eurac research

Bolzano, 16.09.2021

Dear Open Research Award Committee,

We would like to nominate our colleague, **Johannes Rainer, leader of the Computational Metabolomics Team at the Eurac Institute for Biomedicine**, as a candidate for the Open Research Award.

Johannes is a bioinformatician. He develops methods and software for the **analysis of high throughout omics data**. The analysis of such large datasets, e.g. thousands of metabolites or proteins, measured on thousands of individuals, requires an open and continuous exchange of methods, solutions and software tools between researchers worldwide.

Johannes has established successful tools and practices that are heavily **oriented towards open and collaborative scientific research**. He has promoted method and data sharing through multiple open access initiatives. Open science is **a real passion to him**, as he dedicates a considerable amount of time to create scientific resources that are rooted in the open access philosophy.

How openness is expressed in Johannes' work

Openness is an attitude and Johannes is **continuously engaged in creating networks**. He values collaboration as the key engine of science. To enhance collaboration, his style is **using open-source software tools**, mainly the R software package (the most important software for statistical data analysis), extensive and well-written documentation, and reproducible research techniques.

Johannes became the key figure of the **Open Seminar Series (OSS)**, a grassroot voluntary initiative aimed at stimulating the scientific environment at the Institute for Biomedicine. Over the last five years, the OSS has proven to be **fundamental for**

creating connections between researchers, originating new ideas and new projects, and not lastly, **giving a sense of familial environment to the many students and researchers from abroad**.
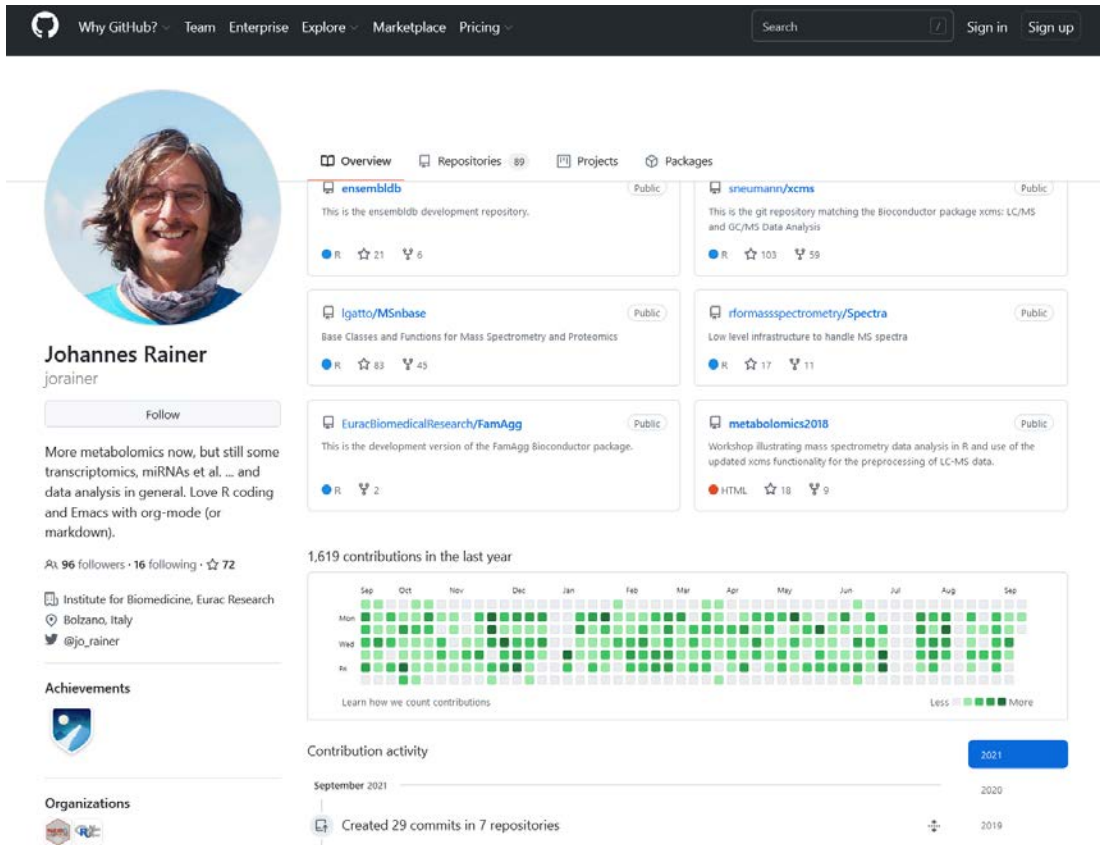

Figure 1. Screenshot of Johannes Rainer's github page at https://github.com/jorainer

Johannes' mission: improving openness, transparency, inclusion and reproducibility within the Institute, the research community and beyond

Johannes strongly believes in **open software and method development** to ensure transparency, provide a community approach to problem solving, enable reproducibility, and encourage help requests from the broad community in an unrestricted way.

