

AndrewsLab Handbook

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Part I

Welcome

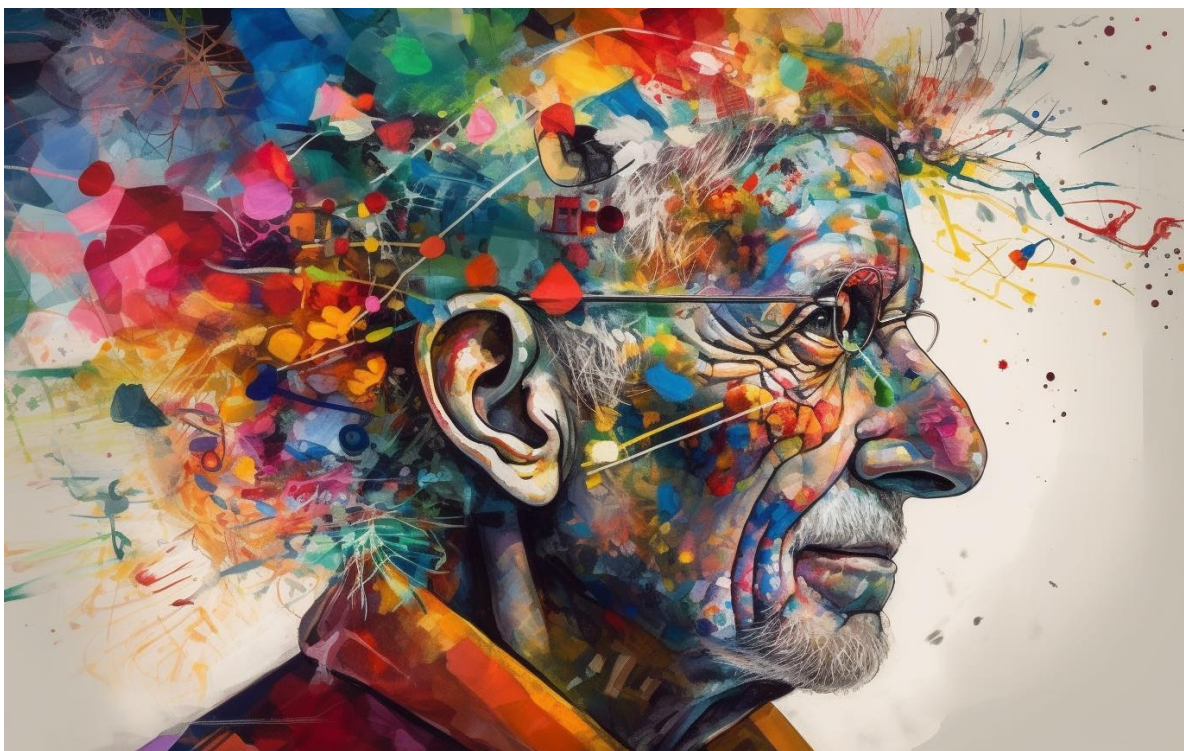


Figure 1: Interplay Between the Genome and Exposome in Dementia - An Illustration by Midjourney

Welcome to the Andrews Lab. As a member of our team, you are joining a group of dedicated researchers committed to advancing our understanding of the causal pathways that underly the development of Alzheimer's disease and related dementias.

Our lab is a dynamic and collaborative environment where curiosity, creativity, and critical thinking are valued and nurtured. We believe that every member of our team brings unique perspectives and skills that enrich our research and contribute to our shared mission.

This handbook is designed to provide you with a comprehensive overview of our lab's operations, policies, and procedures. It serves as a guide to help you navigate your journey with us, whether you are a new member just starting out or an existing member seeking to refresh your knowledge.

In this handbook, you will find information about our lab's history, our team, the research we conduct, and the resources available to you. You will also find detailed protocols for our common procedures, guidelines for data management and authorship, and information about our ethical standards and compliance requirements.

We encourage you to read this handbook thoroughly and refer to it often. However, please remember that it is not meant to cover every possible scenario or answer every question. When

in doubt, do not hesitate to ask. Open communication is key to our lab's success, and we are here to support you.

We are excited to have you on board and look forward to the contributions you will make to our lab. Together, we will continue to push the boundaries of genetic epidemiology and bioinformatics, making discoveries that have the potential to transform human health.

Welcome to our team!

Shea Andrews

Principal Investigator

About the Lab

Mission Statement

The Andrews Lab at the University of California, San Francisco, aims to transform the diagnosis and treatment of Alzheimer’s disease and related dementias. Through pioneering research in genetic epidemiology, we are developing predictive risk models that will serve as the foundation for personalized medicine that improves patient care. By integrating genetic factors—such as monogenic variants, polygenic architecture, and family history—with environmental factors consisting of individual-level lifestyle & behavioral exposures and broader macro-environmental factors, our models will empower patients and healthcare providers with actionable insights. Our ultimate objective is to enable targeted, effective interventions that will improve patient outcomes and reduce health disparities in Alzheimer’s disease across diverse communities.

Lab Philosophy

In the Andrews Lab, our philosophy serves as the cornerstone of our scientific journey, influencing both the research questions we ask and the ethical standards we uphold. Grounded in principles of scientific integrity, collaboration, innovation, and team science, we aim to cultivate an environment that promotes inclusivity, values lifelong learning, and adheres to the principles of open science. Team science is central to our ethos, reinforcing the idea that individual accomplishments are a reflection of collective effort and that our greatest achievements stem from open collaboration and mutual support. This philosophy is not merely a collection of ideals; it’s a commitment to conducting research that is meaningful, ethical, and poised to make a lasting impact in the scientific community.

Team Science

At the heart of our lab’s philosophy is the concept of Team Science. We firmly believe that we are greater than the sum of our parts. In this lab, your success is everyone’s success, and the same holds true in reverse. We are all collaborators here, each contributing unique skills and perspectives that enrich our collective work. I am committed to promoting not just your research, but also your professional growth, and I expect the same level of cooperation and openness from you in return.

Collaboration is a cornerstone of our lab philosophy. We believe that the best science is done when diverse minds come together to solve complex problems. This extends to collaborations within the lab, across departments, and even internationally. We encourage lab members to engage in interdisciplinary research and to seek external collaborations that can enhance the impact of our work.

