

# Hosting Virtual Events

**Arne Bakker**

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Health Research Alliance Spring Members Meeting  
March 22, 2021



# Scientific meetings at CZI

At CZI, we want to build and support collaborative scientific communities

Our goal is to increase collaboration and dissemination of knowledge within and between scientific communities, and between those communities and CZI

We do this through the planning and execution of meetings, workshops and hackathons, and through the support of collaboration tools.



Arne Bakker



Andréa Clavijo



Vivian Chung

# Programs



Imaging



Neurodegeneration Challenge Network



Open Science

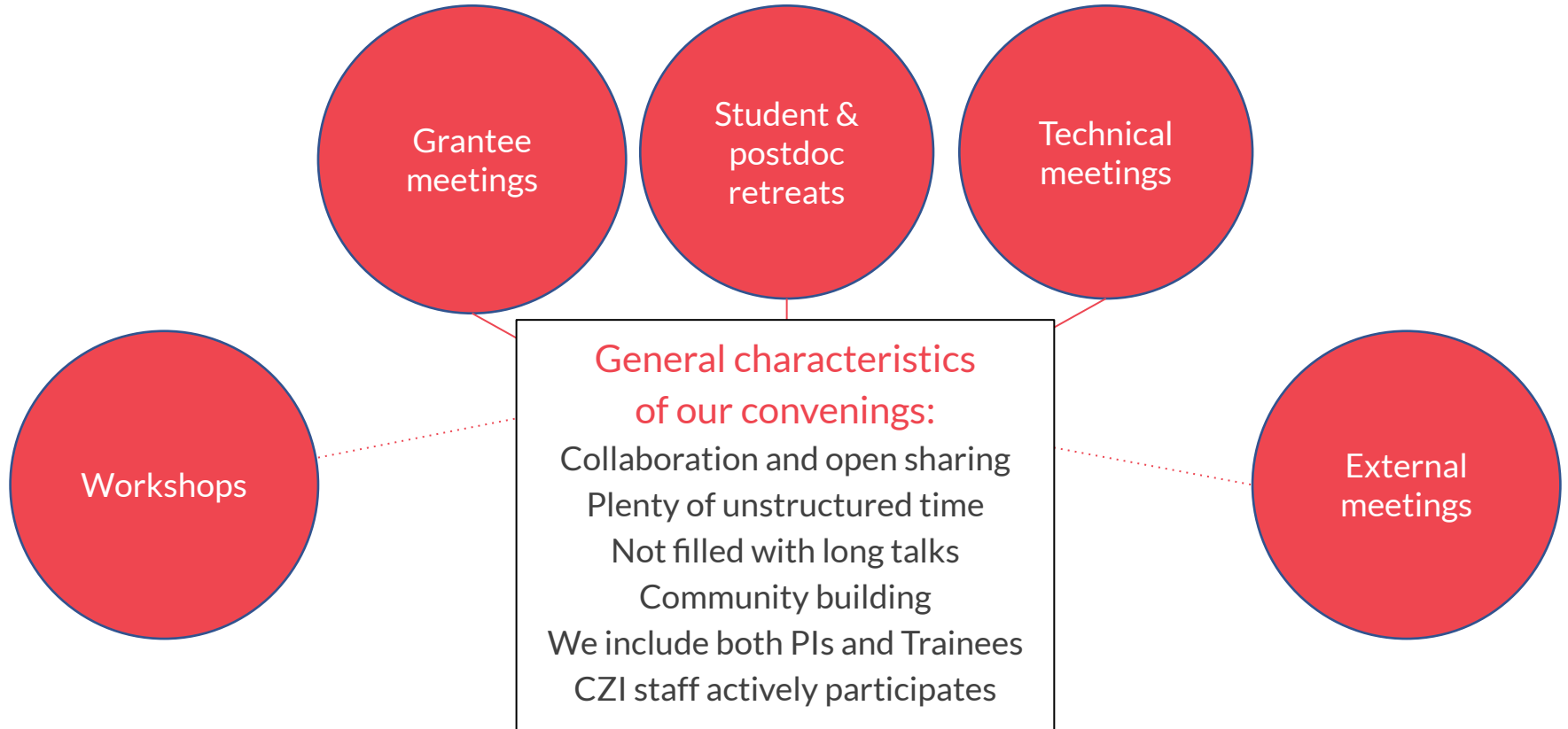


Single Cell Biology



Science in Society

# Scientific meetings at CZI

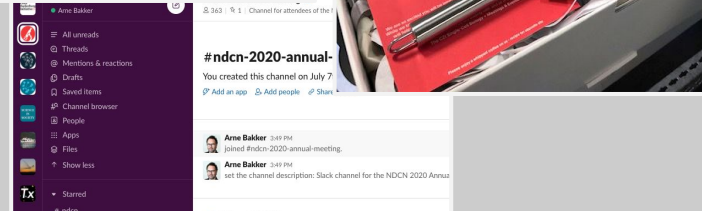
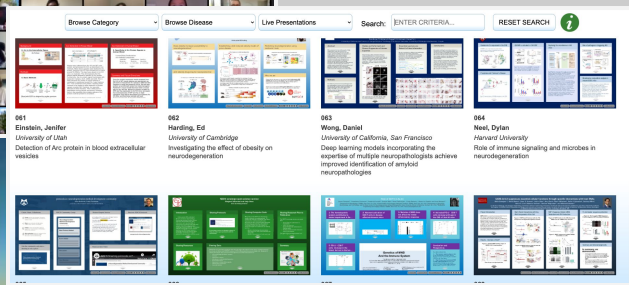
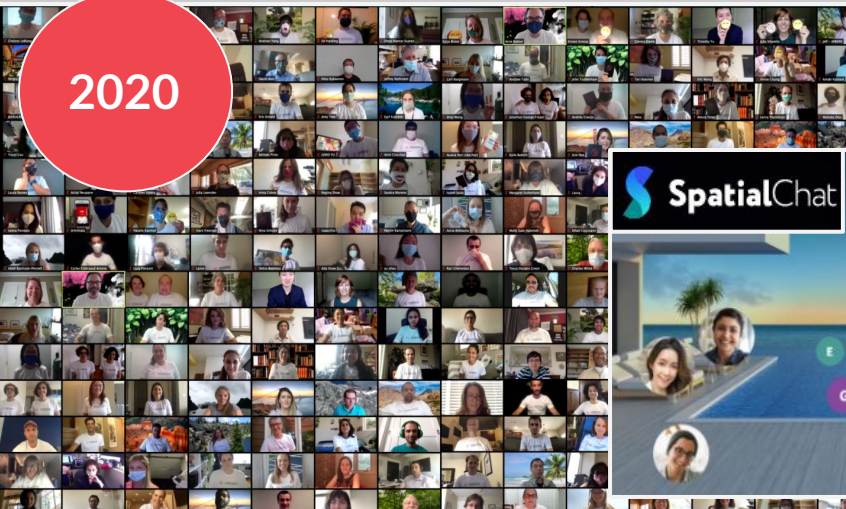


# Meetings in the age of COVID-19

2019



2020





# Goals & Objectives

# Setting goals & objectives

Before you make any decisions about the agenda, meeting platform or anything else, set your goals and objectives. Then shape the format of your meeting based on these goals.

*You will have better success if you decide on the platforms, tools and agenda items of your meeting **after** you have set your goals than if you design the meeting based on the available tools*



# Setting goals & objectives

Before you make any decisions about the agenda, meeting platform or anything else, set your goals and objectives. Then shape the format of your meeting based on these goals.

- *Why is the meeting being held? What is the purpose?*
- *What needs are being met through this meeting?*
- *Are you building off momentum from previous meetings?*
- *After the meeting is over, what does success look like?  
What do you hope to feel excited about afterwards?*
- *Do you have all the information you need to plan this meeting, or do you want to connect with attendees to set the goals?*





# Setting goals & objectives

Before you make any decisions about the agenda, meeting platform or anything else, set your goals and objectives. Then shape the format of your meeting based on these goals.

