
Email from Concha Gil (on the 27th of September)

Dear Dr Locard and Dr Bouyssié,

We are preparing a new issue of the EuPA News and we would like to give you the opportunity to highlight the current activities related to the “EuBic”.

The next bulletin is scheduled for **December 2019**. The contribution should be ideally due to **the 15th November 2019**.

We are available for any question, comment, or help.

The issue will have the following tentative table of contents:

- Message from the EuPA President
 - Activities of EuPA Committees
 - o Conference and Communication Committee
 - o Education Committee
 - o EuPA Journals Committee
 - o Funding Committee
 - o EuPA initiatives Committee
 - News from the EuPA initiatives.
 - o Affinity Binder Knock-Down
 - o EuBic
 - o Biobanking
 - o Standardization
 - o IMOP
 - o Food and Nutrition Proteomics
 - o Cost action CliniMARK
 - Activities of the Young Investigators Club
 - Meeting reports
- EuPA 2018 and EuPA 2019
- Forthcoming meetings
- Announcement and comments about HUPO & EuPA 2020 in Stockholm

We hope that you will consider our invitation positively. Below you will find the instructions for authors

Many thanks you for your help

With our best regards,

Dr. Concha Gil

On behalf of the EuPACCC

R,S.V.P.

Instructions to authors

Manuscripts to be published in the EuPA news must be short (no more than **four A4 pages, 2 cm margin, 1,5 space** between lines in the original submission, that can be no more than two pages in the printed version of the bulletin). Use **Times New Roman 12 pt font**, except for the title (14 pt, bold type). The authors, affiliation and e-mail will be located at the end. A photograph of the contributor(s) will be included.

In special cases, and in agreement with the editors, longer contributions can be admitted.

Contributions must be submitted at least 30 days before the release of the issue.

Previous EuPA news doc:

https://docs.google.com/document/d/1-V9U6qDLQXDNH_wz_qqpGucy32utd3ty9xuLWqLwn7M/edit#

EuBIC: the EuPA initiative for computational mass spectrometry

The European Bioinformatics Community (EuBIC) is the EuPA initiative for mass spectrometry (MS)-related bioinformatics. Its aim is to improve bioinformatics for MS-based research through the setup of community-driven dynamics, thereby improving collaboration, funding, publication, and training activities. Through its different activities EuBIC tries to raise awareness for the benefits of open science and continuously supported open software.

Mass spectrometry data analysis and integration requires proficiency in a combination of scientific fields, including bioinformatics and biostatistics. Despite being of critical importance, research groups often lack sufficient knowledge about these fields. One reason for this lies in the unavailability of adequate educational resources, help and support. We started the European Bioinformatics Community (EuBIC) initiative in November 2015 (Vaudel, 2016) to bring together the MS and bioinformatics communities in an open, collaborative and constructive environment. The initiative is carried enthusiastically by the bioinformatics community and welcomes everyone willing to help.

EuBIC organizes a dedicated yearly conference, bringing together researchers in the fields of mass spectrometry and bioinformatics, junior scientists and industry partners from across Europe. Every year, this conference alternates between a Winter School with keynote talks and workshops, and a Developers' Meeting consisting of collaborative project sessions with the participants (hackathons). Additionally, the EuBIC initiative actively contributes to bioinformatics hubs, and provides various workshops and presentations during international MS (e.g. annual conference of American Society of Mass Spectrometry) and proteomics (e.g. Human Proteome Organization congress, EuPA congress) conferences.

Winter Schools and Developers' Meetings

The EuBIC Winter Schools on computational MS are sponsored by the European Proteomics Association (EuPA) and several MS companies. They bring together scientists from both academia and industry to present and discuss their research in workshops, keynote lectures, flash

talks and poster presentations. We already hosted two Winter Schools, the first one in Semmering, Austria in 2017 (Willems et al., 2017)(<https://doi.org/10.1016/j.jprot.2017.04.001>) and the second in Zakopane, Poland in 2019 (Kopczynski et al., 2019)(<https://doi.org/10.1016/j.euprot.2019.07.002>).