Sharing—be it materials, data, or opportunities—is a fundamental aspect of our collaborative culture. We don't see each other as competitors; we are collaborators, both within these walls and in the broader scientific community. When one of us succeeds, it's a win for all of us. Conversely, setbacks are not borne alone; we rally around each other to find solutions.

By embracing the principles of Team Science, we aim to create a lab environment that is not just productive but also supportive, inclusive, and conducive to the personal and professional growth of all its members.

Scientific integrity

In the Andrews Lab, we uphold the highest standards of scientific integrity. This means conducting research that is rigorous, transparent, and ethical. We are committed to the responsible handling of data, from collection to analysis and reporting. Any form of data manipulation or scientific misconduct is unacceptable. Our aim is to contribute to the scientific community with work that can be trusted and built upon.

Accountability: Accountability is a key aspect of our lab culture. Every lab member is responsible for the quality and integrity of their work, from the planning stage to publication. Regular lab meetings and internal reviews are platforms where we hold ourselves and each other accountable, ensuring that our research meets the high standards we set for ourselves. Mistakes are an inevitable part of the scientific process, and they are not setbacks but learning opportunities. The key is not in avoiding mistakes, but in how we handle them. If you encounter a problem, try to resolve it independently first. If that fails, bring it to my attention as soon as possible. There's no room for covering up errors; transparency is crucial. Together, we will work to correct the issue, learn from it, and move forward.

Open Science: We are strong proponents of open science, believing that scientific knowledge is a public good. Whenever possible, we publish in open-access journals, share our data and code, and engage with the broader scientific community and the public. This commitment to openness increases the impact of our work and contributes to a more collaborative and transparent scientific community.

Innovation and Adaptability: In the Andrews Lab, innovation and adaptability go hand in hand as core values that drive our scientific inquiry. We encourage lab members to think creatively, question existing paradigms, and explore novel approaches to complex problems. Innovation is not confined to groundbreaking ideas but also extends to the methodologies, tools, and techniques we employ in our research.

However, more than innovation is required; the ability to adapt is equally crucial. Science is an ever-evolving field, and unexpected challenges or results are inevitable. We value adaptability as a complementary skill to innovation, enabling us to pivot our research focus or methodologies when warranted by new findings, technical advancements, or unforeseen challenges. This dual commitment to innovation and adaptability ensures that we are not only at the forefront of scientific discovery but also equipped to navigate the complexities and uncertainties that come with pioneering research.

Lifelong Learning

Science is a constantly evolving field, and we are all perpetual students. In the Andrews Lab, we emphasize the importance of continuous learning—whether it’s mastering a new research technique, staying updated on the latest literature, or developing soft skills like communication and leadership. We encourage lab members to attend conferences, workshops, and webinars, and to always be curious.

Inclusivity and Diversity

Our lab is committed to fostering an environment where all individuals feel respected, included, and valued. We believe that diverse perspectives enrich our research and make us more effective scientists. We strive to recruit lab members from diverse backgrounds, including but not limited to race, gender, sexual orientation, and socioeconomic status, and we are committed to their professional development.

Part II

Lab Policies

Getting Started in the Lab

Whether you are an undergraduate student, graduate student, postdoctoral associate/fellow, or associated research staff, starting in a new lab can be a daunting experience. The onboarding process is crucial for ensuring that newcomers feel comfortable and familiar with the lab's procedures, protocols, and guidelines. As you get started you may have a number of questions or uncertainties about your role, your project, our research, or life at UCSF. Just remember that we are here to support you every step of the way, so we encourage questions and feedback during the onboarding process.

New Lab Member Essentials

Important UCSF Sites

- [Office of Diversity and Outreach](#): UCSF DEI policy
- [My Access](#): UCSF Online Services
- [UCSF PeopleConnect](#): Integrated portal for HR
- [UCnet](#): Benefits
- [UCPath](#): Payroll
- [Campus Life Services](#): Information on UC discounts, perks, housing, community organizations etc

Onboarding Tasks

Introductions

- Make sure to take a moment to introduce yourself to other Andrews lab members. We will also introduce you to our collaborators in the Center for Population Brain Health and Memory and Aging Center.

Organize to collect your UCSF ID

- [Get UCSF ID Card](#): Make an appointment or drop-in at the Mission Bay Campus.

Lab Website

- Email Shea a headshot and short bio about your self to be included on the [Andrews Lab Website](#).

Work Computer

This is a list of software you should install on your work computer. If something is missing please add it!

Required software to install

- IDE: [VScode](#)
- R: [R](#), [RStudio](#)
- Terminal: [iTerm2](#) or [Warp](#)
- [Homebrew](#)
 - [Git](#): Cloning git repo's requires using SSH. See [Generating a new SSH key and adding it to the ssh-agent](#) and [Adding a new SSH key to your GitHub account](#)
- VPN Pulse Secure: [UCSF request access](#)
- Reference Manager: [Papers](#) or [others](#)
- [Slack](#):
- Office 365: [UCSF request access](#)
- Zoom: [UCSF request access](#)
- wifi: [UCSFwpa - Secure Wireless](#)

Advanced software to install - project dependent

- [miniforge](#): A package manager that combines Mamba's speed with Conda Forge's environment management for easy software setup.
- [Snakemake](#): A workflow management tool that automates data analysis pipelines using a Python-based language.
- [Docker](#): A platform for packaging applications into containers to ensure they run consistently across different environments.

Optional software to install - Shea regularly uses these

- [Oh My ZSH](#): Bring some life to your terminal!
- [Dropbox](#): Save everything in the cloud.
- [iStat Menues](#): Better tracking of your computers resources
- [tadam](#): Pomodoro timer for focusing
- [Magnet](#): Better management of windows
- [Bartender](#): Take control of your menu bar

Wynton Account

Wynton is UCSF's High Performance Cluster

- [Request an account](#)
- [Set up VSCode ssh forwarding](#)

List Servs

Global Email list serves that Shea needs to add new employees too.

