2020 BioImage Analysis Survey:
Community experiences and needs for the future

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Abstract

In this paper, we summarize a global survey of 484 participants of the imaging community, conducted in 2020 through the NIH Center for Open BioImage Analysis (COBA). This 23-question survey covered experience with image analysis, scientific background and demographics, and views and requests from different members of the imaging community. Through open-ended questions we asked the community to provide feedback for the open-source tool developers and tool user groups. The community's requests for tool developers include general improvement of tool documentation and easy-to-follow tutorials. Respondents encourage tool users to follow the best practices guidelines for imaging and ask their image analysis questions on the Scientific Community Image forum (forum.image.sc). We analyzed the community's preferred method of learning, based on level of computational proficiency and work description. In general, written step-by-step and video tutorials are preferred methods of learning by the community, followed by interactive webinars and office hours with an expert. There is also enthusiasm for a centralized location online for existing educational resources. The survey results will help the community, especially developers, trainers, and organizations like COBA, decide how to structure and prioritize their efforts.

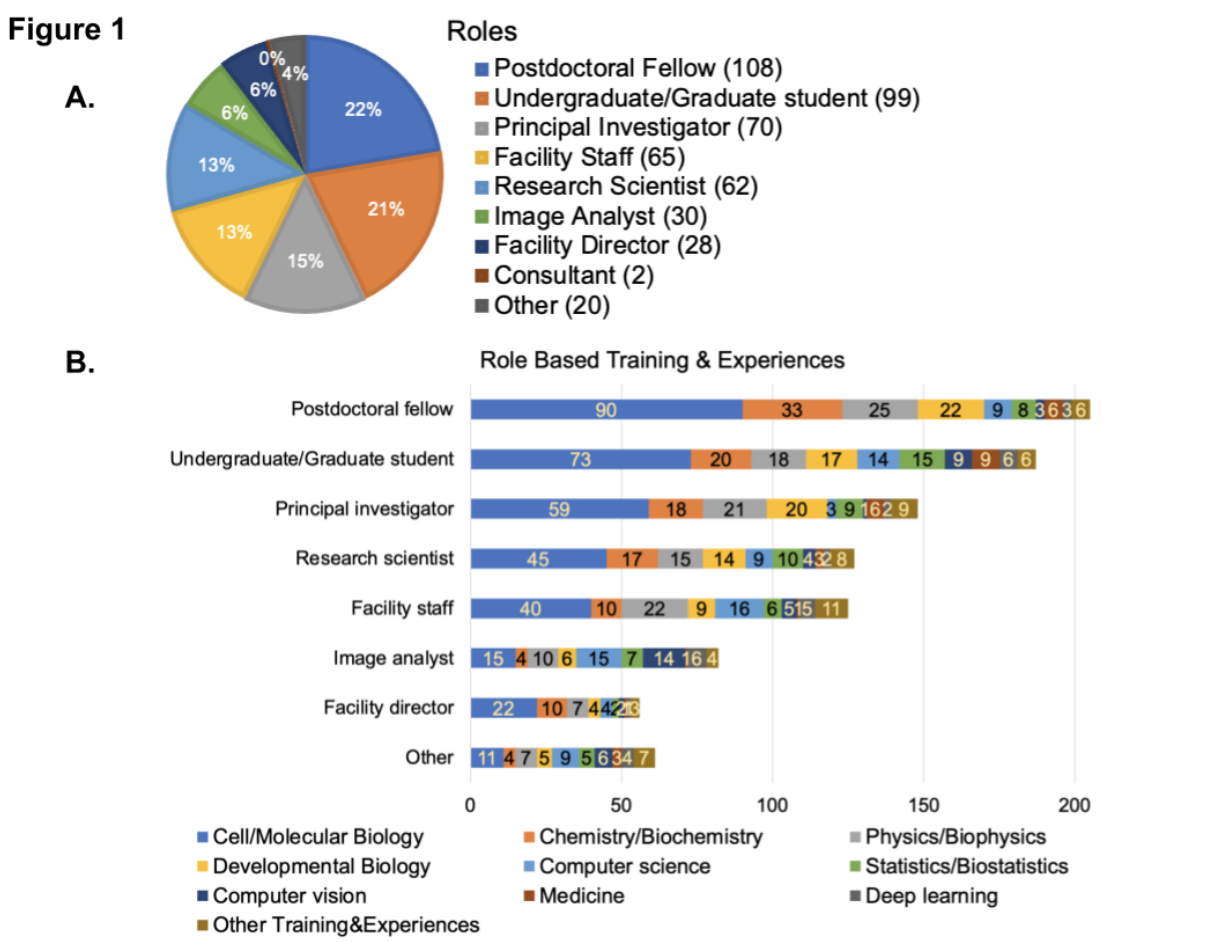
Impact statement:

The Bioimage analysis community consists of software developers, imaging experts, and users, all with different expertise, scientific background, and computational skill levels. The NIH funded Center for Open Bioimage Analysis (COBA) was launched in 2020 to serve the cell biology community's growing need for sophisticated open-source software and workflows for light microscopy image analysis. This paper shares the result of a COBA survey to assess the most urgent ongoing needs for software and training in the community and provide a helpful resource for software developers working in this domain. Here, we describe the state of open-source bioimage analysis, developers' and users' requests from the community, and our resulting view of common goals that would serve and strengthen the community to advance imaging science.

Results

Participants

Of the 484 survey participants, the majority were from North America (60%) and Europe (34%), followed by Asia, Australia, South America, and Africa (Supplementary Fig 1A). 43% of participants were in training (either “postdoctoral fellow” or “undergrad/graduate students”; Figure 1A). Most participants described experience and/or training in the biological sciences, including cell/molecular biology, chemistry/biochemistry, followed by physics and developmental biology (Figure 1B), though the small proportion of participants whose role was “Image analyst” or “Other” reported computational backgrounds more often. This is consistent with a 2015 survey from the Network of European BioImage Analysts (NEUBIAS) [1], which is a network working toward bridging the efforts between life science, computer science, and digital image processing [2].

