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Tutorial How to present scientific work

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How to present scientific work

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I Goals of a scientific presentation

The purpose of a scientific presentation is to report results of your research in a way that is understandable for your audience. In this module, you are going to present a scientific article, which contains the research for somebody else, but presenting the results of a paper or non-published data is a similar process.

You have to address a biological question, and show how you have tried to answer it. The presentation has to remain simple so it is understandable by everyone. It has to be to the point, and do not divert from main objective.

The most important element of a presentation is that **people clearly understand the question you are addressing**. With that in mind, they will be more motivated to follow you because they will try to know how you proceeded to answer your question.

II Reading and analyzing a paper

II. 1. Find the main question of the article

In order to present research, you need to know what you are going to talk about and most importantly you need to know what is the question you are addressing. A scientific paper, even if sometimes looks a bit complicated, usually revolves around one, maybe two main questions or findings. To build your presentation, you need to know what is the main finding (or the two-three main ones) you are going to present. In most cases, the title of the paper tells what is the main finding.

Example.

Read the following title and abstract of a recent article (can also be found free to download at http://www.pnas.org/content/113/35/9716.full.pdf) [1]:

Superresolution intrinsic fluorescence imaging of chromatin utilizing native, unmodified nucleic acids for contrast Dong et al. 2016 PNAS.

Visualizing the nanoscale intracellular structures formed by nucleic acids, such as chromatin, in nonperturbed, structurally and dynamically complex cellular systems, will help expand our understanding of biological processes and open the next frontier for biological discovery. Traditional superresolution techniques to visualize subdiffractional macromolecular structures formed by nucleic acids require exogenous labels that may perturb cell function and change the very molecular processes they intend to study, especially at the extremely high label densities required for superresolution. However, despite tremendous interest and demonstrated need, label-free optical superresolution imaging of nucleotide topology under native non-perturbing conditions has never been possible. Here we investigate a photoswitching process of native nucleotides and present the demonstration of subdiffraction-resolution imaging of cellular structures using intrinsic contrast from unmodified DNA based on the principle of single-molecule photon localization microscopy (PLM). Using DNA-PLM, we achieved nanoscopic imaging of interphase nuclei and mitotic chromosomes, allowing a quantitative analysis of the DNA occupancy level and a subdiffractional analysis of the chromosomal organization. This study may pave a new way for label-free superresolution nanoscopic imaging of macromolecular structures with nucleotide topologies and could contribute to the development of new DNA-based contrast agents for superresolution imaging.

Q. What is the main finding here?

A. The main finding can be found in the sentence starting with "Here, we investigate a photoswitching process of native nucleotides (...)". What the sentence says is that the authors have used an intrinsic property of fluorescence of DNA in order to do perform microscopy images (in so-called "super-resolution").

Q. How did the authors obtain this finding?

A. The answer is rather specialized: they have used a method called "single-molecule photon localization microscopy (PLM)." More details will have to be found inside of the paper.

II.2. Find the arguments that answer this question

Once you understand what is at stake in the article you are reading, you can start reading the methods and the results parts. Usually, the main result, the one which is the most powerful to answer the question addressed, is present in figure 1 or 2. This result is worth putting emphasis on and spend enough time. In many papers, especially in genomics, the following figures are complementary information about the first figure and validate the main results or bring more arguments to it. As a result, first result is usually useful to emphasize, followed by more secondary figures. Usually, the main arguments to answer the questions are contained in the different figures, with one figure corresponding to a section of the results.

Example.

Check the abstract and caption of figures of reference [2] at http://emboj.embopress.org/content/early/2016/02/02/embj.201592862

Q. What is the main finding of the paper? What experiments were done to prove this ? A. The main result is that mitochondria are involved in aging (and also that removing mitochondria prevents cell from aging). To achieve this, the authors have damaged cells with X-ray, as a proxy for aging (figure 1) and see how mitochondria are involved in the process of aging (figure 1 and 2). Genomics was used to prove it (figure 2). Moreover, they show that an important protein involved in aging (and cancer), mTOR, is related to mitochondria metabolism (figure 4).

III Qualities of a good presentation

III.1. Be clear about the goal

The most important quality of a scientific presentation is to clearly state what is the biological question (identified during the reading of the article), and how this question was addressed. You need to clear state in one of your slide, usually at the end of the introduction slides, what is the main finding of the paper.

III. 2. Show how this question has been answered

The rest of the presentation is to develop the main idea and show how it was proven with experiments and/or analysis. For this, the best is to separate the different results into different slides, each time with a title stating was is the result. For instance, one slide in case of example in II.2 could have for title: "mTOR recruits mitochondria in aging process". This is not the only way to proceed, but at least this guarantees to have a certain flow in the presentation.

III. 3. Target the audience

Very importantly, one needs to think about who one is speaking to. Overall, you should think whether your audience is a specialist in your field or not. It is usually not the case, so you should present the results for a broad audience, with an introduction of several slides that explain the context of the study. It is also a good opportunity for you to research the subject.