- Calendar invites for Lab Meetings: Shea
- Center for Population Brain Health: Tamar Simone
- Memory and Aging Center: [MAC ARF](#)
- Institute of Human Genetics: Aubrey Carstension

Mobile

- Email: [UCSF enrollment](#)
- wifi: [UCSFwpa - Secure Wireless](#)

Materials to Review

As a new member in the lab, there may be several materials that you should read or study to get a better understanding of the lab's research projects and protocols. The timeframe and sequence for reading or studying these materials will vary depending on the project(s) you will be working on. However, it's important to make sure you have a basic understanding of the lab's research and protocols before starting your work. It's also essential to ask questions and seek help from Shea and/or lab members if you need clarification or assistance.

- **Background Material:** Joining the lab comes with an expectation of foundational knowledge. Our [Reading List](#) offers a selection of introductory papers to help you get started. Please consult with Shea to identify which topics are most pertinent to your research project.
- **Technical Manuals:** Each project will use specific software tools, Shea will guide you on specific papers to read.
- **Grants:** For those involved in grant-funded projects, Shea will provide you with the relevant grant details.
- **Publications:** Read some of the lab's recent publications to get a sense of the research questions and methods used by the lab members.

Training Basics

At the end of the hiring process HR will have sent an “Welcome to the University of California, San Francisco” email outlining trainings that need to be completed. These include:

- HBS Timekeeping system
- Office Ergonomics
- HIPAA 101
- WarnMe
- UC Cyber Security Awareness Fundamentals
- UCSF Foundations of Diversity, Equity and Inclusion
- UC Preventing Harassment & Discrimination: for Non-Supervisors or UC Preventing Harassment & Discrimination: for Supervisors, Faculty, MSP if you supervise others.
- Document: COVID-19 Prevention Training
- Any other required training found in your required training

Read the Lab Handbook

Hey you are already doing this! When you are finished, please utilize Git to clone the repository and push a new commit adding your name to the [Signatures](#) page acknowledging that you have read and comprehended the contents of the Andrews Lab handbook.

Working in the lab

This section of our handbook is designed to acquaint you with the general lab and institutional policies that underpin our daily operations and long-term objectives, ranging from work hours and time off to professional development and performance evaluations. They reflect our commitment to creating a supportive, productive, and enriching lab environment for all members.

Work Hours

I expect all lab members to be responsible and accountable for their research projects and to set reasonable goals and expectations for themselves regarding their lab work schedule. While I encourage you to manage your time in a way that suits your personal productivity rhythms, regular attendance is beneficial for your own development as well as for the collaborative spirit of our lab. Being present and engaged helps us to work together more effectively and support one another's research pursuits.

Full time lab members should aim to be on-site three days per week, with two of these days being Tuesdays and Thursdays to attend lab meetings. While work hours are flexible to accommodate varying personal schedules and research needs, they should generally overlap with core business hours of 8:00 AM to 6:00 PM.

However, life is full of surprises and responsibilities beyond the lab. If you foresee any changes in your availability, just let me know—open communication will help us work together to find the best solution for everyone.

Time Off

Taking time away from the lab is an important part of leading a balanced life and can have great benefits for productivity after returning to work. All lab members are encouraged to fully utilize their entitled paid time off as stipulated in their contracts. During this time, I strongly endorse a complete break from work-related activities, including refraining from checking emails, to ensure a true break.

Lab members should inform me about their time off as early as possible, so that I can plan accordingly and ensure that lab activities continue smoothly. They can inform either in person

or via email, and I would appreciate it if they could provide me with specific details about the dates and the duration of their absence.

Currently, there are no restricted periods for taking time off. However, I ask everyone to be considerate of their own project timelines and those of collaborative efforts. Please plan your absences thoughtfully, avoiding critical phases of research when your presence may be integral to our progress.

Code of Conduct

All lab members are expected to adhere to the [UCSF Researcher Code of Conduct](#). We are all expected to perform our research with integrity, to uphold ethical values and to demonstrate competence in our areas of research.

Lab members should also be mindful of their behavior and language to promote a respectful and inclusive work environment. Discrimination, harassment, and bullying will not be tolerated.

Responsible conduct of research is foundational to our scientific integrity and credibility, all lab members are required to uphold the highest standards of honesty, accuracy, and objectivity in their work. See the [RCR](#) section for more details

Performance Reviews

Performance Evaluations

Annual performance evaluations are essential for all non-probationary career employees, in line with [UCSF guidelines](#). These evaluations aim to fairly assess employee performance, set objectives for the upcoming period, and review the achievement of previously set goals. They play a critical role in enhancing job performance aligned with the lab's and institution's goals, improving individual performance, acknowledging contributions, and supporting professional development. Evaluations also offer an opportunity to address any concerns, suggest improvements, and fulfill both internal and external documentation requirements for individual performance.

The evaluation cycle follows the calendar year, starting on January 1 and concluding on December 31, with evaluations due by mid-March of the subsequent year. This process ensures a structured approach to recognizing achievements, fostering growth, and maintaining high standards of performance within our lab environment.

Probationary Periods

New lab members hired into a Career position serve a six-month probation period, unless otherwise extended pursuant to policy or contract. A mid-point assessment will be conducted half-way through the probationary period.

Individual Development Plans

At the start of the Academic Year (August/September), Shea will convene a State-of-the-Lab meeting to review the lab's progress, achievements, challenges, and envisaged paths forward. This meeting is designed to foster transparent communication, celebrate the lab's collective and individual accomplishments, and outline the objectives for the upcoming year.

Integral to the State-of-the-Lab is the completion of an [Individual Development Plan](#), a tool aimed at defining and achieving their professional career goals. Shea will discuss the IDP with each person one-on-one. Additionally, the State-of-the-Lab provides a forum for all members to share their goals and receive feedback

Professional Development

I highly encourage everyone to pursue professional development opportunities that will further their careers. UCSF provides a range of resources to support professional development, such as workshops, seminars, and courses. Additionally, there are opportunities for lab members to attend conferences, present their research, and network with colleagues in their field. I am happy to write letters of recommendation or support their applications for these opportunities. In order to gain access to these resources, lab members should consult with Shea or the institution's professional development office to identify relevant opportunities and funding sources.

Slack

Use the [#seminars](#) Slack channel to share any upcoming seminars, conferences or professional development opportunities with the rest of the lab!