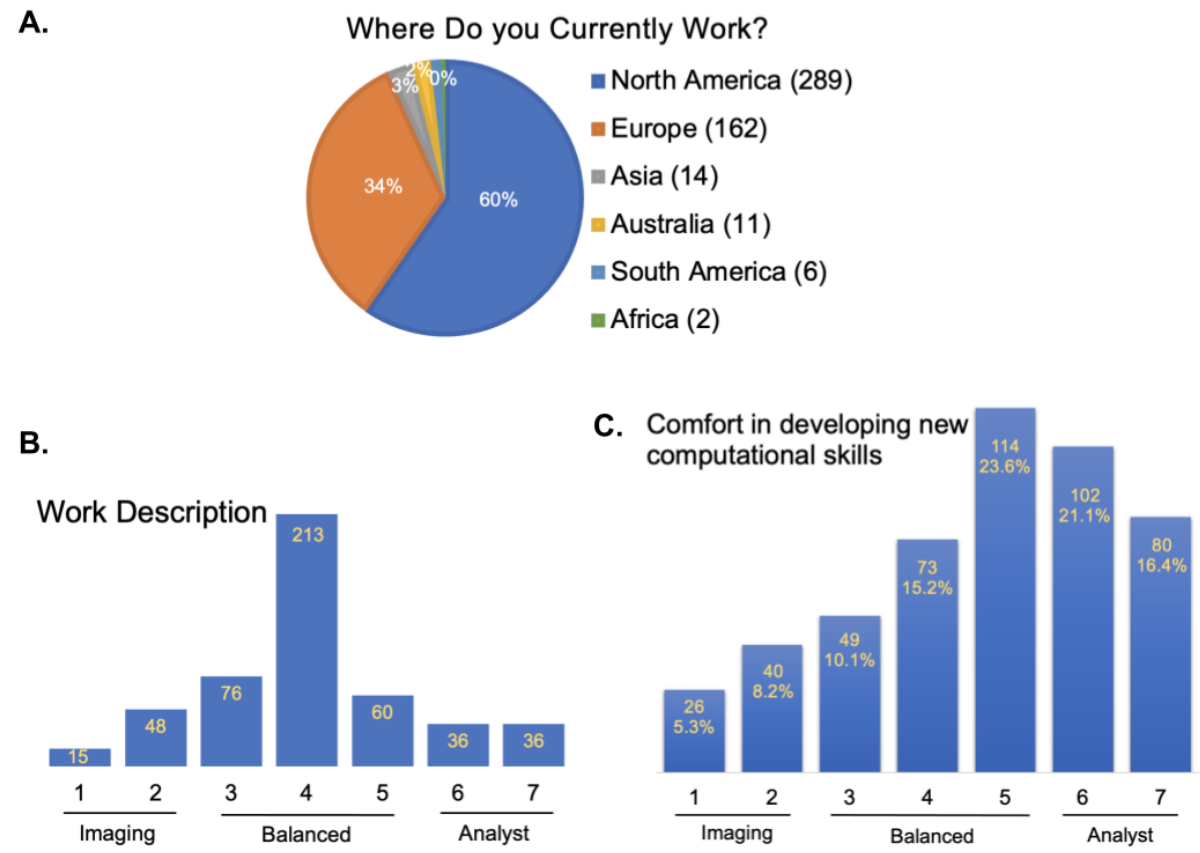


A. Responses to the multi-choice question of “Which of the following roles best describe you?”.

Respondents had the option to provide additional answers.

B. Responses to the checkbox question of “Which of the following do you have significant formal training in or experience with? Select all that apply”. Responses were broken down by the major categories from part A.

Supplementary Figure 1



A. Responses to the multiple choice question of “Where do you currently primarily work?”

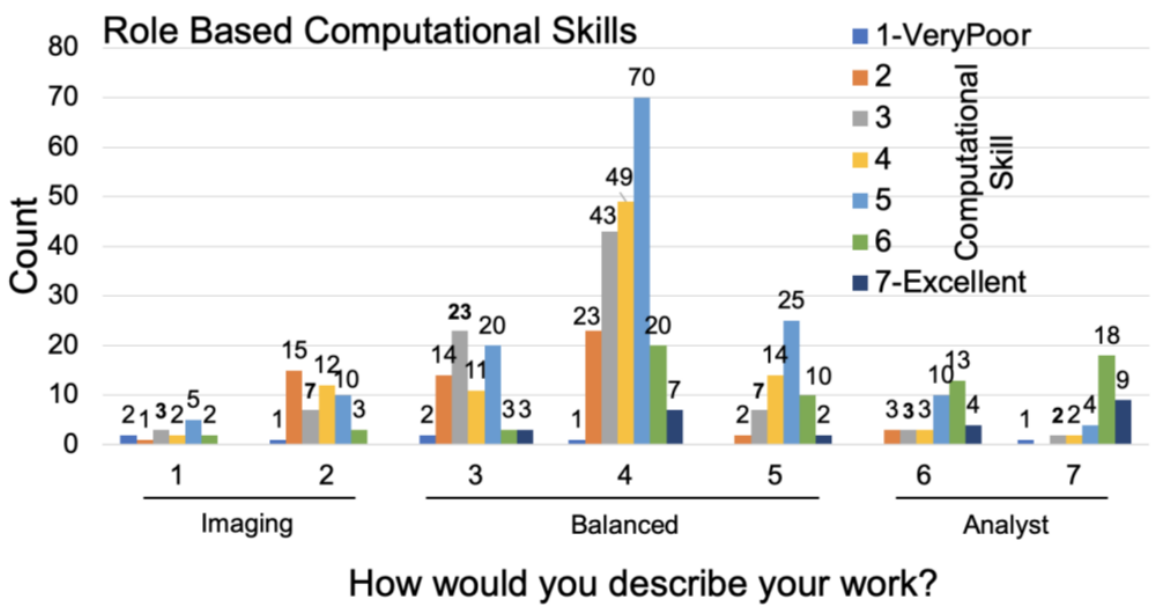
B. Responses to the question of “How would you describe your work?” along a linear scale, with 1 representing *nearly entirely imaging* (sample prep, optimizing/deciding on imaging modalities, acquiring images, etc), and 7 representing *nearly entirely image analysis* (finding the right tools to analyze a particular experiment, optimizing the analysis, data mining). Responses were categorized into three groups: “Imaging” (scores 1&2), “Analyst” (scores 6&7), and “Balanced” (scres 3 to 5).

C. Responses to the question of “How would you rate your comfort in developing new computational skills?” along a linear scale, with 1 representing *very uncomfortable* and 7 representing *very comfortable*. Responses were categorized into three groups of “Imaging”, “Balanced”, and “Analyst” as described in B.

We next asked participants to describe their work along a linear scale, with 1 representing mainly imaging (sample preparation, optimizing/deciding on imaging modalities, acquiring images, etc.) and 7 representing mainly image analysis (finding the right tools to analyze a particular experiment, optimizing the analysis, and data mining). The group of respondents with scores of 1 and 2 are hereafter described as “imaging”, the group with scores of 3-5 are described as “balanced”, and the group with scores of 6-7 as “analysts”. The majority of respondents fell into the “balanced” category (Supplementary Figure 1B).

We also asked participants about their level of computational skills, on a scale of 1 to 7. Computational skills tracked somewhat with job roles, with the imaging, balanced, and analyst groups showing mean computational skills of 3.59, 4.17, and 5.40, respectively (Figure 2). On average, the community feels they are more comfortable than not in developing new computational skills, rating themselves a 4.73 out of 7 (Supplementary Figure 1C).

