optimization-of-computing-performance-for-bioinforma>



#### **4.8 2013-03-20: English online article on Mr. SymBioMath on andaluciabioregion.es**

An article<sup>10</sup> on Mr. SymBioMath has been published on the website of Andalusia BioRegion.

#### **4.9 2013-03-26: German online press article on Mr. SymBioMath on derstandard.at**

The Austrian newspaper Der Standard has published an online article<sup>11</sup> on Mr. SymBioMath on their webpage.

#### **4.10 2013-04-09: German newspaper article on MrSymBioMath in OÖEN**

On 10th of April 2013 the Austrian regional newspaper Oberösterreichische Nachrichten published an article<sup>12</sup> on MrSymBioMath.

#### **4.11 2013-10-31: Spanish press article on the Mr. SymBioMath project on SaberUniversidad.es**

A spanish press article<sup>13</sup> describes the Mr. SymBioMath project.

#### **4.12 2016-11-18: Spanish press article on the Mr. SymBioMath project**

Project partner SAS has issued a press announcement on the mentioned date (in press).

## **5 Social networks**

### **5.1 Facebook**

The Mr. SymBioMath consortium set up a Facebook page for the project<sup>14</sup>.

---

<sup>10</sup>[http://www.andaluciabioregion.es/en/entity\\_item.cfm?iid=469](http://www.andaluciabioregion.es/en/entity_item.cfm?iid=469)

<sup>11</sup><http://derstandard.at/1363706116544/Die-DNA-ist-ein-Speicherfresser>

<sup>12</sup>[http://www.nachrichten.at/ratgeber/beruf\\_bildung/Big-Data-Forschung-fuer-die-Medizin;art121,1098253](http://www.nachrichten.at/ratgeber/beruf_bildung/Big-Data-Forschung-fuer-die-Medizin;art121,1098253)

<sup>13</sup><http://www.saberuniversidad.es/article/ACTUALIDAD/1636185/revolucion/omica/con/acento/andaluz.html>

<sup>14</sup><https://www.facebook.com/MrSymBioMath/>

## References

[AnnexI] Mr. SymBioMath Consortium. Mr. SymBioMath Annex I: Description of Work. Grant Agreement Number 324554, FP7-PEOPLE-2012-IAPP, October 2012.