III. 4. Make relevant slides

Usually all slides come with a title on the top and a visual below it. A powerful way to design slides is to always put a strong statement, or a result in the title, such as "gene X does Y", which is always better than the rather vague title "gene X". Asking a question is also powerful, because then your job is to answer the question.

Don't crowd your slides with material. Less is better. Usually you can put one graph, maybe more if they need to be compared. If something stands alone, generally speaking put it on a separate slide. Too much text is not good usually, but at times it can be fine. For instance, if you have to introduce definitions, you can have more text that you read. Less fun than pictures, but fine in the context of a lecture. Keep things visual for a scientific presentation.

Example of a good slide:



As you can see, the design is simple, everything is clear. The title clearly states a question (mTOR recruits mitochondria) while the content of the slide answers the question in one simple graphic which easy to comment.

IV Presentation outline

IV.1. Main questions

Half of the presentation should be about introducing the topic and the main question, and presenting the main result. Rest of the presentation will be focused on more detailed results. Introduction is important because your audience is usually not familiar with the topic, and even if they are, everybody likes to get a bit of context and have a refresh on certain notions. People are not working on your question directly and even if they know a lot about what you do, they will appreciate 5 minutes to get into it again. The brain functions this way is that it needs to immerse itself in a topic for a while before really starting to understand what things are about. So staying longer on the introduction is always better than barely introducing the topic.

In the context of the presentation you have to build, giving a bit of information in the introduction about the topic means that you need to do a bit of research about the topic and illustrate what is said in the introduction of the paper. Usually, figures are only for results so you will have to build your own visuals. At times, there is a diagram of the method in figure 1 that you can take. But overall, you need to do some research to know best what to put in the introduction. Usually, try to talk about things which are useful to understand the question in the paper, but don't divert. Be focus on the main question. For instance, if you had to present the paper on the human genome project, in the introduction you will present the historical context of the project, the partners involved, and probably the methods that were used to do the research. Once the topic is introduced, you need to formulate the main question. For instance, the main question could be: is gene X involved in process Y?

- IV.2. Possible outline for a presentation of 20 minutes (adjust to a factor X depending on the time of your speech).
 - 5 minutes: introduction + what is the question
 - 5 minutes: main question + main result
 - 10 minutes: more detailed results incl. a summary slide.

Please find an example of a good presentation with harmonious simple slides at the following URL: http://www.biosurvey.ou.edu/swan/PowerPointGuidelines.pdf

Example.

Please find the slides for a presentation given during a journal club to present a scientific article in Appendix.

Q. What is the main question of the presentation? What are the main results? What qualities do you find in the presentation? What is missing?

A. Positive aspects: slides remain simple (despite some with several graphs), titles are sharp, a nice concluding slides sums up the different findings and brings something new to the table. Negative aspects are that there is not much of introduction and the main question is not very clear. But remember also that you need to target your audience. In the context of a meeting within the lab, intro can be less prominent as people may know a lot about the topic.

V The speech

V.1. Golden rule

Slower is better than faster. If you are stressed, try speaking slower. You may loose a bit of your audience if you talk slower, but very fast paces stress everybody and understanding comes difficult, even for people interested in what you say.

V.2. General attitude

Be friendly to audience, talk in their direction. Try to be positive (not always easy).

Always give time to people to discover a slide. Start by the title. The title should tell what the slide is about. If you first start by rephrasing the title, your speech for this slide will be more focused. For instance, if the title is "Gene X is involved in the function of Y", start by saying something like "Next we showed that gene X is involved in the function of Y". Once that sentence is pronounced, you will easily be able to comment anything that is on the slide.

Take time to describe the graphs. Do not only tell what the result is, but help the audience by showing them how your graph works. For instance, if there is a 2D plot with one variable plotted against another, take time to explain these variables. Almost all speakers rush through the slides and do not dare explaining the way the graphs work. This is not usually a good strategy, because if someone does not understand the graph at the beginning, and you use lots of those, the person will never catch up during the presentation. So insist on explaining how your method works, and once it is clear to everyone, move on to the next figures.

Example.

Please have a look about the graphics below [3].



Figure 1. Total open genome (accessibility) before and after UV treatment, in various regions of the genome: promoter, exon, intron and intergenic.

Q. Have would you present this figure ?

A. You need to explain both axis and the different categories each time: "For each regions of the genome, either promoter, exon, intron or intergenic in x-axis, the value of total open genome is given in y-axis, before and after treatment with UV", or something approaching. If the result is complex, involving several variables, take time to explain all the variables and how they combine in the diagram/graph.

VI Tools for presentation building

LibreOffice.

Free of rights, LibreOffice in itself does not suffer problems, it is impossible to expect 100% compatibility if you run your presentation built with LibreOffice on a machine with Microsoft Office. Some shapes or text boxes might not always be positioned the way you initially planned. As a result, always save as pdf to avoid such compatibility versions.

Microscoft Powerpoint 365.