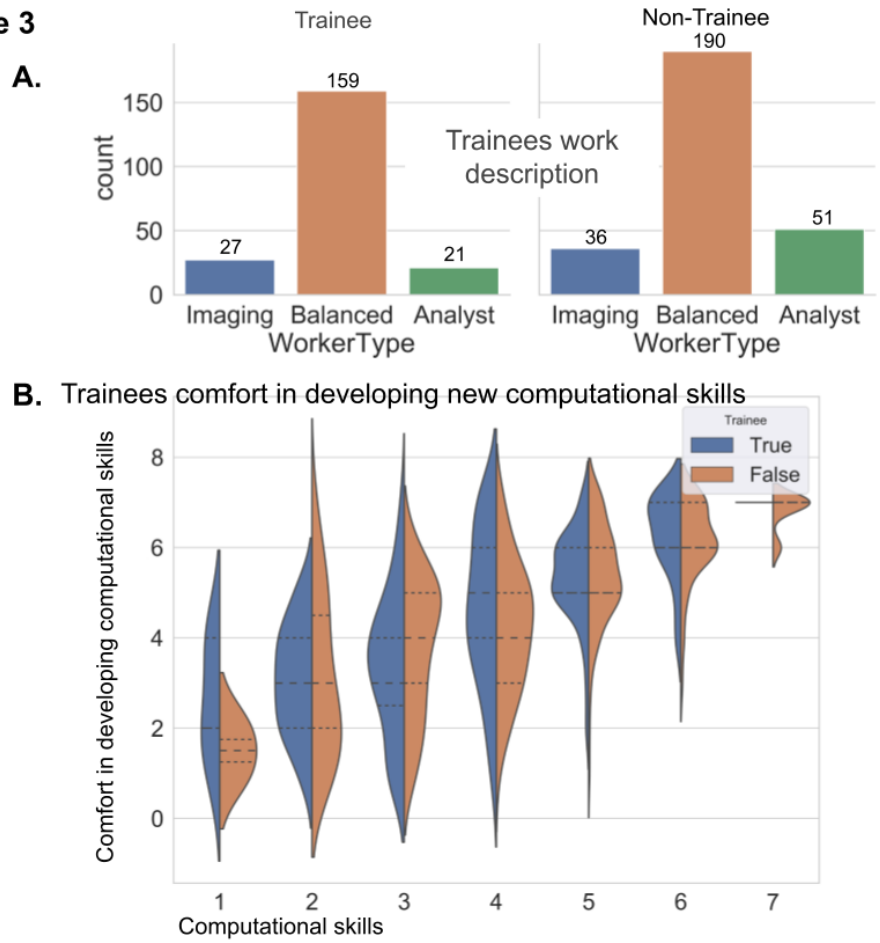
Figure 2



Responses to the question of “How would you rate your computational skills?” along a linear scale with 1 representing *Very poor* and 7 representing Excellent. Responses were cross-matched with the work duties (graphed in Supplementary Figure 1B).

Because almost half of the survey participants were from the trainee group and because trainees may have particular requests that need to be addressed, we wanted to know how our measures of job class, computational skill, and computational comfort differed for trainees vs non-trainees. Cross-matching the work duties as shown in Supplementary Figure 1B with the role description as shown in Figure 1A, showed the trainee group was relatively evenly drawn from the imaging, balanced, and analyst groups. A large number of survey respondents were from the balanced group, regardless of their trainee status (Figure 3A). While trainees were missing from the highest self-reported skill level, reported comfort in developing new computational skills increased with reported existing skill level and was comparable between trainees and non-trainees (Figure 3B).

Figure 3



A. The trainee vs non-trainee groups' job description were drawn by cross-match of the work duties (graphed in Supplementary Figure 1B) and role description (graphed in Figure 1A)
B. Responses to the question of "How would you rate your comfort in developing new computational skills?" (graphed in Supplementary Figure 1C), cross-matched with the

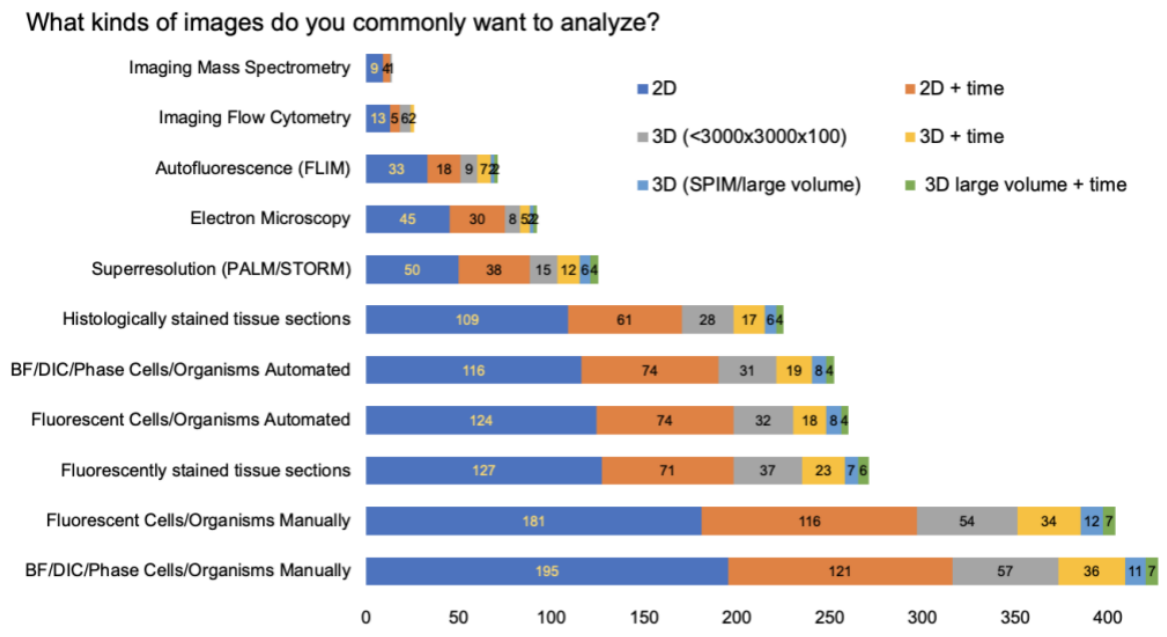
responses to the question of “How would you rate your computational skills?”, and separated based on the trainee group.

Needs and commonly-used tools

Types of images analyzed (modality, technique, specimen, etc.)

In response to our question “*What kinds of images do you commonly want to analyze?*”, brightfield (BF/DIC/Phase) and fluorescent two-dimensional (2D) images from cells and organisms were the top most-commonly analyzed images among the survey participants (Figure 4), which were mainly captured by manual field selection as opposed to an automated system. Overall the majority of images to be analyzed were 2D, followed by 2D timelapse images, 3D volumes, and then 3D timelapse images.

Figure 4



Responses to the checkbox grid question of “What kinds of images do you commonly want to analyze?”. Respondents had the option to provide additional answers.