UCSF & Bay Area

There are numerous opportunities to attend workshops, seminars, and symposiums at UCSF and within the Bay Area. These include, but are not limited to:

- Institute of Human Genetics Seminars

- Memory and Aging Center Lecture Series
- Center for Population Brain Health Works in Progress
- [The Office of Career and Professional Development](#)
- UCSF Dementia Day
- Bay Area Alzheimer's Disease Researchers Symposium
- Institute for Human Genetics Genotech Symposium
- [Gladstone Bioinformatics Workshops](#)

Conferences

The general expectation for conferences - particularly national and international - is that to attend you have submitted an abstract that has been accepted for a poster or oral presentation. A couple of standard conferences. When thinking of what conferences to attend, consider what you want to get out of it, larger conferences offer much larger potential for exposure and the ability to meet with most people in our field. However, smaller conferences are more intimate and offer better opportunities to network.

- [Alzheimer's Association International Conference \(AAIC\)](#)
- [American Society of Human Genetics \(ASHG\)](#)

In addition to these larger conferences there are also consortium level meetings

- Alzheimer's Disease Genetics Consortium (ADGC) Meeting
- Alzheimer's Disease Sequencing Projects (ADSP)
- [Alzheimer's Disease Research Centers Meetings](#)

Institutions offering career development workshops

- [Skills for Health and Research Professionals \(SHARP\) Training](#)
- [Cold Spring Harbor Laboratory](#)
- [Advanced Psychometric Methods for Cognitive Aging Research \(ΨMCA\)](#)
- [Harvard Catalyst](#)
- [Stanford](#)

Letters of Recommendation

I am honored that you have asked me to write a letter of recommendation for you, and I take this responsibility seriously. In order for me to help you get into the program you want, please provide the following materials to assist me in writing the letter:

- CV
- Personal statement
- Details on the program you are applying for (website, etc.)

In addition to these materials, please provide me with answers to the following questions, or any other additional information about you that you would like to be highlighted in the letter:

- What are your strongest attributes?
- What are you most proud of (academic or personal life)?
- What sets you apart from other applicants?
- How would your peers describe you? What makes you a good team player
- What do you want to make sure the program knows about you?
- How can I best advocate for you in the letter?

This information will aid me in crafting a compelling and personalized recommendation that aligns with your aspirations and the program's expectations.

Leaving the Lab

Transition is a natural part of the laboratory life cycle, recognizing that each member has unique career aspirations. Shea is committed to supporting these professional goals and encourages open dialogue about future plans. This transparency ensures a seamless transition for both the individual and the lab. Should a situation arise where a member's departure is involuntary, we promise to offer clear, constructive feedback and explore all possible solutions. In instances of funding cessation, we pledge to assist in identifying new opportunities, striving to preserve amicable relationships with departing members under any circumstances.

Planned and Voluntary Separation from the Lab

Staff members should refer to [UCSF Offboarding](#) for guidance. Written formal notification of your voluntary resignation should be sent to Shea as soon as possible. This will allow for timely processing of your separation (minimum of 10 business days required).

Involuntary Separation or Termination

While not expected, there may be times that a lab member needs to leave the lab unexpectedly due to loss of funding or conduct that violates the expectations of the lab and University. Disciplinary or performance issues will be addressed respectfully and directly, with adherence to University policy regarding the terms of employment.

Offboarding tasks

Files and Backups

When you leave, your lab computer will be wiped and repurposed for new researchers.

Therefore, all of your files related to publications and analyses should be on Box or Wynton:

- Spreadsheets, documents, presentations and images should go on Box in your folder here. One exception is if the files are already on the drive in a project- or paper-specific folder.
- Large datasets used in publications or useful to other members should already be on Wynton. If some such data is not already there, transfer it.
- Any code that you have used to processed data or generate results for publications should be pushed to a AndrewsLab GitHub repository
- Experimental data should be in Box.

Slack and GitHub

Former lab members' access to the Lab Slack and GitHub will be reviewed at the start of each academic year. This allows for the finalization of any ongoing projects and publications. Access will be maintained temporarily to facilitate this process but will be revoked once these tasks are concluded.

Communication

Effective communication is paramount for a lab to function cohesively and productively. Our lab, a scientific community within the larger University of California, San Francisco (UCSF) ecosystem, thrives on regular interactions. These exchanges foster connections, enhance morale, facilitate the sharing of information, and help to identify and mitigate challenges in our research endeavors. It is crucial that when we communicate, both within our lab and with external colleagues, we adhere to the following principles:

- **Respectfulness:** Approach every interaction with respect, acknowledging the value of each member's contributions.
- **Clarity of Expectations:** Clearly articulate goals, responsibilities, and expectations to avoid misunderstandings.
- **Honesty:** Maintain transparency and honesty in all communications, fostering a culture of trust.
- **Constructive Feedback:** Offer feedback in a manner that is supportive and aimed at growth, recognizing that constructive criticism is a foundation for development.
- **Confidentiality:** Respect the privacy of sensitive information, ensuring that what is confidential remains so.
- **Inclusivity:** Promote an inclusive environment where diverse perspectives are welcomed and valued, recognizing that diversity strengthens our research and enriches our community.

Meetings in the Lab

Lab, project, and institutional meetings are integral to keeping abreast of each other's research, fostering collaborations, and furthering our professional development. Therefore, all full-time staff and trainees are encouraged to attend these meetings in person whenever possible.

Lab Meetings

The Andrews Lab convenes every Tuesday and Thursday from 11 AM to 12 PM. These sessions are primarily designed for members to present updates on their research progress. We will also engage in discussions on professional development topics such as writing, presenting, and

journal clubs. To ensure productive meetings, all participants should arrive prepared with any necessary materials or updates pertinent to their projects.

One-on-One Individual Meetings

In addition to broader lab meetings, one-on-one meetings offer tailored feedback on research projects and professional development. Staff and trainees should come ready to discuss their project's progression, any challenges encountered, and any questions or concerns they have. It's also a time to review goals and set new ones.

These meetings are ideally held at regular intervals—weekly, biweekly, or monthly—to best accommodate the staff/trainee's and Shea's schedules.

! Important

Responsibility for these meetings lies with the staff/trainee, who should provide an agenda to Shea at least one day prior. If there are specific materials for review, such as manuscript drafts or abstracts, these should be submitted at least one week in advance.