Practical considerations:

- *How large will the meeting be?* → platform limits
- *Sharing science or connecting researchers?* → interactivity
- *Global reach or local groups?* → accessibility and bandwidth
- *Open meeting or closed?* → registration and logins
- *Working meeting?* → breakout functionality





# Meeting Platforms

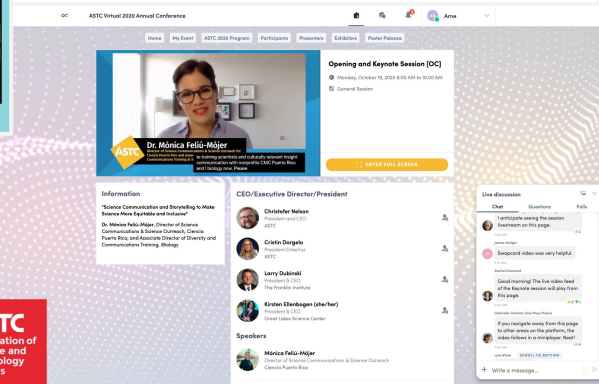
# Meeting platforms

How do attendees participate in the main meeting?

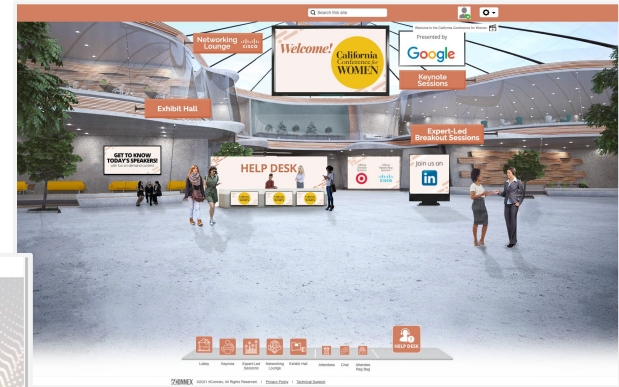
Three main choices:



Application-based



Web-based



Virtual convention space



# Meeting platforms

How do attendees participate in the main meeting?

## Three main choices:

- Application-based platform:  
*Zoom meeting / Zoom webinar / Microsoft Teams / Google Meet / ...*
- Web-based platform:  
*Swapcard / Attendify / Whova / Hopin / ...*
- Fully customizable convention space:  
*Cvent / 6Connex / Adobe Connect / ...*

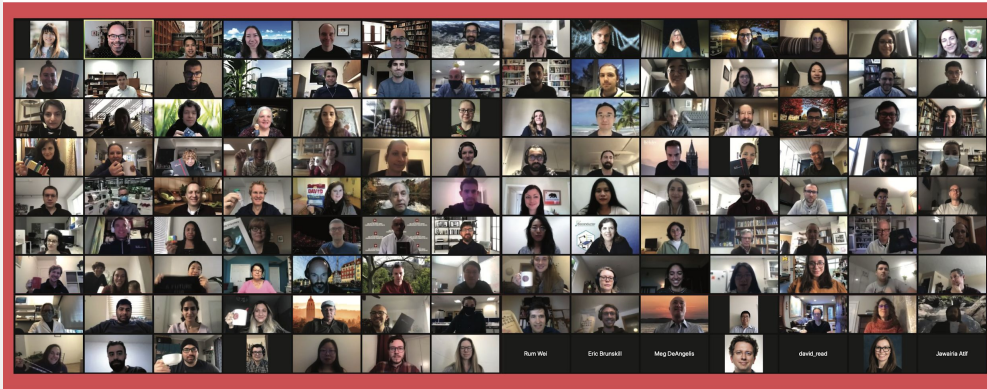
Lots of options! Many people have made lists comparing platforms



# Meeting platforms: CZI uses Zoom



## CZI Seed Networks 2020 Annual Meeting



Zoom as main meeting platform

> Bioconductor: HCA data access	11
> Azimuth	47
> Cell Annotation PlatformFeedback	29
> Cellxgene	27
> DCP & Lattice	10
> Bioconductor: scaleable clusteri	8
> Napari	5
> Meta	3
> Scanpy	26
> Scvi-tools	11
> SPRING	6
> VISION	21