Figure 1: picture of participants of the EuBIC Winter School 2019.

The Developers' Meetings is an event dedicated to computer scientists and developers, in the field of bioinformatics applied to MS, where they can discuss and work together in an open and constructive spirit. The program is split between keynote lectures and multiple hackathon sessions where the participants develop bioinformatics tools and resources that address outstanding needs in the bioinformatics community and among biologists using MS data. Our first Developers' Meeting took place in Ghent, Belgium in 2018 (Willems et al., 2018).

In total, our three conferences attracted about 250 participants from all over Europe and featured twenty-two different high class keynote speakers from the research area. The next Developers' Meeting will take place in January 2020 in Nyborg, Denmark. This event, like the previous ones, is expected to significantly contribute towards increasing the visibility of bioinformatics applications for analyzing MS proteomics data. Furthermore, as this EuBIC meeting will gather several established experts in the field of computational MS, it will provide the perfect opportunity to nurture fruitful international collaborations. Especially the hands-on sessions will

stimulate the start of new collaborative projects. The registration to the Developers' Meeting 2020 has already opened (deadline December 23, 2019) and six collaborative projects - proposed by community members - were selected. More information is available on <https://eubic-ms.org/2020-dev-meeting>.

Recent EuBIC activities

Definition of guidelines for reproducible MS data analysis

The number of datasets published on public repositories is in constant increase (Deutsch et al., 2019; Perez-Riverol et al., 2019). This constitutes a highly valuable resource for meaningful biological data in the form of scientific publications, as well as billions of mass spectra obtained from a wide range of biological samples that can be integrated or re-analysed in other biological contexts. While the quantity of available data is tremendous, there is a growing concern regarding the reproducibility of the associated bioinformatics analysis. The methods sections of research manuscripts, or supplementary files, often do not contain all the information necessary to interpret the analysis results and/or to reproduce them, such as complete and detailed experimental designs, or the correct parameters necessary to run the involved software tools. Therefore, it is necessary to increase the awareness of authors on providing truly reproducible procedures and results. EuBIC started to work on the definition of a new set of guidelines (<https://eubic.github.io/ReproducibleMSGuidelines>) as a support for authors to write complete material and methods sections, as well as editors and reviewers to evaluate data availability of submitted papers. This project is fully community-driven, and we encourage everybody to contribute in order to refine and extend the definitions of these guidelines.

New EuBIC website: eubic-ms.org

In partnership with the EuPA Educational Committee (EC), the Proteomics Academy web resource (<https://www.proteomics-academy.org>) has become the central communication portal for EuBIC since its creation in 2015. To increase the visibility of EuBIC itself, we recently decided to set up a new website dedicated to the initiative at <https://eubic-ms.org>. There, people will find all information regarding past and upcoming EuBIC activities. The EuPA educational

activities will remain on the Proteomics Academy. The job fair webpage (<http://jobs.proteomics-academy.org/>) developed in collaboration with the Young Proteomics Investigators Club (YPIC - eupa.org/ypic) remains accessible at the same location. The job platform has recorded several offers over the past months and statistics of November 2019 list 14 open job positions at different levels (PhD, post-doc, staff scientist and bioinformatician). We thus encourage all EuPA members and young scientists searching for a new position to visit this webpage.

How to get involved?

The EuBIC community is open to everybody working in computational proteomics and mass spectrometry. You can join us by sending an email at info@eubic-ms.org or by using the contact form available from the eubic-ms.org website. We will then send you an invitation to join our Slack workspace (<http://eubic.slack.com>), which is our extensively used platform to interact with other EuBIC members. Additionally, you can follow and retweet our latest activities from our Twitter account ([@EuBIC_ms](https://twitter.com/EuBIC_ms)). By joining us, you will be part of a community effort, and thus contribute to the sustainability of these scientific activities, which we expect to foster the development of the computational MS field.

Acknowledgments

The EuBIC organizing committee would like to thank the European Proteomics Association for its support and funding since the creation of the initiative. We would also like to underscore the remarkable work accomplished by all organizers of the previous Winter Schools and Developers' Meetings.

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