As-Needed Meetings

If my door is open, feel free to request an ad-hoc meeting. These are intended for issues that don't necessitate a scheduled meeting or when rapid feedback is necessary. Additionally, Shea will make rounds to touch base informally throughout the week.

Seminar Series

See the [UCSF Events Calendar](#) for upto date information on UCSF seminars.

- [Insitute of Human Genetics](#): Seminars from UCSF IHG faculty or invited speakers held Biweekly on Thursdays, 3-4:30pm
- Memory and Aging Center Lecture Series: Seminars from UCSF MAC faculty or invited speakers held weekly on Mondays, 10-11am
- Center for Population Brain Health Works in Progress: CPBH staff trainees provide updates on their research works in progress.

Internal Communication

Our primary means of communication is Slack, but we also talk with outside collaborators via email, zoom, and social media.

! Important

As the PI, Shea juggles a lot of commitments and often works outside of standard work hours. Should you receive messages or emails from him during these times, please know there is no expectation for an immediate response or to adjust to his schedule. Additionally, Shea appreciates your understanding and reminders if there's something you're awaiting from him that hasn't yet been delivered.

Slack

We use Slack as our primary means of communication within the lab. If you plan on sending an e-mail to someone within the lab, try a slack message instead. **You'll find that almost all messages you write on Slack should be in a channel, and not in a Direct Message.** This is because Slack's value is in its search functions: they make it easy to find messages about a particular project long after they have been posted. This only works well if messages are grouped in the right channels; we can't search each other's direct messages.

! Important

Direct messages should only be used for confidential conversations (like advising discussions with Shea) or for incidental messages that nobody else needs to read (like "are we meeting now?").

How and where to post

Every project has its own channel (like #mendelian-randomization). Some of these channels will be large due to it covering multiple subprojects people are working on, as these start to become unwieldy we will make channel-children.

In addition to project-specific channels, we have a variety of channels for organizational purposes.

#general is where we share various thoughts and ideas across the lab that are not specific to a given channel and lab-wide announcements.

#journal-club is for posting interesting papers that you have come across.

#lab-meeting is for organizing lab meetings, posting agendas, or meeting minutes.

#wynton is for discussing using wynton and computational resources.

#check-in is where, each work day, we post a quick overview of what we plan on working on for the day.

check-in

The daily check-in serves to keep all lab members informed about ongoing work, facilitate collaboration, and help individuals manage their time effectively. All full-time lab members are required to post a brief summary of their daily work plans. This can be done either at the beginning or end of the workday. If posting in the morning, please address “**What did you accomplish yesterday, and what are you planning to work on today?**”. If posting in the evening, the focus should be on “**What did you accomplish today, and what are your goals for tomorrow?**”. For part-time lab members, please post a check-in only on the days you are actively working on Andrews Lab projects. Lab members are encouraged to review each other’s check-ins to offer help, resources, or collaboration where applicable.

There is no need to provide a check-in if you are not working on a particular day due to a holiday, vacation, or other reasons.

journal-club

In an effort to foster a culture of continuous learning and to keep the team updated on the latest scientific developments, all full-time lab members are required to actively participate in our Slack channel, #journal-club. Each full-time lab member must post at least once a week - but more often is better! - sharing a scientific paper they find interesting and is relevant to the lab’s research focus or broader scientific community. Please also include a link to the paper and a brief statement (2-3 sentences) on why you think it is interesting or relevant. Lab members are encouraged to read the shared papers and engage in discussions, either by asking questions, providing insights, or sharing related work.

See Journal Club for some suggestions on how to develop a habit of keeping up with the literature.

Expectations of Lab Members

What You Should Expect from Me as Principal Investigator

What I Expect from Lab Members

When Things Don't Go Right in the Lab

Making and Disclosing Mistakes and/or Problems

Resolving Conflicts (with peers or PI)

Problem Solving Strategies (The SMARTER Approach)

Open Science

Safety

Equipment

Standard Operating Procedures and Protocols

Record-Keeping Practices and Lab Notebooks

Data

Management and Integrity

Data Analysis and Interpretation

Intellectual Property and University-Owned Data

Data Sharing and Open Science

Responsible Conduct of Research

Responsible Conduct of Research (RCR) encompasses ethical practices and standards in scientific research, ensuring integrity, accuracy, and the consideration of societal impacts in both basic and clinical studies. It is a fundamental aspect for researchers at all levels, from students to senior faculty, essential for a thriving research career.

[UCSF RCR training](#) provides details on RCR training schedules and access to course materials, external resources, grant proposal templates, and tailored training programs for different types of trainees, ensuring all members understand and engage with the principles of responsible research.

Compliance

Writing and Adhering to Compliance Protocols

Authorship in the Lab

Proper Citation and Writing with Integrity

Fabrication, Falsification, and Plagiarism (FFP)

Conflicts of Interest and Conflicts of Commitment

Use of Artificial Intelligence

Part III

Resources

Compute

Local Machine

Oh My Zsh

I like to install Oh My Zsh on my local machine for autocomplete etc

- [OhMyZsh](#): Mange your zsh configuration
- [zsh-autosuggestions](#)

High Performance Computing

[Get Started with Wynton Job Submission File Transfers](#)

[Wynton Bioinformatics Open Data Resource](#)

```
/wynton/group/databases
```

```
ssh sjfandrews@log1.wynton.ucsf.edu
```

```
/wynton/group/andrews
```

[Getting started with HPC](#)

Mamba

Conda and Mamba are tools that help you install and manage software packages and their dependencies, which are other packages that a software needs to function properly. They're especially useful when different projects need different versions of the same software package. Conda, created by Anaconda, Inc., is well-known for its ability to create isolated spaces (called environments) for your projects, ensuring that the software packages of one project don't interfere with those of another. Mamba is a faster version of Conda, doing the same job but more quickly. Both of them support many programming languages, making them versatile tools for managing software in your projects.

Install [Mambaforge](#) in your home directory

Cookiecutter

A command-line utility that creates projects from cookiecutters (project templates), e.g. creating a Python package project from a Python package project template.