Breakouts for smaller sessions

# Social interactions

Virtual meetings have brought different ways of networking

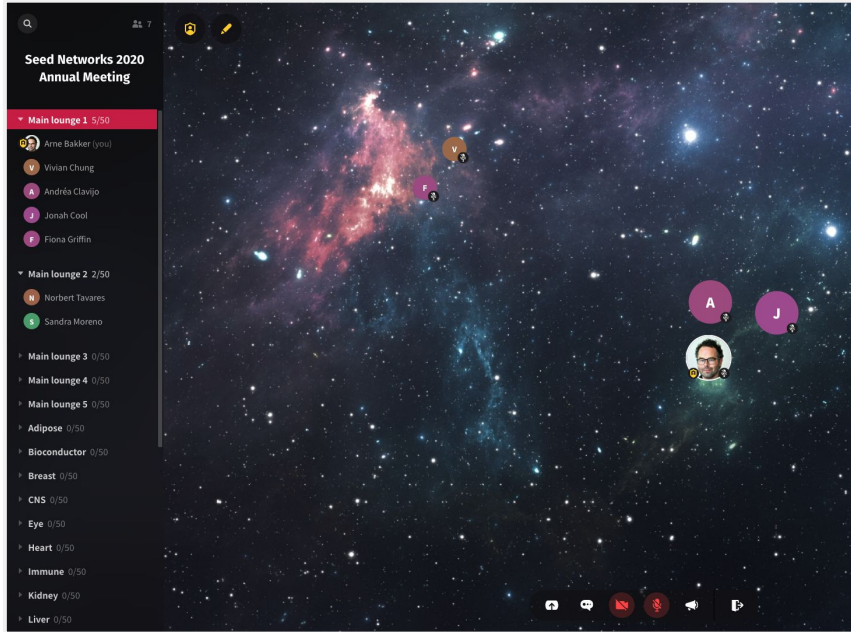
- Zoom breakout rooms: *Many recent updates*
- Move yourself around in 2D: *Spatial Chat / Kumospace / Wonder / Gather.town*
- 1:1 connections: *Icebreaker.video*
- Virtual conference space: *6Connex / Cvent / Remo*
- Fun & games: *Go Game / Scavenger hunt / Happy hour hangout / ...*

## Tips

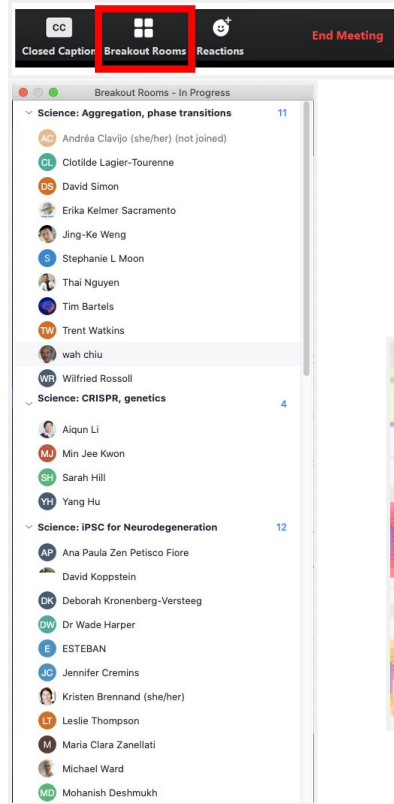
- Include clear instructions & be available for questions
- Additional networking at the end of the meeting day gives flexibility to your attendees



