Developing a set of guidelines for your research field: a practical approach

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ABSTRACT Since 2008, the autophagy community has periodically published a set of guidelines, currently titled “Guidelines for the Use and Interpretation of Assays for Monitoring Autophagy.” The newest version of the guidelines was published in 2016. There are many reasons for establishing a set of guidelines in a given research field. This Perspective explores some of these reasons, including standardizing nomenclature for better communication, improving reproducibility, and making it easier for newcomers to enter the field. It also includes the approach I have used to generate and update the guidelines that are now widely used in the autophagy field. The suggestions are not meant to be formulaic, and the method is certainly not perfect. Instead, this should be viewed as a starting set of, well, guidelines.

INTRODUCTION
The autophagy guidelines encompass a discussion of the currently accepted best methods for monitoring the different types of autophagy and include standards for data interpretation, as well as cautions concerning known methodological problems. The initial version of the guidelines (Klionsky et al., 2008) arose as a result of my observations at a conference at which it was clear that researchers newer to the field could benefit from having a resource that indicated best practices. Autophagy is connected to many aspects of human health and disease (Klionsky and Emr, 2000; Baxt and Xavier, 2015; Pierrefite-Carle et al., 2015; Rubinsztein et al., 2015; Saito and Sadoshima, 2015; Shibutani et al., 2015; Morishita and Mizushima, 2016) and has brought in a large number of researchers from a wide range of disciplines. These researchers might be experts in their own areas but not be familiar with the methods used in studying autophagy. Of course, they could look at various published papers and try to decide on an appropriate method, but I thought it would be useful to have the preferred methods available in one location, not as a set of protocols, but instead with suggested experimental approaches along with descriptions of how the experiments should be interpreted, also including caveats or cautions. As a simple example, assessing the appearance of green fluorescent protein (GFP)–microtubule associated protein 1 light chain 3 (LC3) puncta is a common method of monitoring macroautophagy; however, what are the criteria for determining whether a cell is positive for macroautophagy based on this marker? The consensus in the guidelines is that the number of puncta per cell should be counted, or at least the number of puncta used to classify a cell as being positive needs to be clearly stated in the Methods section.

Indeed, one critical aspect of the guidelines concerns an important issue—data reproducibility, a topic that has recently attracted considerable attention. Reproducibility is much more likely to be attained within a field if the researchers agree on the methodology and if they follow best practices based on a consensus of a majority of the people carrying out these experiments. Going back to the example of GFP-LC3, is one punctum enough to count a cell as “positive”? Probably not, but this needs to be explicitly stated. Furthermore, although LC3 is likely the most commonly used marker to monitor macroautophagy (primarily because this protein, unlike most of the autophagy-related proteins, remains associated with the completed autophagosome), it also participates in other processes, such as LC3-associated phagocytosis. Accordingly, most sections of the guidelines end with Cautionary Notes, followed by a brief conclusion. For example, in the section on Atg8/LC3 Detection and Quantification, one of the cautionary notes states, “LC3-I also associates with the membranes of nonautophagic structures.” Therefore the guidelines are meant to help researchers avoid potential pitfalls that could drastically alter the interpretation of their data. Of importance, we note in the guidelines, “these cautions are not meant to be a deterrent to undertaking any of these experiments or a hindrance to data interpretation.” In other words, we want to make it clear that the guidelines are only meant to guide, not to restrict. Along these lines, we also state, “by discussing the merits and limits of particular autophagy assays, we hope to encourage technical innovation in the field.”
Another key concept in the autophagy field concerns flux, which is worth a brief description. As I just noted, LC3 is the primary marker used to follow macroautophagy in mammalian cells. This protein is typically up-regulated after macroautophagy induction; hence an increase in the amount of LC3 might be interpreted as an indication that a particular treatment or stress condition has resulted in a higher level of macroautophagy. The problem is that a part of the LC3 population is also degraded in the lysosome during the final stages of macroautophagy. Thus we need to consider both increased synthesis and degradation (Figure 1). A mutation or treatment that blocks fusion of the autophagosome with the lysosome or degradation of LC3 within the lysosome will also result in an increase in the amount of LC3. Therefore it is critical to use a fusion or degradation inhibitor in conjunction with the analysis of the given mutation or pharmacological inhibitor to determine the true reason for the increase in LC3. The different interpretations could result in completely opposite conclusions about what happened and how to proceed. The seminal paper making this point was published in 2005 (Tanida et al., 2005); however, I routinely see papers submitted to Autophagy in which the authors did not adequately address this issue. Thus this fundamental point about autophagic flux is clearly emphasized in the guidelines.