Install [cookiecutter](#) using mamba

Snakemake

Snakemake is a versatile, Python-based workflow management system that enables the creation of reproducible and scalable data analyses. It operates on the principle of defining “rules” that explicitly state how to produce output files from input files. These rules, which can incorporate shell commands or scripts in any language, are written in a Snakefile. Snakemake takes care of determining the correct order of rule execution based on their dependencies. It also supports parallelization of jobs, making it suitable for high-throughput computations. Furthermore, Snakemake workflows are self-documenting, meaning they can serve as a record of your data analysis, enhancing reproducibility. It’s widely used in bioinformatics, but its application can extend to any field that involves pipeline-based data analysis.

Install [Snakemake](#) using mamba

Install [sge](#) snakemake profile using cookiecutter

Installing Mamba and Snakemake (Detailed Instructions):

Log into your wynton account and switch to a development node:

```
```{bash}
$ ssh username@wynton.ucsf.edu

$ ssh dev2 (because you can't use "git" on log1)
```
```

In your web browser:

Go to: <https://github.com/conda-forge/miniforge#mambaforge> to find “Mambaforge.”

Then find “Linux” under OS, then “x86_64 (amd64)” under Architecture, then “Mambaforge-Linux-x86_64” under Download. Right-click on the “Mambaforge-Linux-x86_64” link (copying the link).

In your Wynton terminal:

```

```{bash}
$ wget paste_the_mamba_link_here # So, your command looks like: "wget http://etc"

$ bash Mambaforge-Linux-x86_64.sh # make sure that you have this "Mambaforge" file by typi
```

```

Then, accept the license terms when wynton asks you. Confirm the location when wynton asks you. Initialize Mambaforge when wynton asks you.

Mambaforge should now be installed:

You should get the following message:

“Thank you for installing Mambaforge!”

Log out of wynton (write “logout”) and log back in for the changes to take effect: Log first into log1 and then dev2 (or dev1).

Next, do a full installation of Snakemake:

In your web browser:

Go to: https://snakemake.readthedocs.io/en/stable/getting_started/installation.html#

Find the “Full installation” instructions. (The Wynton commands are “conda activate base”, then “mamba create -c conda-forge -c bioconda -n snakemake snakemake”, then “conda activate snakemake”).

Confirm the changes when wynton asks.

In your web browser:

Go to: <https://github.com/AndrewsLabUCSF/sge-wynton> and type the wynton command line instructions:

```

```{bash}
$ mkdir -p ~/.config/snakemake

$ cd ~/.config/snakemake

The final wynton command line,

$ git clone git@github.com:AndrewsLabUCSF/sge-wynton.git (may fail)
```

```

If it fails, follow the instructions in the lab handbook, “Git on the UCSF HPC Server Wynton” in the “Compute” section of the lab handbook to get git clone to work properly.

Note: If you already have the `key_pair` file, overwrite it when wynton asks you.

```
```${bash}
Print rulegraph
snakemake --rulegraph | dot -Tpdf > images/dag.pdf

Install conda/singularity envs, dont run workflow
snakemake --use-conda --conda-create-envs-only
```
```

Git (and Git Clone) on UCSF HPC Server Wynton

On Wynton (open a terminal):

```
$ ssh your_wynton_username@log1.wynton.ucsf.edu
```

You can't use git on log1, so switch to a development node:

```
$ ssh dev2
```

You can't use 'git clone' yet (You need an authorization key):

```
$ git clone git@github.com:AndrewsLabUCSF/sge-wynton.git
```

failure

Generate public/private (ed25519) key pair:

```
$ ssh-keygen -t ed25519 -C your_email_address_assoc_with_GitHub
```

Enter the filename in which to save the key:

```
$ key_pair
```

Enter passphrase (empty for no passphrase):

(optional; You can just hit return)

Enter same passphrase again:

(optional; You can just hit return)

Your identification has been saved in `key_pair`. Your public key has been saved in `key_pair.pub`. The key fingerprint is:

Your `key_fingerprint` your_email_address_assoc_with_GitHub

Type "`ls -la`" to check that your `key_pair` and `key_pair.pub` exist.

Open a connection to your authentication agent:

```
$ eval $(ssh-agent)
```

Agent pid (new number each time)

Move your `key_pair` and `key_pair.pub` files into a new folder called “.ssh”:

```
```{bash}
$ mkdir .ssh # if .ssh doesn't yet exist

$ mv key_pair .ssh

$ mv key_pair.pub .ssh
```
```

SSH-ADD your files and assign the necessary permissions:

```
```{bash}
$ ssh-add .ssh/key_pair

$ chmod 600 .ssh/key_pair.pub

$ ssh-add .ssh/key_pair.pub
```
```

Copy the contents of your `key_pair.pub` file to paste in GitHub (This command gives the file’s contents):

```
$ cat .ssh/key_pair.pub
```

Your_key your_email_address_assoc_with_GitHub

Paste the contents of `key_pair.pub` into the following location:

Log onto GitHub and click on your personal account, then click on “settings”.

Click on “SSH and GPG keys”.

Click on “New SSH key” and paste the entire contents of `key_pair.pub` (including your email address associated with GitHub) into the new “Authentication Key”.

Save this key, after giving a title.

Prepare for “git” and “git clone”:

```
$ ssh -T git@github.com
```

(You may get this message: . . . Are you sure you want to continue connecting (yes/no)?):

```
$ yes
```

On GitHub:

Click on “<> Code” in green on the desired repository page.

Click on SSH.

Copy the code in the box to use in your git clone command (see below) - use the SSH code.

On Wynton:

```
$ git clone git@github.com:AndrewsLabUCSF/sge-wynton.git
```

Success!

Logging out and logging back into Wynton:

```
```{bash}
$ ssh your_wynton_username@log1.wynton.ucsf.edu

$ ssh dev2 (or dev1, etc)
```
```

Open a connection to your authentication agent:

```
$ eval $(ssh-agent)
```

Agent pid (new number each time)

Add your key pair:

```
```{bash}
$ ssh-add .ssh/key_pair

$ ssh-add .ssh/key_pair.pub
```
```

Prepare for 'git' and 'git clone' on Wynton:

```
$ ssh -T git@github.com
```

Hi GitHub_username! You've successfully authenticated, but GitHub does not provide shell access.

Push some previously committed files:

```
$ git push etc
```

Success!