# Social interactions: examples



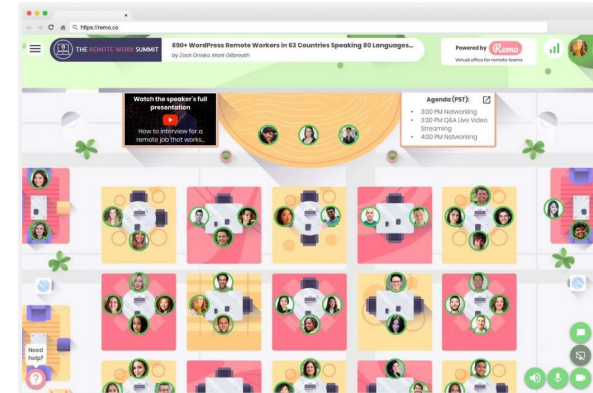
Spatial Chat



Zoom breakouts



The Go Game



Remo

# Poster platforms



NEURODEGENERATION  
CHALLENGE NETWORK

2020 ANNUAL MEETING  
July 13-15



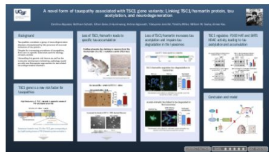
Browse Category

Browse Disease

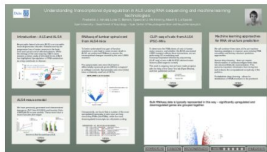
Live Presentations

Search: ENTER CRITERIA...

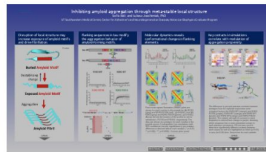
RESET SEARCH



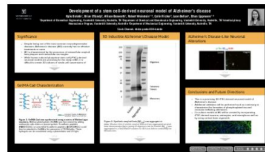
**001**  
**Alquezar, Carolina**  
*University of California, San Francisco*  
A novel form of tauopathy associated with TSC1 gene variants: Linking TSC1/hamartin protein, tau acetylation, and neurodegeneration



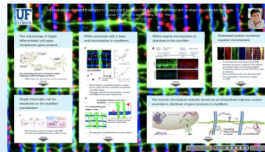
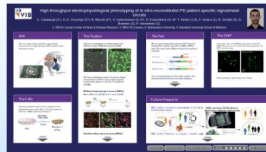
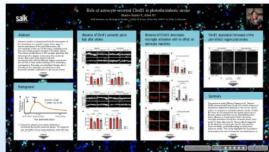
**002**  
**Arnold, Frederick**  
*Duke University*  
Understanding transcriptional dysregulation in ALS using RNA sequencing and machine learning technologies



**003**  
**Bali, Sofia**  
*UT Southwestern Medical Center*  
Inhibiting amyloid aggregation through metastable local structure

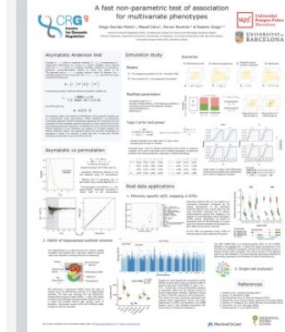


**004**  
**Balotin, Kyle**  
*Vanderbilt University*  
Development of a stem cell-derived neuronal model of Alzheimer's disease



iPoster Sessions (aMuze)

1. Computational Tools



**01. A fast non-parametric test of association for multivariate phenotypes**

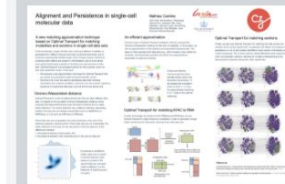
Diego Garrido Martin, Miquel Calvo, Ferran Reverter, Rodolfo Guigo

Abstract

The availability of phenotypic data at multiple levels, from the organismal to the molecular, in large cohorts of genotyped individuals is continuously increasing, enabling genome-wide association studies (GWAS) and quantitative trait loci (QTL) mapping analysis. Most of these analyses test for association with genetic variants a single trait at a time, even though many biological phenotypes are intrinsically multi-trait, size and connectivity of brain regions, levels of blood lipids, facial and allometric traits, composition of the gut microbiota, gene networks, abundances of alternative splicing isoforms, single-cell gene expression across tissues and organs, etc. Because of the correlated structure of these traits, joint (i.e. multivariate) analysis often results in increased statistical power to detect genetic associations. In this context, multivariate distance matrix regression offers an interesting non-parametric approach. However, its current statistical framework relies on permutations, which makes impractical its usage in large-scale datasets. Here we have derived the limiting distribution of its test statistic, allowing the ultra-rapid computation of asymptotic  $p$  values. We illustrate our method by applying to two different genomic contexts: single-specific splicing QTL mapping in GTEx and GWAS of MRI-derived volumes of hippocampal subfields in the ADNI cohort. We believe that our multivariate approach can be also of interest for the analysis of single-cell datasets.