In addition to providing a useful resource, the guidelines can also serve to set a standard for the field. For example, in the section on Autophagy Inhibitors and Inducers, the guidelines state, “The main concern with pharmacological manipulations is pleiotropic effects of the compound being used. Accordingly, genetic confirmation is preferred whenever possible.” Furthermore, the guidelines also note, “if using a knockdown [i.e., genetic] approach, at least 2 ATG genes should be targeted.” Knocking out or knocking down a single gene to examine the requirement of the corresponding protein for autophagy is insufficient because, as noted for LC3, some gene products are involved in other processes. Perhaps one might consider this obvious, but I can assure you that not everyone does. Why not make it clear that your research field demands a certain level of rigor for its published papers? Along these lines, another goal of the guidelines is to simplify the review of papers. Rather than having to elaborate on why a particular experiment was carried out incorrectly, a reviewer could briefly note the problem and then refer to the guidelines. Conversely, authors can, and do, use the guidelines to defend their experimental approach against inappropriate criticism by a reviewer who may not be as familiar with the field.

One caution is that there is a difference between standardization and stagnation. We try to emphasize repeatedly in the guidelines that “These guidelines are not meant to be a formulaic set of rules, because the appropriate assays depend in part on the question being asked and the system being used.” Similarly, “Throughout the guidelines we have noted that it is not possible to state explicit rules that can be applied to all experimental systems … they are not meant to constrain imaginative approaches to monitoring autophagy.”

One of my goals for the guidelines has been to build the autophagy community and maintain a level of collegiality. Having the best methods clearly spelled out makes the field more open to new researchers. In addition, the guidelines have directly fostered interactions among researchers located proximal to each other; simply noting the number of people working on autophagy in particular geographical areas has led to the formation of regional autophagy networks. Whereas the first set of guidelines focused on mammalian cells, the second version of the autophagy guidelines included yeast and other model organisms (Klionsky et al., 2012a), greatly expanding the text and the relevance to other researchers and resulting in a tremendous increase in the number of contributors. Along these lines, I need to emphasize that the guidelines themselves represent a community effort—there is no way I could generate these guidelines entirely on my own, and I rely on input from the many members of the autophagy community.

It is worth noting that the guidelines are not intended solely for the use of new investigators or investigators new to the field of autophagy. The current version of the guidelines has >2400 authors. That is an extremely large number of people who have looked over the guidelines (and in principle agreed to follow them) and provided input, new ideas, and new methods. It is impossible for one person or one lab to keep track of all of the updates and changes in this rapidly developing field, whereas >2400 people have a much better chance of doing so. Thus the guidelines represent a tremendous collective resource.

So, let’s assume that you are considering the need to generate a set of guidelines for your field. How do you go about it?

PREPARING A SET OF GUIDELINES

1. Getting community support for standardization

Perhaps the first issue to consider is how to initiate a community discussion of standardization and how to get the majority of researchers in a field to accept the resulting guidelines. One possibility is to start by discussing this issue at a meeting/conference at which many of the researchers in the field are in attendance (e.g., this could be a workshop session at an annual meeting or part of a business discussion at a conference). Is there a need for a set of guidelines, or is everyone in the field in complete agreement about the best methods to use and how the results should be interpreted (I am pretty certain about the answer)? Furthermore, will the community respond to this question in a positive manner? Considering the autophagy field, one of the first community efforts was to standardize the nomenclature for what are now called autophagy-related (ATG) genes (Klionsky et al., 2003). Before this effort was undertaken, at least 10 different names were being used to identify genes/proteins that played a role in autophagy in different fungi, let alone in more complex eukaryotes. Thus it was becoming quite confusing to know which gene or protein was actually being referred to—for example, APG1, AUT3, CVT10, GSA10, PAZ1, and PDD7 are all now combined as ATG1. The issue was discussed at a conference at which most of the labs working on autophagy in fungi were
represented, and a consensus was quickly reached that it would be worthwhile to adopt a uniform nomenclature; the nomenclature established for fungi was subsequently accepted for most model organisms. Perhaps as important, I think that this effort helped establish the autophagy community. Along these lines, I suggest that it is best to be as inclusive as possible when considering who should be considered to be part of the community—this will help to ensure more effective and widespread acceptance of the guidelines.