We recommend version 365 because it comprises some new ameliorations which are extremely useful, such as automatic alignments. The levels of zoom are also much better handled than previous versions and certain behaviors of the software that were a bit annoying at times in earlier versions have been corrected.

Adobe Acrobat reader DC.

Needed to open presentations you will save as pdf. Pdf is a convenient program readable on almost all machines.

Shutter (or other screenshot tools)

Shutter is a very easy to use tool to make captures of part of your screen. By doing copy/paste, you can rapidly insert whatever is visible in your screen inside of your presentation. Downloading available at http://shutter-project.org/

References

[1] Dong B et al. Superresolution intrinsic fluorescence imaging of chromatin utilizing native, unmodified nucleic acids for contrast. Proc Natl Acad Sci U S A. 2016 Aug 30;113(35):9716-21.

[2] Correia-Melo C et al. Mitochondria are required for pro-ageing features of the senescent phenotype. EMBO J. 2016 Apr 1;35(7):724-42.

[3] Schick et al. 2015. Journal of Cell Science.

Appendix

Example of scientific presentation of an article given in the context of a journal club.

Journal club 17/09/2014 Nature biotechnology papers on RNA-seq quality control

David Fournier

Several sources of variation contribute to differences in analysis of RNA-seq data



A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium

SEQC/MAQC-III Consortium*

Variations between sequencing platforms And detection of splice variants

We present primary results from the Sequencing Quality Control (SEQC) project, coordinated by the US Food and Drug Administration. Examining Illumina HiSeq, Life Technologies SOLiD and Roche 454 platforms at multiple laboratory sites using

Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study Variation between sequencing platforms and library preparation

Sheng Li^{1,2,24}, Scott W Tighe^{3,24}, Charles M Nicolet⁴, Deborah Grove⁵, Shawn Levy⁶, William Farmerie⁷, Agnes Viale⁸, Chris Wright⁹, Peter A Schweitzer¹⁰, Yuan Gao¹¹, Dewey Kim¹¹, Joe Boland¹², Belynda Hicks¹², Ryan Kim^{13,23}, Sagar Chhangawala^{1,2}, Nadereh Jafari¹⁴, Nalini Raghavachari¹⁵, Jorge Gandara^{1,2}, Natàlia Garcia-Reyero¹⁶, Cynthia Hendrickson⁶, David Roberson¹², Jeffrey Rosenfeld¹⁷, Todd Smith¹⁸, Jason G Underwood¹⁹, May Wang²⁰, Paul Zumbo^{1,2}, Don A Baldwin²¹, George S Grills¹⁰ & Christopher E Mason^{1,2,22}

Detecting and correcting systematic variation in large-scale RNA sequencing data Variations due to measurement errors

Sheng Li^{1,2,11}, Paweł P Łabaj^{3,11}, Paul Zumbo^{1,2,11}, Peter Sykacek³, Wei Shi⁴, Leming Shi⁵, John Phan⁶, Po-Yen Wu⁶, May Wang⁶, Charles Wang⁷, Danielle Thierry-Mieg⁸, Jean Thierry-Mieg⁸, David P Kreil^{3,9} & Christopher E Mason^{1,2,10}

A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium

SEQC/MAQC-III Consortium*

We present primary results from the Sequencing Quality Control (SEQC) project, coordinated by the US Food and Drug Administration. Examining Illumina HiSeq, Life Technologies SOLiD and Roche 454 platforms at multiple laboratory sites using

> SEQC: Sequencing quality control consortium Funded by the food and drug administration (FDA)

Protocol



Gene and splice variants detection varies with gene annotations used but not with site of measurement



Site, pipeline choice and filtering method influence the quality of analysis



Dilutions of RNA in titration experiments show Mostly expected fold changes in gene expression With some variation between sites and platform



Relative gene expression measurements agree across platforms



Consistency score varies with platform, site and pipeline used



Variation coming from different methods to prepare libraries

Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study

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ABRF: Association of biomolecular resource facilities

Transcript coverage show mostly variation between protocols to extract RNA



Variation coming from measurement errors

Detecting and correcting systematic variation in large-scale RNA sequencing data

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ABRF: Association of biomolecular resource facilities

A high percentage of genes are differentially expressed when comparing two different sites



A majority of differentially expressed genes is reproducible across sites





Comparison

Heterogeneity across sites can be explained by several bias



Conclusions

Variable assessed by QC	Observations/problems	Possible solutions for problems
Platform to acquire expression data	RNA-seq > microarray, especially for low expression levels Outputs of the different sequencing platforms show similar patterns of differential expression genes	
Platform to acquire expression data	Splice variant detection varies across platform Consistency of samples (titration) not always good	Increase read length, choose proper annotation, decrease error rate Consistency: pay the vendor to do the job
Measurement (differences between operators)	High variability	Better ways to prepare libraries, perform spike-in controls, automation of tasks, increase read length
Library preparation	Differences in nucleotide composition between methods	Improve standardization of procedures

References

- Diagram on sources of variation: Kratz& Carninci, Nat Biotech 2014
- All papers mentioned are from the current issue of Nature biotechnology