Presented by  
Diego Garrido Martin

Institution  
Centre for Genomic Regulation (CRG), The Barcelona Institute for Science and Technology, Barcelona (Spain), Section of Statistics, Department of Genetics, Microbiology and Statistics, Universitat de Barcelona (UB), Barcelona (Spain), Universitat Pompeu Fabra (UPF), Barcelona (Spain)



**02. Alignment and Persistence in single-cell molecular data**

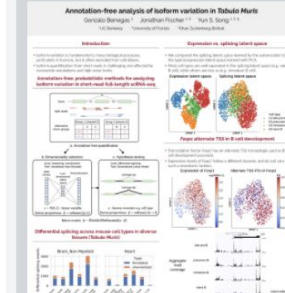
Matthieu Carrière

Abstract

In the last decade, single cell data sets combining different modalities or generated from different tissues have been produced extensively due to numerous experimental breakthroughs. Even though several methods for correcting batch effects are present in the literature, less is known about more general techniques capable of handling very general pairs of data sets. Optimal transport has emerged recently for this purpose, due to its very wide application range. In this work, 1) We propose a new approximation technique for Optimal Transport that can speed up computation while being theoretically correct, 2) We show how it can be used for generating data sets including information from several modalities, and how it can be used for capturing dynamics in longitudinal data sets, such as the human spinal cord.

Presented by  
Matthieu Carrière

Institution  
Inria Sophia Antipolis



**03. Annotation-free analysis of isoform variation in Tabula Muris**

Dimitrios Benetos, Jonathan Friedman, Yuh-Sung Song

Abstract

Isoform diversity is a fundamental aspect of higher eukaryote biology but is often ignored in single cell studies, due to quantification challenges with short read technologies. We have developed a suite of tools for quantification, dimensionality reduction, and hypothesis testing of isoform variation from short-read full-length single-cell RNA-seq, focusing on splice junction usage. Our methods do not require transcriptome annotations and leverage probabilistic count models to handle noise and sparsity of single cell data. We find a strong cell-type-specific isoform variation signal across diverse mouse tissues, including a large proportion of unannotated splice junctions.

Presented by  
Dimitrios Benetos

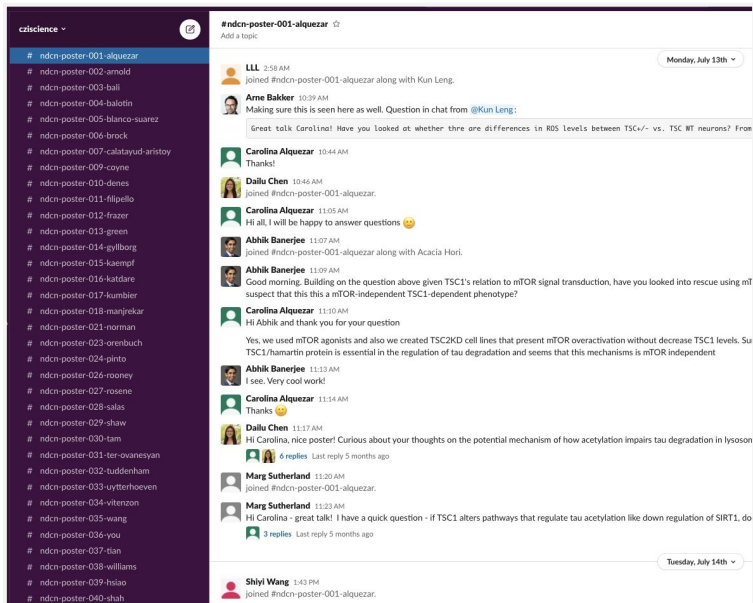
Institution  
UC Berkeley, University of Florida, Chan Zuckerberg Biohub