If there is an agreement that a set of guidelines would be beneficial, the next issue becomes deciding who will be in charge of writing it. I think that a small group should be appointed to draft the first set of guidelines. Ultimately, someone must sit down and write the first version, and it is easier to get a group of people to revise a draft than it is to get them to write one. That is, revision by committee is preferable to writing by committee. Thus I recommend that one person, or at the most two or three people, write the initial version.

2. Write the guidelines

A. Create a draft version. This is perhaps the most difficult part of the process, and there are different aspects to consider before getting started, as follows:

i. Scope. As noted in the Introduction, the autophagy guidelines have increased in scope with each iteration, with the first version focusing on mammalian cells. It is important to realize that you do not need to worry about including every topic in the initial version of the guidelines; the article can expand and evolve over time. Limiting the scope for the first draft will obviously make it easier to write.

ii. Conflicts and corrections. Similar to scope, I think it is reasonable to conclude that the authors of the draft should not worry about getting every single statement to be perfect; input from all of the authors will improve the quality. In the case of conflicting opinions, the guidelines can reflect current controversies or divergent points of view while still pointing out the best ways to interpret the results, along with known caveats. In the case of the autophagy guidelines, input from literally thousands of authors has, one hopes, reduced erroneous information. Moreover, errors that have been introduced or become apparent as the field advances can be eliminated in the next version.

iii. Terminology. As with the unification of the ATG gene names, I think it is useful to adopt an accepted terminology for the field. There are nomenclature committees in place for most model organisms, and these can be relied on as the basis for standardized gene/protein names (Klionsky et al., 2012b).

iv. How and where are the guidelines to be published? There may not be a single best answer to this question. One general consideration is whether they should be published as an article or exist only as an online resource. Although the guidelines are meant to be flexible and evolving, I think it is good to have standards that are clearly in place from one day to the next. Thus I prefer a published article that sets the standards for a given period of time, with the expectation that they will be reviewed and revised periodically.

Having established answers for these initial considerations, there is no getting around the fact that the first draft has to be written. In addition, I think that one person needs to have the ultimate responsibility to keep the manuscript moving forward and make the final decisions on what to add and what to remove (in my experience, it is difficult to complete a large undertaking of this nature if every decision needs committee approval, but I strongly advise seeking a consensus). For the first version of the autophagy guidelines, I wrote an initial draft and then sent it to a small group, mostly the associate editors of the journal Autophagy and/or people I considered likely to respond, for comment. Even at this stage, it is a good idea to establish some parameters for the responses you are soliciting.

B. Solicit responses.

i. Set a deadline for the response. The reason is obvious, but as you get toward the end and the completion is in sight, potential contributors need to know that there is an end date for being included as an author and/or for having suggested changes included in the text.

ii. Spell out precisely the information you need with regard to name, affiliation, and approval for someone to be listed as an author. You cannot be too specific about this if you want to save time in the long run (Supplemental Figure S1). For example, it is not unreasonable to state, “Provide your name as you want it listed in the paper. Write this information in the following order: first name, middle name or initial, and then your family name/surname. Use capital letters only for the first letter.” Otherwise, you may get responses such as “KENT, CLARK” or even “CLARK KENT” and not know which name is the last name, let alone that someone will have to change this to only first letters being capitalized. Furthermore, in some countries, it is standard to write the surname first, without being followed by a comma, which can make it quite confusing for placement in the author list. Be very specific in your instructions, such as indicating that you want the full first and last names, not just initials. Similarly, spell out precisely what you need for the affiliation. For example, including the city is requested, whereas the street name is not. With regard to the article text, I suggest a clear indication along the lines of, “Responses that suggest ‘It would be nice to add something about…’ that do not include the suggested text, or ‘It would be good to have a reference for this…’ without providing the actual reference, will generally be ignored” (you do not have time to find references or write text that may fit with what someone else has in mind). The contributor must write what they want included at the appropriate location. If they have a reference to include, they should indicate it. A test letter to a small group is probably a good idea, so you can find out what you overlooked, before sending the invitation out to hundreds of people.