He **actively supports the Bioconductor community,** specifically dedicated to the analysis of biological data, as a member of the Community Advisory Board and the Code of Conduct committee. He also contributed annotation packages for the Bioconductor's AnnotationHub.

He is a **founder of the "R for Mass Spectrometry" initiative,** www.rformassspectrometry.org, which highlights Johannes' **positive attitude**, by valuing and especially **encouraging contributions from the community and by actively reaching out to developers** to ask for contributions.

All data analyses performed by Johannes and his Team are done **using R markdown and *github* repositories** to enable reproducibility and collaborative efforts. Repositories are open to the whole scientific community upon acceptance of publications.

Within the Institute Johannes provides package versions for the different releases of our core data sets, facilitating data analysis for the whole institute, and manages and maintains R-software on the Institute's scientific computing infrastructure to enable **reproducibility**. **All datasets are made available through public repositories** unless prevented by legal or privacy constraints (see Gene Expression Omnibus examples in **Figure 2**).

He **favors reviewing articles for open peer review journals** such as *PLOS Computational Biology*.

Finally, documenting his attitude to the broadest dissemination and openness, the scientific activity of Johannes and his team are always disseminated to a lay audience through his twitter account, https://twitter.com/jo_rainer, which has a great number of followers.

Joining and expanding open research projects initiated by Johannes is easy. His attitude has enhanced the whole Institute's research environment and network.

Accessing data and methods from Johannes and his team is extremely easy thanks to his efforts in providing extensive documentation and well-organized software and data packages. More than that, his work is influencing heavily the general attitude of data

scientists at the Institute to favor open, collaborative and reproducible research, significantly increasing the quality of our scientific output.

Johannes' research encourages knowledge transfer within the specific and the broad research community, enabling interdisciplinary research and intercultural exchange.

While developing methods and tools that are mainly dedicated to solve problems in the statistical analysis of omics data, the same methods and software are applied to other fields. The R and Bionconductor communities **don't have boundaries**. For this reason, the developed **open access tools are especially beneficial to scientific researchers from disadvantaged countries**.

Johannes Rainer: brief summary of the scientific and open research activity
- Developer of several open source R packages, most of which are part of the Bioconductor project.
- Member of the Bioconductor Community Advisory Board, https://bioconductor.org/about/community-advisory-board/, with the mission to reach out and involve the scientific community
- Member of the Bioconductor Code of Conduct committee.
- Contributor of annotation packages for Bioconductor's AnnotationHub.
- Founder of the "R for Mass Spectrometry" initiative https://www.rformassspectrometry.org.
- Highly active in providing help and support for users of the various software packages (e.g. https://github.com/sneumann/xcms/issues).
- Created workshops and tutorials to illustrate usage of the developed software packages. (e.g. https://jorainer.github.io/SpectraTutorials/).
- Workshops at various conferences as well as in the "Bioconductor CSAMA summer schools" (e.g. https://www.huber.embl.de/csama2019/#home).
- Manages R-software package versions and releases (using docker/singularity) on the Institute's calculation cluster to ensure reproducibility.
- Data sets available through public repositories; e.g. Gene Expression Omnibus https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE95120 ; https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE78210
- Open peer reviewer for PLOS Computational Biology
- Organizer of Open Seminar Series at the Eurac Institute for Biomedicine
- Authored >50 scientific publications with >2500 citations and an H index of 25

Figure 2: Summary of Johannes Rainer scientific and open research activity

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An attitude to generating educational resources for formal and informal education

Johannes is a great visual and verbal **communicator**. He created workshops and tutorials to illustrate usage of the developed software packages. All materials are always provided for free, as github repositories including all data, scripts, documentation, as well as rendered workshop material (e.g. https://jorainer.github.io/SpectraTutorials/).

He held **workshops at various conferences** as well as in the "Bioconductor CSAMA summer schools" (https://www.huber.embl.de/csama2019/#home), one of the main bioinformatic summer schools in Europe.

Overall, the figure of Johannes Rainer particularly summarizes the attention and sensitivity towards an increasingly open, transparent, reproducible and comprehensible scientific research. If we had to choose a Eurac testimonial in this field, we would choose him.

We hope that our testimony can help you recognize Johannes valuable contributions.

Sincerely,

Cristian Pattaro
Group leader, Biostatistics & Epidemiology, Eurac Research Institute for Biomedicine

Christian Fuchsberger
Group leader, Computational Genomics, Eurac Research Institute for Biomedicine

Francisco Domingues
Group leader, Biomedical Informatics, Eurac Research Institute for Biomedicine

Hagen Blankenburg
Data Steward at the Eurac Research Institute for Biomedicine