VirtualPosterSession.org

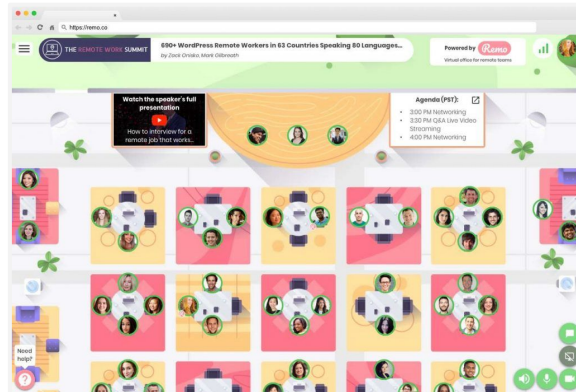




# Poster sessions



Slack channels for posters  
(do not recommend!)



Remo tables for posters

> 01 - Diego Garrido Martín	2
> 02 - Mathieu Carrière	2
> 03 - Gonzalo Benegas	2
> 04 - Jackson Loper	3
> 05 - Viktor Petukhov	6
> 06 - Ye Zheng	2
> 07 - Shou-Wen Wang	1
> 08 - Vitalii Kleshchevnikov	1
> 09 - Arya Kaul	6
> 10 - James Zou	1
S Siyuan	
> 11 - Fangming Xie & Ethan Armand	6
> 12 - Florian Schmidt	1
> 13 - Shani Amarasinghe	0
> 14 - Jinzhuang Dou	3
> 15 - Ansley Conchola	1
> 16 - Renee Conway	0
> 17 - Michael Wasney	2
> 18 - Monika Litvinukova	0
> 19 - Jamie Marshall	3
> 20 - Sebastian Wallace	0
> 21 - Parker Wilson	4
> 22 - Tallulah Andrews	12
> 23 - Shuai Guo	0
> 24 - Rebecca Back	2
> 25 - Gregory Booth	4

Zoom breakout  
rooms for posters



# Agenda & Production

# Agenda drafting

- Start with your goals & objectives
- Avoid long talks on Zoom
- Build in plenty of breaks
- Build in buffers & transition time
- Do people platform hop or not?  
Are there Parallel Sessions?
- Social session at the end can stay 'open' for post-meeting networking
- Start with a blank slate and move around sessions until it feels right



Meeting agenda		
Closed caption is available during all Zoom sessions		
Tuesday, November 17th		
Time (Pacific Time)	Session	Meeting link
8:00 AM - 8:15 AM	Welcome & opening	Main Zoom meeting
8:15 AM - 9:00 AM	Overview of the first year of the Seed Networks program	
9:00 AM - 9:45 AM	Keynote: <a href="#">Dr. Keolu Fox, University of California San Diego</a>	
9:45 AM - 10:00 AM	Break	
10:00 AM - 11:15 AM	<b>Project talks (parallel sessions, <a href="#">talk titles</a> below the Meeting Agenda):</b> <ul style="list-style-type: none"><li>● <b>Session 1: Aging &amp; Lifestyle</b><ul style="list-style-type: none"><li>○ Shyam Prabhakar</li><li>○ Jimmie Ye</li><li>○ Peter Sims</li><li>○ Mark Eckert</li></ul></li><li>● <b>Session 2: Genetics &amp; Computation</b><ul style="list-style-type: none"><li>○ Abbas Rizvi</li><li>○ Nelson Johansen</li><li>○ Allen Wagner</li><li>○ Kasper Hansen</li></ul></li><li>● <b>Session 3: Spatial Approaches</b><ul style="list-style-type: none"><li>○ Rita Manco</li><li>○ Douglas Shepherd</li><li>○ Rebecca Beuschel &amp; Veronika Kedlian</li><li>○ Kai Kessenbrock</li></ul></li><li>● <b>Session 4: Cancer</b><ul style="list-style-type: none"><li>○ Ram DasGupta</li><li>○ Harikrishna Nakshatri</li><li>○ Matthias Mann</li><li>○ Bo Yuan</li></ul></li></ul>	<a href="#">Zoom Link 1</a>  <a href="#">Zoom Link 2</a>  <a href="#">Zoom Link 3</a>  <a href="#">Zoom Link 4</a>
11:15 AM - 11:45 AM	Break	
11:45 AM - 12:30 PM	<b>Lightning talks:</b> 3-minute talks of poster presenters <ul style="list-style-type: none"><li>● Emily Holloway</li><li>● Jamie Marshall</li><li>● Paul Cheng</li><li>● Riccardo Calandrelli</li><li>● Gregory Booth</li><li>● Shou-Wen Wang</li><li>● James Zou</li><li>● Jinzhuang Dou</li><li>● Ye Zheng</li></ul>	Main Zoom meeting
12:30 PM - 12:45 PM	Closing & overview of day 2	
12:45 PM - 1:30 PM	Networking session: Network with your network	