iii. Indicate in the letter that the modified text must be noted clearly, for example, with a different color font or highlight. In addition, the contributor must indicate separately (e.g., in their email) which page(s) has been modified so you do not have to search through the entire manuscript, which takes time and might lead to a change being overlooked. Finding changes also becomes problematic because the version of the guidelines you are currently working on may be substantially different from the revised one you receive from an author months after it was first sent out. You can suggest that the contributor return only the relevant page(s) rather than the entire manuscript. In addition, specify that the returned text be given a specific title, such as “Guidelines XY,” where “XY” correspond to the name, or first initial and last name, and so on, of the contributor. Having hundreds of documents with only the name “Guidelines” in your download folder can be problematic if you ever want to distinguish among them.

iv. Point out that the goal is not for people to promote their own work per se (an exception to this is the glossary; see paragraph 2E). Thus it might become necessary to edit out information that might even be interesting (e.g., describing the progress of one lab) but does not meet the specific goals of the guidelines (i.e., this is not a review article). You need to be cautious when...
incorporating the new text; changes can be made, and text eliminated, later, but before insertion, it is prudent to consider whether the added text enhances the guidelines.

v. Note that if figures are included, the contributors need to indicate that they have permission to reprint them (if appropriate) and provide the relevant citation information. Specify the application format that you want used for figure preparation, and I suggest that you also indicate the font you want used for the labels in the figure.

C. Modify the text. I next started to expand the number of contributors by sending out additional email invitations to a large group of scientists from an EndNote-generated list (see paragraph 3E). I think it is best to go slowly at this stage. First, you do not want to have too many people working on different versions of the text simultaneously, which can make it difficult to reconcile all of the different changes. Second, revisions of the text should become less frequent with increasing input. At some point you can invite hundreds of people at a time and expect relatively few changes. Third, there are practical concerns with sending out emails, especially ones with attachments, to hundreds of people:

i. Some email servers set a limit on how many emails you can send (and they will not tell you what those limits are), supposedly to cut down on spam mail.

ii. I suggest putting the current version of the manuscript in Dropbox or some similar location and generating a shared URL link (you can use a URL shortener such as the one available from Google [https://goo.gl] to reduce its length). This will allow you to share the file without having to send it as an attachment (which can count against your mailbox size limit if each sent mail is saved automatically). Note, that in some countries, in particular China, the authors may have problems accessing the file through this link.

iii. You may be able to set up a group email list, which counts as a single email.

D. Obtain additional input. See 3. Identify additional authors. I note here the possibility of using a wiki approach or Google Docs or something similar for modifying the text of the manuscript. I have not tried this because I have been concerned about the difficulty of handling the potentially overwhelming number of responses and counterresponses; if you have >2400 authors, this could become unmanageable. Perhaps for the development of the initial draft, a shared document would be a consideration.

E. Send the revised draft back to all of the authors. Ask them to verify the spelling of their names and their affiliations in addition to checking all of the text or at least that part that is relevant to their area of expertise.

F. The third version of the autophagy guidelines (Klionsky et al., 2016) incorporates the glossary that had previously been a separate article. The glossary is literally an alphabetical listing of terms that are relevant to the field of autophagy. Thus it includes in particular additional topics, correction of minor errors, and the inclusion of unpublished observations that may save researchers considerable time.

An obvious question is whether you need or want a glossary. I found it useful to generate a glossary for the autophagy field (Klionsky, 2010; Klionsky et al., 2010, 2011); there are a large number of proteins being analyzed, regulatory factors, pathway names, and drug and chemical treatments, which can be difficult to keep straight without a quick reference guide.

3. Identify additional authors

After having written the first draft and received feedback after one or more rounds of soliciting comments, I start to expand the number of contributors to the main text and glossary. This allows coverage of additional topics, correction of minor errors, and the inclusion of unpublished observations that may save researchers considerable time.

A. I rely extensively on identifying researchers who have published a paper(s) in the field. To find them, I search through EndNote (other reference management systems can probably be used, but I will refer to EndNote throughout).

B. Word search. I use the standard search function and use “autophagy” with “All Fields” as the parameter. Obviously, the search can be modified or limited by restricting the search parameter to “Title,” “Abstract,” or “Keywords” or by changing the search word to “autophag*,” which would also capture “autophagic” and “autophagosome.”