LabScrum

LabScrum adapts the Scrum framework from software development for research laboratories. It applies agile principles to scientific research to improve collaboration and streamline workflows. Research projects are divided into “sprints” with regular communication through stand-ups and retrospectives. This approach helps teams adapt to changes and work efficiently.

LabScrum sprint cycle

Our LabScrum framework is as follows. Every quarter, we identify key milestones. These encompass tasks with firm deadlines like grant applications, progress reports, conference abstracts, and presentations, as well as those with flexible deadlines, such as paper submissions. The quarter is divided into five sprints, each spanning three weeks, with an additional free week. Each sprint involves a planning meeting, four scrum meetings, a review, and a retrospective. Meetings are scheduled on Tuesdays and Thursdays.

Note

This is our initial attempt at implementing LabScrum for project management, and we anticipate making revisions to better suit the lab's needs

Sprint Planning

The objective of the planning meeting is to establish concrete, measurable sprint goals for each team member. Every member should arrive at the meeting with a preliminary sprint plan detailing their overarching goals and the associated subtasks to be accomplished by the sprint's conclusion. This plan is then adjusted based on feedback regarding prioritization and logistics. The sprint goals should align with upcoming quarterly milestones, ensuring they contribute to the lab's long-term research objectives. Employing SMART goals ensures the sprint goals are feasible within the sprint's timeframe.

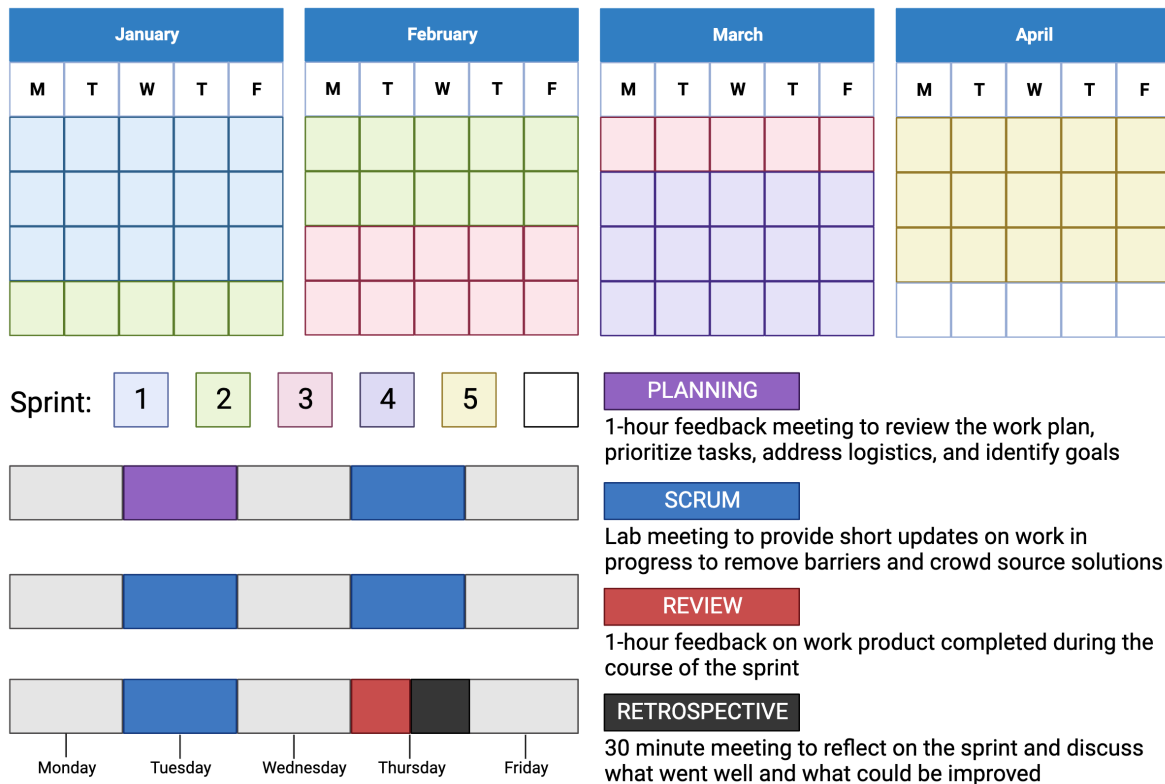


Figure 2: LabScrum Outline



Tip

SMART Goals are **S**pecific **M**easurable **A**chievable **R**elevant **T**ime-Bound.

An example of a SMART-goal statement might look like this: Our goal is to [quantifiable objective] by [timeframe or deadline]. [Key players or teams] will accomplish this goal by [what steps you'll take to achieve the goal]. Accomplishing this goal will [result or benefit].

Scrum meetings

Scrum meetings offer brief updates on each team member's progress. They aim to collectively identify solutions to challenges and pinpoint colleagues who might help. While solutions might become evident during the scrum itself, sometimes a separate discussion with colleagues afterward is necessary. The format for updates isn't rigid; it can be slides, a verbal summary, or even raw code. However, each update should tackle these three key questions:

1. What tasks have you completed since our last meeting?
2. What will you focus on next?
3. Are there any obstacles hindering your progress?

Sprint Review

Upon concluding the sprint, we present the accomplishments of each team member and assess the progress against their initially set sprint goals. This presentation will utilize a slide deck format. It serves as a platform to receive in-depth feedback on the completed tasks, pinpoint challenges faced, prioritize upcoming tasks, and establish new objectives informed by the review and feedback.

Sprint Retrospective

The Sprint Retrospective is held after the sprint review to reflect on the past sprint and identify opportunities to enhance the effectiveness and enjoyment of future sprints. The goal is to foster a culture of continuous learning. By consistently evaluating our methods and results, we ensure that we're continually adapting and evolving based on real-world feedback and experience. The key questions to address are:

1. What went well in the last sprint?
2. What could be improved?
3. What will we commit to improving in the next sprint?

Beyond these central questions, the retrospective also serves as a venue to discuss any issues related to team dynamics, communication, or collaboration. It's also a moment to recognize and appreciate the hard work and contributions of team members. It's important to celebrate successes, both big and small!