Types of analysis tools used

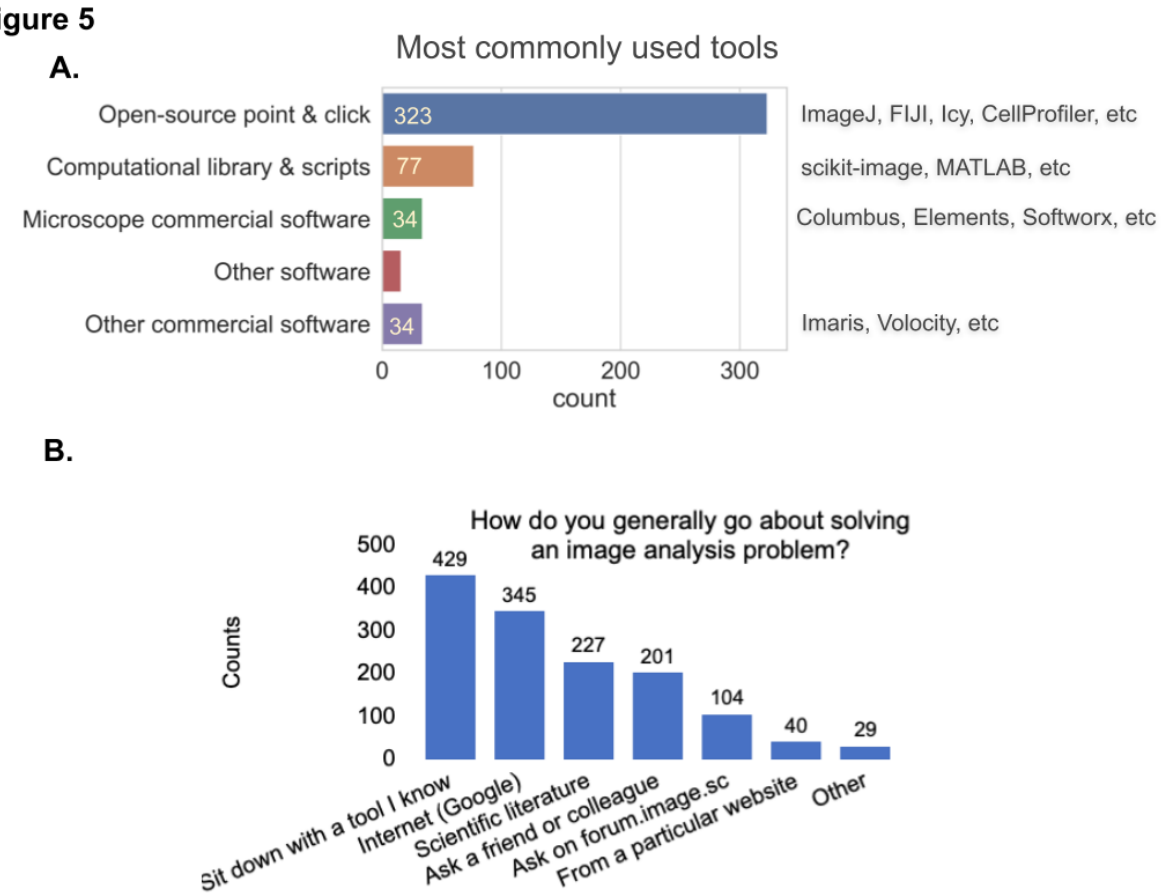
When we asked "*What image analysis tools do you use the most?*", the vast majority of respondents reported the category of "open source point and click software". The question described such tools to include ImageJ [3,4], Fiji [5], CellProfiler [6], Icy [7], etc., all of which are the most commonly used tools among participants (Figure 5A). The next most common tools were "computational libraries and scripts" (such as scikit-image [8] and MATLAB [9] libraries), followed by commercial software on the user's microscope and other commercial software. While these may be representative of the broader community, we note that most promotion of the survey was via a forum for open-source tools (forum.image.sc) [10] and by Twitter accounts related to open-source tools, presumably increasing their final representation in the survey.

Approaches, image analysis problems, and tips for developers and users

Commonly used approaches to solve image analysis problems

We next wanted to better understand what approaches our participants take to solve their image analysis problems. The most popular approaches are: sit down with a familiar tool, search the web, look up solutions in the scientific literature, ask a friend or colleague, and/or ask on the Scientific Community Image forum (forum.image.sc) (Figure 5B).

Figure 5



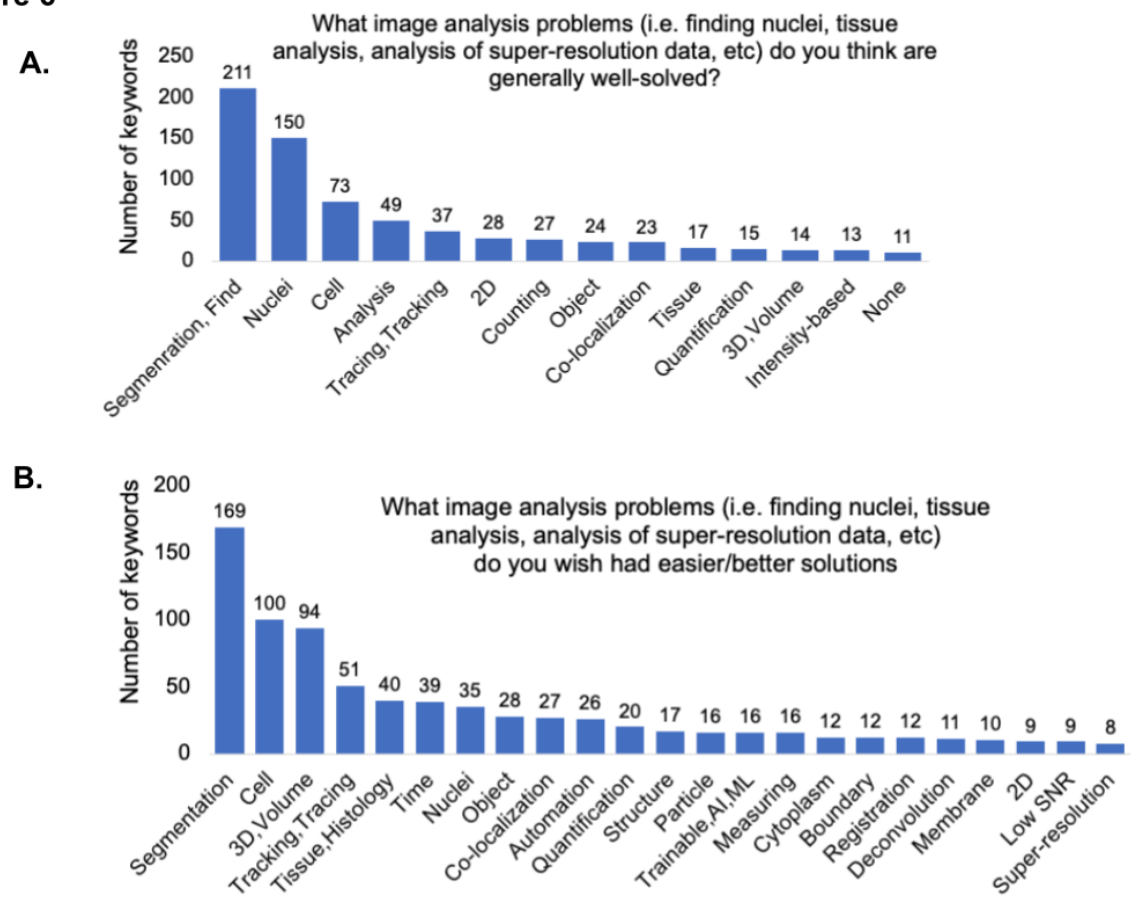
A. Responses to the multiple choice question of "What image analysis tools do you use the most?". Respondents had the option to provide additional options.
B. Responses to the checkbox question of "How do you generally go about solving an image analysis problem? Check the approach(es) you use them the most". Respondents had the option to provide additional options.

Well-solved image analysis issues and those needing better solutions

To assess the community's thoughts on the success of currently existing tools, we next asked participants via open-ended questions to describe which image analysis problems they thought were already well-solved and which they wished had better solutions. We analyzed the free-text responses by parsing them, using Python scripts as described in the methods section. Responses containing "detection" and/or "segmentation" were the most common for both questions; likely this reflects the huge diversity of biological objects our participants are trying to detect (Figure 6A-B). The answers with a much higher relative rank in the "well-solved" category

were “Nuclei” and “2D” and in the “wish were better solved” category were “3D/Volume” and “Tissue/Histology".

Figure 6



A. Keyword analysis of the open-ended question of “What image analysis problems (i.e. finding nuclei, tissue analysis, analysis of super-resolution data, etc) do you think are generally well-solved?”.
B. Keyword analysis of the open-ended question of “What image analysis problems (i.e. finding nuclei, tissue analysis, analysis of super-resolution data, etc) do you wish had easier/better solutions?”.