C. Year. For the previous guidelines, I generally searched over a 4-year range, searching by each year individually. That is, my search included “All Fields” using “autophagy” and “Year” with the appropriate four-digit year. For autophagy, this now yields ~3000–4000 hits per year. It is tempting to create separate files for each year to keep the number of papers in a more manageable range (after doing this a few times, 4000 begins to seem quite manageable). However, I recommend merging the files (by copy and paste) to generate one large EndNote file, which makes subsequent reductions easier (see the next paragraph).

D. Reduce the number of reference files.

i. I suggest first making a backup copy of the EndNote library. The easiest way to start reducing the number of references you need to handle in your working copy of the library is to “Find Duplicates” under the “References” menu. In some cases, the same publication will appear in more than one year (e.g., year accepted and year published). You can easily eliminate these duplicates within one EndNote library, but not between libraries.

ii. I next eliminate “Commentary” and “Review.” This can be done with the “Any Field” category (equivalent to “All Fields,” which is the name of the option when you search PubMed through EndNote). Of course, you may decide to keep papers that fall within these categories.

iii. Search for duplicate authors. I typically do this before I start to search through the EndNote references and also during the entire
search process. For example, I will search for authors who I know to be relatively prolific and eliminate the multiple entries for these authors with the caveat that I check each reference to verify the corresponding author (not always the last person listed, and sometimes there is more than one) and to ensure that the email address is the same as the one I am using for the invitation (if there are different email addresses, I add them to the invitation list, but typically use a secondary one only if necessary; see paragraph 3F).

iv. Once I have invited an author (see paragraph 3E), I search for other papers by the same person. This is one place where it is helpful to have a single combined library. I recommend using the “Notes” category for searching. If you search by “Author,” you can use only the last name and initials, whereas “Notes” allows you to use first and last names.

E. Scan the paper. Starting with the most recent year (because locations/affiliations, and hence email addresses, change, and the most recent is usually correct), I individually search each entry. That is, I use the URL link in EndNote and open the paper. I then run a quick search of the full HTML or PDF version for “autophagy,” “Atg8,” or “LC3.” This allows me to eliminate papers that use the term “autophagy” once in the Introduction or Discussion but are otherwise not focused on the topic. Obviously, this is time consuming; however, I also find it to be very beneficial. First, I learn a lot just skimming through the paper (and since essentially all of these papers are in my field, I consider it worthwhile). Second, I find new topics and words that I want to add to the main text or to the glossary. For each paper that passes this simple criterion, I send out an email invitation to the corresponding author(s). A sample letter is provided in Supplemental Figure S1 as a guide.

F. Keep records. It is important to keep careful track of all invitations. I do this with an Excel spreadsheet, where I note last name, first name, and email address. When people respond, I highlight the last name and add their affiliation. Some email messages bounce back, and then I try a second email address if it is available. Otherwise, I note that the message was not delivered in case I subsequently discover a new email address.

G. Additional authors. My goal is to be inclusive. This helps build the community and also helps meet the goal of achieving participation by the majority of the researchers in the field. There is really no point here in trying to be exclusive.

i. Reviewers. In the most recent version of the guidelines, I invited people who reviewed papers for the journal Autophagy even if they had not authored a paper in the field over the time period of my search. I reasoned that if these people are reviewing papers, I certainly want them to be familiar with, and participate in the preparation of, these guidelines.

ii. As part of my invitation letter, I inform the invitee that he or she is welcome to extend the invitation to people in the lab and colleagues in other labs who work in the field of autophagy. It is at least as important for the undergraduates, graduate students, postdocs, and technicians who are at the bench to be familiar with these guidelines as it is for the principal investigators. I suggest that you make it clear, however, that you need a direct email indicating approval to be listed as an author from each person. That is, it is fine to “nominate” someone to be an author, but you do not want to take additional time sending out invitations (or searching for email addresses), and you must have an official approval from each author. Thus the original invitee needs to forward the invitation to any other people they consider appropriate.

iii. In addition, for the most recent version, I posted an invitation as an Editor’s Corner (the frontispiece) in Autophagy (Klionsky, 2014). As indicated, one goal is to be inclusive. In addition, there is the practical aspect that some people might be accidentally overlooked when you are dealing with hundreds or even thousands of authors. By posting an invitation and asking invitees to send invitations to colleagues, you minimize the number of people who are missed. Not incidentally, you also diffuse the responsibility for having made this type of regrettable mistake.