# Agenda drafting

## Flow & energy

- How is information shared?  
*Sage on a stage vs. Interactive sessions*
- Considering flow contributes to the success of your meeting
- Mix up session types for increased attention  
*Presentations vs. Panels vs. Breakouts vs. Workshops vs. Networking*



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12:30 PM - 12:45 PM	Closing & overview of day 2	
12:45 PM - 1:30 PM	Networking session: Network with your network	<a href="#">Spatial Chat</a>

# Run of show

- Have clear roles and responsibilities

## *Running a virtual meeting is not a 1-person job*

I recommend 3 people to run a successful multi-day meeting

Someone moderating should *not* be assigned to tasks like admitting attendees

- TEST TEST TEST (then test again)  
Meeting planners have moved into the realm of A/V professionals
- Have one host be available at all times for questions. Especially if you're platform hopping



Wednesday, March 3rd		
Time (Pacific Time)	Session	Job Duties
7:30 AM	Planning meeting team to meet on Zoom	ALL Check link Start recording Start closed captioning Mute everyone on entering - Welcome slide with music - Arne - Admitting attendees - Andréa - <a href="#">Slack announcements</a> - Vivian
8:00 AM - 8:15 AM	<b>Welcome &amp; opening</b>	Zoom Host - Andréa - <a href="#">To share screen Master slide deck</a> - Andréa - Welcome - Vlad - Team Introductions - Vlad - Agenda overview - Vlad - Housekeeping - Andréa - For private questions - Andréa - Share pdf link in chat & Slack - Arne
8:15 AM - 8:45 AM	<b>Overview of CZI Science:</b> Cori Bargmann & Phil Smoot	Zoom Host - Andréa - <a href="#">To share screen Master slide deck</a> - Andrea - Introduction - Vlad - Cori (Head of Science) 8:15 - 8:45 AM - AC to run slides - both to share screen - Phil (Head of Science Technology) 8:30 - 8:45 AM - AC to run slides - both to share screen - <a href="#">Time keeper</a> (no need to chime) - Vivian
8:45 AM - 9:05 AM	<b>Overview of the CZI Imaging Program:</b> Stephani Otte & Vladimir Ghukasyan	Host - Andréa - <a href="#">To share screen Master slide deck</a> - Vlad - <a href="#">Time keeper</a> - (no need to chime) - Vivian
9:05 AM - 9:35 AM	<b>Biolmaging North America:</b> Alison North & Teng-Leong Chew	Zoom Host - Andréa - <a href="#">To share screen Master slide deck</a> - Melissa - Introduction - Vlad - Moderate Q&A - Vlad - Claire & Alison to share screen - 25 mins talk + 5 mins for Q&A - <a href="#">Time keeper</a> - Vivian - Gather questions copy & paste into Slack - Andréa
9:35 AM - 9:55 AM	Break	



# Final thoughts & resources

Thank you!

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[sciencemeetings@chanzuckerberg.com](mailto:sciencemeetings@chanzuckerberg.com)

[www.chanzuckerberg.com/science/meetings](http://www.chanzuckerberg.com/science/meetings)