Tips for image analysis for users and developers

Suggestions for the Open-Source Tool Creators/ What creators can do

We asked the community to provide open-ended feedback for the tool developers: *“What do you think analysis tool CREATORS (such as software developers) could/should do to make image analysis better and more successful? How best could we encourage them to do it?”*. Through

our analysis of keywords, we conclude that all groups encouraged developers to improve documentations and manuals, user interface, plugins and packages, as well as providing easy-to-follow workshops and tutorials (Figure 7A). They suggested that tool creators form a tight-knit community, in which they could collaborate, review software, and improve documentation. Other suggestions included prizes for best tool instructions and frequent reminders for users to cite analysis tools in publications.

As we expected, users who self-reported spending more time on imaging than on analysis have different perspectives on the greatest needs. We therefore binned the answers into the "imaging", "balanced", and "analyst" categories. The "imaging" group's most common suggestions were for more-user friendly tools, better documentation, and more video tutorials. The "balanced" group emphasized a need for clear documentation with detailed explanations of the parameters, as well as asking for tools that perform better in real-world conditions when ability to improve sample acquisition is limited. The "analysts" also highlighted a need for better documentation, an ecosystem with fewer and more multifunctional tools over a plethora of single-use scripts, and more interoperability between the current open source tools; they also encouraged developers to communicate with users early and often (data not shown).

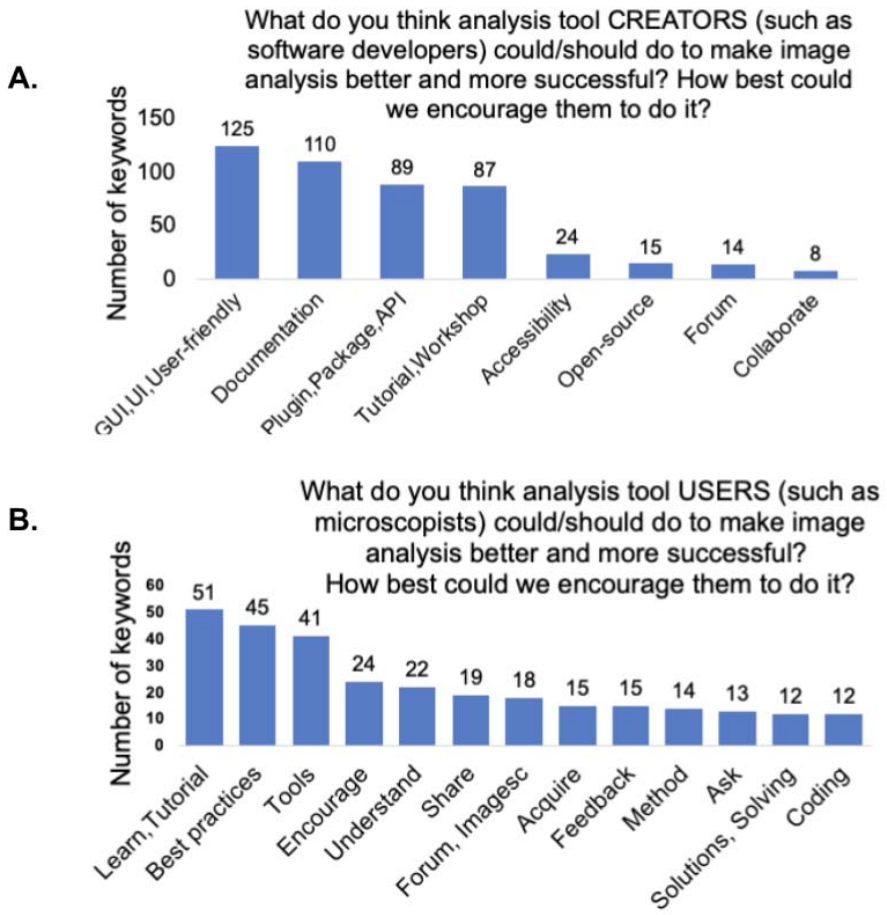
Suggestions for the Open-Source Tool Users

We also asked, *"What do you think analysis tool USERS (such as microscopists) could/should do to make image analysis better and more successful? How best could we encourage them to do it?"*, allowing the community to provide feedback for the tool users. Overall, as shown in Figure 7B, the community asked users to seek out existing tutorials and workshops and learn the tools and basics of image analysis, follow the best practices guidelines for imaging, and ask their image analysis questions on the image.sc forum. By using a single, central forum for image analysis questions, all members could benefit from every user's questions, feedback, and suggestions, which makes it easier for tool creators to provide answers. Respondents also encouraged users to start image analysis when performing pilot imaging and condition optimization experiments, rather than waiting until the completion of larger-scale experiments. Participants also suggested that principal investigators encourage their trainees to take image analysis courses and try new image analysis tools.

Breaking down the answers by role, we found that the "imaging" group asked the users to pay attention to sample quality, to have an understanding of why particular image analysis methods

are applied in certain cases, and to reach out to experts and provide detailed feedback to tool developers with examples. The “balanced” group responded that users should provide analysis workflow details in publications, keep settings consistent during acquisition and analysis, and they encouraged tool users to think about the analysis before and during image acquisition, testing their approach on early data rather than leaving all the analysis for the end. They also emphasized providing feedback for the developers, exploring new tools, and posting questions on the image.sc forum. “Analysts” particularly asked users to take advantage of available tutorials and workshops about the basics of image analysis and open source tools. They also encouraged tool users to clarify their image analysis needs to the developers, provide feedback, request new features, and report bugs, including detailed information and sample images in their bug reports.

Figure 7



A. Keyword analysis of the open-ended question of “What do you think analysis tool CREATORS (such as software developers) could/should do to make image analysis better and more successful? How best could we encourage them to do it?”.
B. Keyword analysis of the open-ended question of “What do you think analysis tool USERS (such

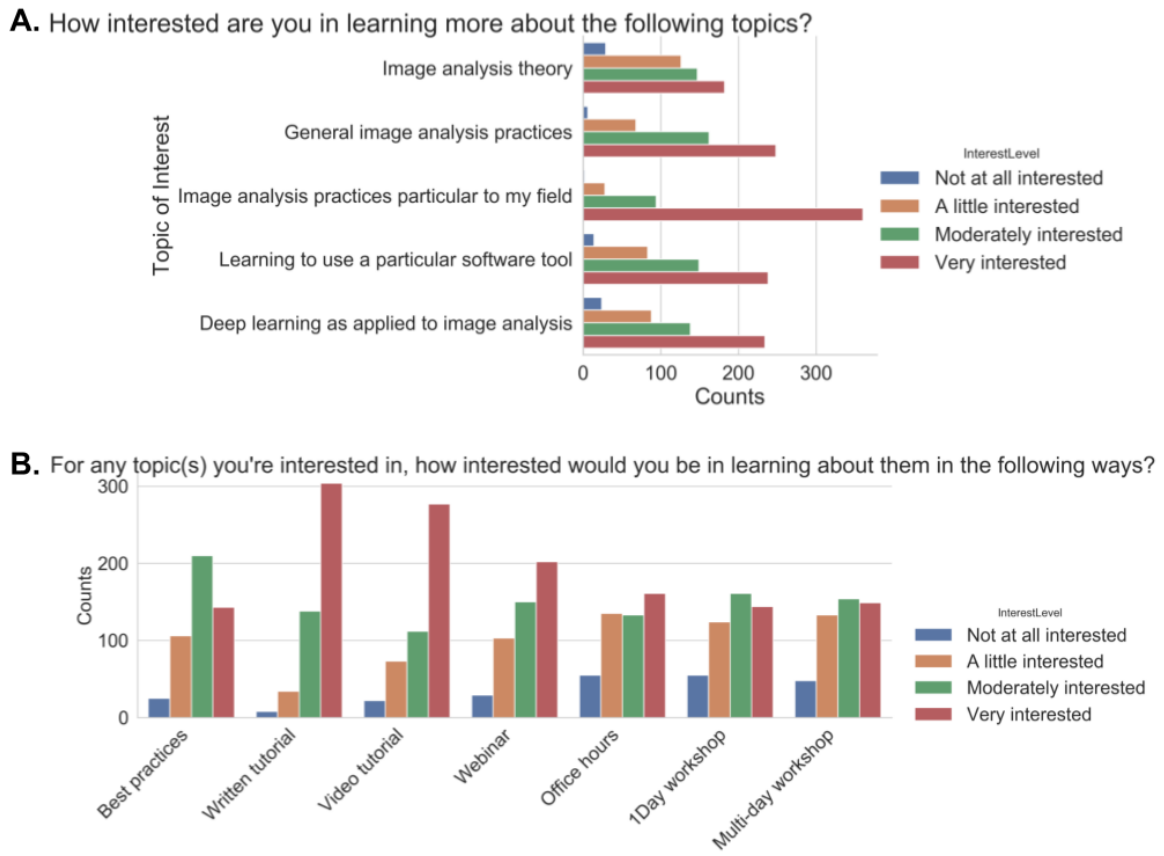
as microscopists) could/should do to make image analysis better and more successful? How best could we encourage them to do it?".