4. Subjective evaluation

Have the autophagy guidelines been useful, and have they achieved their goals? First, I suggest that even getting the majority of the researchers in a field to read through the guidelines is an accomplishment, as it familiarizes them with the current views on best methods. Second, many authors have commented to me that they used the guidelines as they entered the field, during the review of manuscripts, and in grant applications. To further answer this question, I provide some unsolicited quotes from researchers who agreed to be authors on the newest update of the guidelines:

Starting out in the field

• “We as newcomers to the field of autophagy made a great use of the presented information.”

• “The 2012 guidelines were a huge help to us in getting started in this area and we have referred back to them many times as the ‘go-to source.’”

• “This is the first information I send my colleagues when they are inquiring about autophagy.”

Inclusivity and community

• “I truly appreciate this effort as well as your aim to allow the majority of researchers in the autophagy field to contribute and bring forth their views and comments in order to reach the best possible consensus.”

• “In the spirit of inclusiveness, since you’ve generously set that tone, my colleagues … are on the editorial boards of other journals where they can help to enforce these new guidelines … I’ll communicate this latest draft to them.”

• “The current version of the Autophagy Guidelines was the starting point to create the Spanish autophagy network.”

Format, revisions, and updating

• “Especially the part on the databases is critical nowadays.”

• “I think the inclusion of the glossary is a major improvement.”

• “I think it is a great idea to prepare an updated version of the guidelines, given the rapid development of the field and the increasing number of labs and people using assays for monitoring autophagy in different experimental setups, models and physiological and pathological conditions.”

Applications and impact

• “I agree to follow these established guidelines in my own work, and when reviewing manuscripts, whenever possible.”

• “Over the last few years the guidelines have become an indispensable reference for anybody working in autophagy and they have performed an incredibly valuable role in standardizing the
conditions of the different experimental approaches that need to be followed to rigorously study autophagy.”

- “Even experts in the field will benefit from this ‘group’ think.”

Applicable to other fields?

- “I wish other research fields were as well organized with their methods as the autophagy field.”
- “Many fields can benefit from a similar effort that improves the quality and reproducibility of data.”
- “These guidelines are a great tool for those in the field either new or not. I wish more of this type of guidelines were published for many other research topics!”

5. Handling the page proofs

The size of the autophagy guidelines coupled with the fact that the paper had been “reviewed” by >2400 authors led the journal office to bypass the galley proof stage and send page proofs to me for correction. In addition to proofreading everything myself, I wanted to give all of the authors a final opportunity to make changes, in particular to check the spelling of their names and ensure that affiliations were correct. Accordingly, I sent out an invitation letter (Supplemental Figure S2), and it is worth noting some particular points in this regard:

A. I generated a group email list using the Excel spreadsheet of all authors and sent the page proofs as a PDF file along with an explicit set of instructions.

B. I requested that all changes be marked directly in the PDF file, which makes it much easier to locate them (all changes ultimately need to be transferred into a single PDF file).

C. I specifically asked authors to check names and affiliations and noted that although they were welcome to check the remainder of the text, major changes (including adding new references) were not possible at this time.

D. I noted that there was a one-week deadline for comments.

E. I requested that authors not write back if they were not making changes.

CONCLUSIONS

In the Introduction, I mentioned the value of the guidelines with regard to data reproducibility. Along those lines, I want to briefly point out two related considerations. First, the current update of the guidelines uses the standard nomenclature for genes and proteins. Rather than describe the rationale behind this, I refer readers to an article that presents the justification for adhering to a set of nomenclature guidelines (Klionsky et al., 2012b). With regard to data reproducibility, one aspect that would help is ensuring that researchers are referring to the same gene or protein when they use a particular name. Section II includes a catalogue number, but now has an entirely different manufacturer and/or reagent. I do not think there was any intent to mislead the reader. Instead, when forced to check the catalogue number, the researcher realized that the lab was not using the reagent they assumed was being used (or perhaps had been used in the past).

Finally, as I noted earlier, remember that the final product does not have to be perfect—the guidelines can, and should, be updated periodically. Along these lines, as noted, it is not necessary to have a consensus on a single method that is best to monitor a particular aspect of the process you are studying; the guidelines can accommodate conflicting views, perhaps reaching a consensus in a later version, while in the meantime noting the advantages and disadvantages of the respective methods. Remember that the guidelines are meant to be dynamic, reflecting a field of active research, which means that there will frequently be new findings, new methodologies, and new thoughts on data interpretation. Thus the guidelines need to evolve along with the field.

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