Learning materials and their components

Interest in learning new topics

We next asked users to rate their interest in learning more about each of several topics. Participants showed the highest level of interest in learning about image analysis practices specifically related to their own field (Figure 8A). The remaining four areas to be rated, image analysis theories, general image analysis practices, learning to use different software tools, and deep learning approaches for image analysis, showed a similar pattern to each other with a plurality of users stating they were "very interested" followed by "moderately", "a little", and "not at all" interested. These results emphasize that the community shows an appetite for image analysis educational materials.

Figure 8

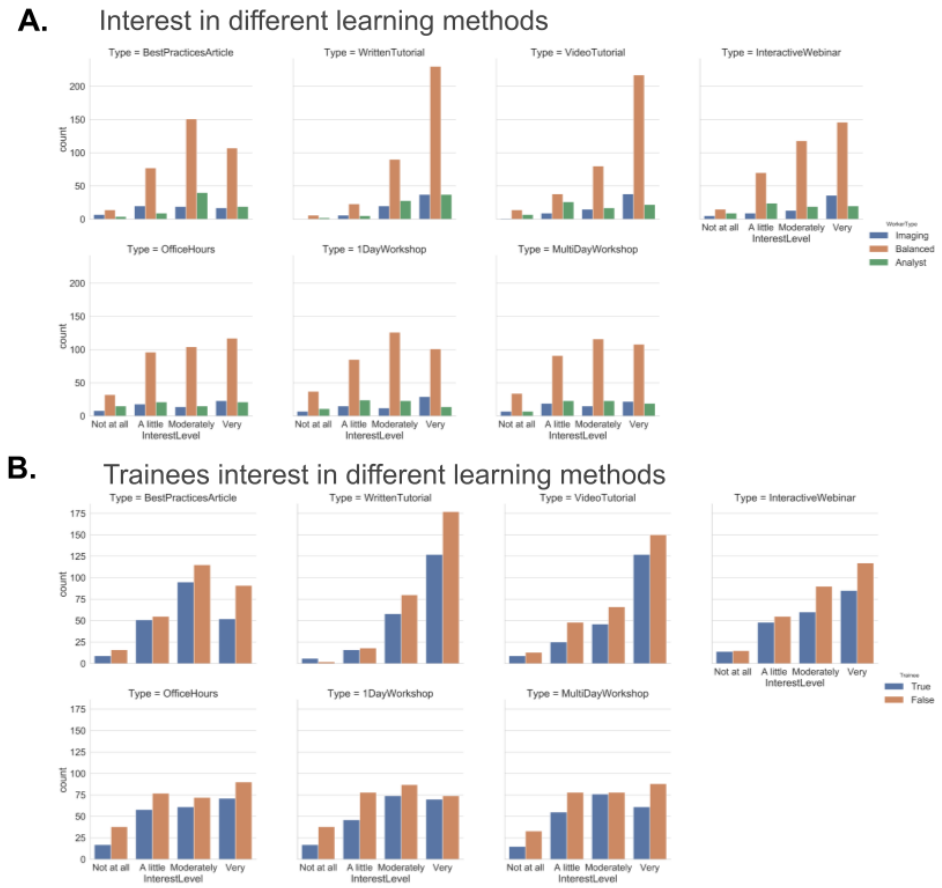


A. Responses to the multiple choice grid question of “How interested are you in learning more about the following topics?”.
B. Responses to the multiple choice grid question of “For any topic(s) you're interested in, how interested would you be in learning about them in the following ways?”.

Delivery format of learning material

To help trainers and developers better prioritize particular types of educational material, we asked “*For any topic(s) you're interested in, how interested would you be in learning about them in the following ways?*”, via a multiple choice grid question. Survey participants in general prefer written step-by-step and video tutorials, followed by interactive webinars and office hours with an expert (Figure 8B). While we hypothesized that we would see differences in preferred format among our “imaging”, “balanced”, and “analyst” groups, we in fact saw minimal differences between those groups (Supplementary Figure 2A); nor did preferences substantially differ between trainees and non-trainees (Supplementary Figure 2B). The preference for written and video tutorials, followed by interactive webinars, remained true across other groups of participants, such as comfort level in developing new computational skills and level of interest in learning new topics (Supplementary Figure 3).

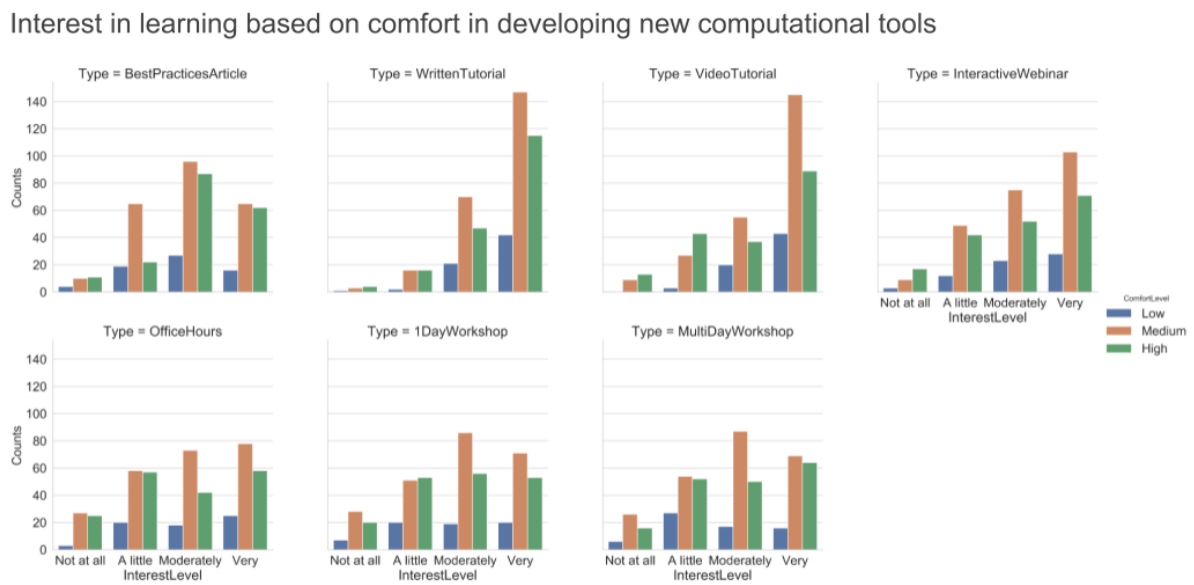
Supplementary Figure 2



A. Cross-matching of the preferences in learning methods (graphed in Figure 8B) with the work duties (graphed in Supplementary Figure 1B), and separating them based on the level of interest (not at all, a little, moderately, and very).

B. Cross-matching of the preferences in learning methods (graphed in Figure 8B) with the trainee group, and separating them based on the level of interest (not at all, a little, moderately, and very).

Supplementary Figure 3



Cross-matching of the preferences in learning methods (graphed in Figure 8B) and comfort level in developing new computational skills (graphed in Supplementary Figure 1C), and separating them based on the level of interest (not at all, a little, moderately, and very).

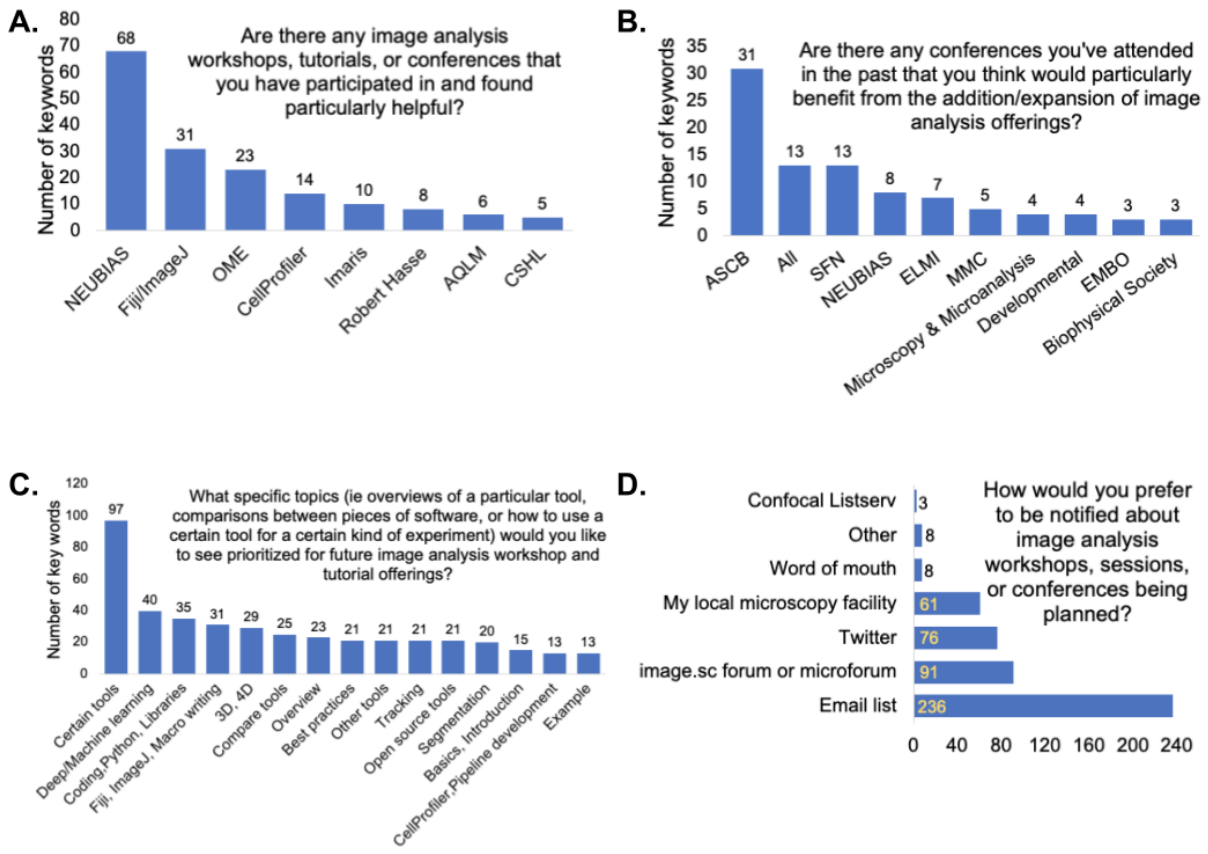
Components of well-received learning materials

We asked participants about their past experiences with workshops and conferences. Survey participants have mostly attended workshops, tutorials, and conferences on imaging and image analysis, and they specifically found NEUBIAS, Fiji/ImageJ, OME, CellProfiler, and Imaris workshops very helpful (Figure 9A). When asked what made those particular resources beneficial, respondents highlighted that those workshops provided image analysis basics and theory, step-by-step and hands-on approaches, real-time feedback, and access to experts while developing a workflow (data not shown).

When asked to name conferences that could benefit from the addition/expansion of image analysis offerings, the most common responses included the following: the American Society for Cell Biology (ASCB), Society for Neuroscience (SFN), Network of European BioImage Analysts (NEUBIAS), European Light Microscopy Initiative (ELMI), and the Microscience Microscopy

Congress (MMC) (Figure 9B). We also asked respondents which subjects they would like to see prioritized for the workshops and tutorials. Most - unsurprisingly - wanted materials for the particular tool with which they work, indicating a strong appetite for practical training, but general suggestions included machine and deep learning, coding, python, different libraries, ImageJ macro writing, overview of different tools, best practices, and different examples (Figure 9C). Finally, the community's preferred method of notification for the image analysis conferences and workshops are through email lists, forums (such as image.sc and the microforum (forum.microlist.org)), Twitter, and their local microscopy facility (Figure 9D).

Figure 9



A. Keyword analysis of the open-ended question of "Are there any image analysis workshops, tutorials, or conferences that you have participated in and found particularly helpful? If yes, what made them beneficial?".
B. Keyword analysis of the open-ended question of "Are there any conferences you've attended in the past that you think would particularly benefit from the addition/expansion of image analysis offerings?".
C. Keyword analysis of the open-ended question of "What specific topics (i.e. overviews of a particular tool, comparisons between pieces of software, or how to use a certain tool for a

certain kind of experiment) would you like to see prioritized for future image analysis workshop and tutorial offerings?".

D. Responses to the multiple choice question of "How would you prefer to be notified about image analysis workshops, sessions, or conferences being planned?"

In the final "Any other thoughts?" open answer response, the community asked for easy-to-follow (at your own pace) beginner's guides, better clarification of best practices, a centralized location to find available image analysis tools, various types of example workflows, interoperable platforms to create a workflow combining different tools, and better tools for hyperspectral image analysis.

Methods

The 2020 BioImage analysis questionnaire was developed using Google Forms and was distributed in the bioimage community around the world using the image.sc forum, microforum, twitter, as well as confocal, imagej, and BioImaging North America (BINA) listservs. Responses were exported via tables, and duplicates were removed; the results were then graphed in Jupyter Notebook (version 6.1.1)[11] using Python3 [12], matplotlib [13], numpy [14], pandas [15], and seaborn [16] libraries or Microsoft Excel (2016 and 2021).

To analyze the short and long answer survey questions, the answers to a specific question were parsed with a Python (3.7) script using PyCharm (2019.3) to find the number of words used in the answers, excluding some commonly used words such as: I, that, in, or, of, at. The outcome file was then checked, and depending on the question, the most used and meaningful words were chosen to create a tag list. The responses were parsed again using the tag list, searching for the number of keywords from the tag list. The final results showed the number of keywords (from the tag list) used in the answers. The corresponding figure was then created based on the counts and tags using Microsoft Excel. The tag names used in the figure were sometimes shortened to fit the figure.

Conclusion

Nearly 500 members of the imaging community from around the world participated in the BioImage Analysis survey, conducted in 2020 through the NIH Center for Open BioImage Analysis (COBA). The most common requests from the participants were for general improvement of tool documentation and for access to easy-to-follow tutorials. There is demand

for the community to focus on centralizing and publicizing existing educational resources, as well as improving tutorials for the imaging community. Our data on user preferences for particular formats and types of material should help COBA, as well as outside developers such as the BioImage informatics index from NEUBIAS [17], decide how to structure and prioritize their efforts.

The Scientific Community Image Forum (forum.image.sc), which is sponsored by COBA, partners with more than 50 open-source image analysis tools and scientific organizations devoted to biological imaging. It was designed to be a central “go-to” place for the community to ask questions and share updates, news, and ideas. While membership in the forum has grown from approximately 10,000 to 17,000 users in 2 years, fewer than 1/4th of users in our survey identified it as something they “generally” use to solve image analysis problems, indicating the forum can still have an even larger impact among the community; anecdotal responses from the survey, as well as our experience training users in image analysis, suggest some users find asking questions on the forum intimidating. Tool developers and other imaging experts all can play a role in creating an even more welcoming community. To ensure the forum lives up to its fullest potential, the community could consider a number of more systematic steps to reduce barriers to participation, such as expanding the existing templates for common questions to make it even easier for users to know which information developers most likely need to answer their questions. Suggestions for improving the forum are always welcome via the various communication routes for COBA: our Twitter address (@COBA_NIH), website (https://openbioimageanalysis.org/), and email address (COBA@broadinstitute.org).

The growth and increased stability of the bioimage analysis community in the last several years is both a triumph and a testament to the many hours that countless members of the community have contributed. With this survey data, COBA hopes to aid the entire community in celebrating its successes and in prioritizing its goals in both the short and longer terms. While individual tools and approaches will no doubt wax and wane in popularity over time, if we share common goals and plans for achieving them, our community will only continue to grow stronger in the years to come.

Human subject statement

This study was exempt from IRB approval based on Category 2 (Surveys, interviews, educational tests, and public observations). Full exemption was granted because we agreed to de-identify the data, so the subjects' identity could not be readily obtained.

Acknowledgements

We thank the biology and microscopy community for providing answers to the survey questions. We also thank Rebecca L. Ledford for her help in opening and publicizing the survey. We thank the members of the Eliceiri, Carpenter-Singh, and Cimini labs for their input on the questionnaire and assessment of needs in the bioimaging community.

Competing interests

The authors declare that there are no competing interests associated with the manuscript.

Author contributions

BAC and ETAD created the survey with editorial input from NJ, KWE and AEC. NJ performed analyses with help and supervision from BAC. The manuscript was written by NJ and BAC, with editorial contributions from ETAD, AEC and KWE. All authors have read and approved the manuscript.

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Data availability statement

The survey questions, responses to each individual question (sorted independently for each question to ensure deidentification), and all code used in creating the results are available at https://github.com/ciminilab/2021_Jamali_submitted.

References

1. Miura K. A Survey on Bioimage Analysis Needs, 2015. Zenodo [Internet]. 2021; Available from: https://scholar.archive.org/work/ait7eta4tnhjzecu5qsj7r623m/access/wayback/https://zenodo.org/record/4648077/files/Bioimage_Analysis_Survey_2015.pdf

2. About [Internet]. 2016 [cited 2021 Aug 4]. Available from: http://eubias.org/NEUBIAS/venue/

3. Schneider CA, Rasband WS, Eliceiri KW. NIH Image to ImageJ: 25 years of image analysis. Nat Methods. 2012 Jul;9(7):671–5.

4. Schindelin J, Rueden CT, Hiner MC, Eliceiri KW. The ImageJ ecosystem: An open platform for biomedical image analysis. Mol Reprod Dev. 2015 Jul;82(7-8):518–29.

5. Schindelin J, Arganda-Carreras I, Frise E, Kaynig V, Longair M, Pietzsch T, et al. Fiji: an open-source platform for biological-image analysis. Nat Methods. 2012 Jun 28;9(7):676–82.

6. Stirling DR, Swain-Bowden MJ, Lucas AM, Carpenter AE, Cimini BA, Goodman A. CellProfiler 4: Improvements in Speed, Utility and Usability [Internet]. bioRxiv. 2021 [cited 2021 Jul 14]. p. 2021.06.30.450416. Available from: https://www.biorxiv.org/content/10.1101/2021.06.30.450416.abstract

7. de Chaumont F, Dallongeville S, Chenouard N, Hervé N, Pop S, Provoost T, et al. Icy: an open bioimage informatics platform for extended reproducible research. Nat Methods. 2012 Jun 28;9(7):690–6.

8. van der Walt S, Schönberger JL, Nunez-Iglesias J, Boulogne F, Warner JD, Yager N, et al. scikit-image: image processing in Python. PeerJ. 2014 Jun 19;2:e453.

9. MATLAB [Internet]. [cited 2021 Jul 14]. Available from: https://www.mathworks.com/products/matlab.html

10. Rueden CT, Ackerman J, Arena ET, Eglinger J, Cimini BA, Goodman A, et al. Scientific Community Image Forum: A discussion forum for scientific image software. PLoS Biol. 2019 Jun;17(6):e3000340.

11. Kluyver T, Ragan-Kelley B, Pérez F, Granger B, Bussonnier M, Frederic J, et al. Jupyter Notebooks -- a publishing format for reproducible computational workflows. In: Loizides F, Schmidt B, editors. Positioning and Power in Academic Publishing: Players, Agents and Agendas. IOS Press; 2016. p. 87–90.

12. Van Rossum G, Drake FL Jr. Python reference manual. Centrum voor Wiskunde en Informatica Amsterdam; 1995.

13. Hunter JD. Matplotlib: A 2D Graphics Environment. Computing in Science Engineering. 2007 May;9(3):90–5.

14. Harris CR, Millman KJ, van der Walt SJ, Gommers R, Virtanen P, Cournapeau D, et al. Array programming with NumPy. Nature. 2020 Sep;585(7825):357–62.

15. Reback J, McKinney W, jbrockmendel, Van den Bossche J, Augspurger T, Cloud P, et al. pandas-dev/pandas: Pandas 1.0.3 [Internet]. 2020. Available from: https://zenodo.org/record/3715232

16. Waskom M. seaborn: statistical data visualization. J Open Source Softw. 2021 Apr 6;6(60):3021.

17. Martins GG, Cordelières FP, Colombelli J, D'Antuono R, Golani O, Guiet R, et al. Highlights from the 2016-2020 NEUBIAS training schools for Bioimage Analysts: a success story and key asset for analysts and life scientists. F1000Res. 2021 Apr 30;10:334.