Further reading

1. May. 2019. [LabScrum Guide](#)
2. Pirro. 2019. [How agile project management can work for your research](#). Nature.
3. Adam. 2019. [A project-management tool from the tech industry could benefit your lab](#). Nature.
4. Brauer. 2021. [“I’ll Finish It This Week” And Other Lies](#). arxiv.

Finally, watch the [YouTube video](#) from our lab meeting where we initially discuss LabScrum for project management.

Statistical Analysis Plan

A Statistical Analysis Plan (SAP) is a comprehensive, detailed document that outlines the strategies and techniques that will be used to analyze the data collected in a research study. The SAP is crucial for ensuring the integrity and objectivity of the research. It specifies the statistical methods for assessing the primary and secondary outcomes, addresses how to handle missing data, and outlines procedures for any subgroup or sensitivity analyses. By pre-specifying these methods, the SAP helps to prevent bias and data dredging, where researchers might otherwise consciously or unconsciously analyze the data in ways that produce desired outcomes. In essence, the SAP serves as a roadmap for data analysis, guiding researchers to adhere to rigorous, pre-established analytical methods.

Below is a SAP template.

Project Title

Background and Objective:

- Provide a clear statement about what is known about the topic. This should include a review of recent and relevant literature to the proposed research.
- Identify gaps in the existing research or knowledge.
- Define the specific problem or question the research will address.
- State the overall objective of your research. This should be a concise statement of what you hope to achieve with the research.

Planned analysis by Aims:

Break down the general research objective into specific aims. These should be clear, concrete goals that you will work towards throughout your research.

Aim 1:

- Define the first specific aim of your research. This should be a clear, measurable goal that directly contributes to your overall research objective.

Hypothesis:

- Formulate a hypothesis for Aim 1. This should be a specific, testable prediction about what you expect to find in your research.

Rational:

- Explain why you have chosen this particular hypothesis and aim. This should include an explanation of why this hypothesis and aim are important and how they will contribute to the overall field of study.

Primary Proposed Analysis:

- Outline the methods you will use to test your hypothesis. This should include a detailed description of the experimental design, data collection procedures, and statistical methods you plan to use.

Anticipated Problems and Alternative Approaches:

- Discuss potential challenges that may arise during your research, as well as how you plan to address them.
- Include contingency plans for unexpected results or complications.
- Consider possible alternative approaches or methods that could be used if the primary approach doesn't work out.

Secondary, exploratory analysis:

- Explain any additional analyses you plan to conduct that are not directly tied to testing your hypothesis. This could include examining relationships between variables not included in your primary analysis, or investigating unexpected findings.
- Note that while these analyses may provide interesting additional insights, they are considered exploratory because they were not part of the original research plan.

Gantt Chart

- Use a Gantt Chart to visualize and manage the timeline of various analytical tasks and project milestones. This allows researchers to easily see the sequence of tasks, their durations, and any dependencies between them.

References

- List of references

Directory Structure

In any research project, especially those involving data analysis, maintaining an organized and standardized directory structure is crucial. This practice facilitates efficient data management and ensures the reproducibility of your research. Here are some key reasons why standardized directory structures are important:

1. **Ease of Navigation:** A well-organized directory structure allows you and others to easily locate files and understand their purpose. This is particularly beneficial when working in a team or when your project is handed over to another researcher.
2. **Reproducibility:** Reproducibility is a cornerstone of scientific research. A standardized directory structure, coupled with good documentation, allows others to understand and replicate your workflow, enhancing the reproducibility of your research.
3. **Efficiency and Error Minimization:** When directories are organized systematically, it reduces the time spent searching for files and decreases the likelihood of errors that can occur from using incorrect files or versions.
4. **Collaboration and Sharing:** If you're collaborating with others or plan to share your work publicly, a standardized directory structure ensures that your colleagues or the wider research community can understand and use your work effectively.
5. **Long-term Maintenance:** Over time, projects can become more complex. A standardized directory structure can accommodate this growth, making it easier to manage and maintain your project in the long run.

In our lab, we adhere to a specific directory structure that includes separate directories for raw data, processed data, scripts, and output files, among others. This structure is outlined in detail below. By consistently using this structure, we ensure that our work is organized, understandable, and reproducible.

Project Directories

Project level directories should be a dedicated git repository for a specific project adhering to a modified [Snakemake directory structure](#). Project level directories should be located in `/wynton/group/andrews/users/username/project`.

Directory Structure

```
.gitignore
README.md
LICENSE.md
workflow
  rules
|     module1.smk
|     module2.smk
  envs
|     tool1.yaml
|     tool2.yaml
  scripts
|     script1.py
|     script2.R
|     Snakefile
config
  config.yaml
  some-sheet.tsv
results
data
docs
resources
```

To push empty directories while ensuring that large or sensitive files are not inadvertently made available on GitHub, you can add the following .gitignore file. This is useful to included in **resources** or **data** directories.

.gitignore to create empty directories

```
# Ignore everything in this directory
*
# Except this file
!.gitignore
```

Data Directories

Datasets obtained from external sources are housed in the `/wynton/group/andrews/data` directory. Project-level directories create soft links to these resources for easy and efficient access. Each dataset is assigned its own directory, adhering to the following structure.

Directory Structure

```
parent/
  .gitignore
  README.md
  LICENSE.md
  data/
  docs/
```

- `parent` is the top-level directory, and should be named according to the dataset.
- `data` contains the original files downloaded from the external resources. Potential sub-directories can include different releases.
- `docs` contains documentation files such as data dictionaries
- `README.md` contains information about the dataset.

The `README.md` should contain the following information.

README

```
# Data
## Description
This directory contains raw data files downloaded from [repository name]. These files serve

## Data Source
Repository Name: [repository name]
Repository URL: [repository URL]
Date of Access: [date when the data was downloaded]

## Data Files
This section describes the data files included in this directory.

file1.extension: Brief description of what this file contains.
file2.extension: Brief description of what this file contains.
...

## Data Structure
Briefly describe the structure of the data. For example, if the data is tabular, describe t

### Data Download and Processing
Describe the process of downloading the data from the repository and any steps taken to pro

## Usage Notes
```


Include any additional information that users of the data should be aware of. This could include:

Contact Information

For any additional questions or clarifications, please contact:

Name: [Your name]

Email: [Your email]

Grants

UCSF Office of Sponsored Research

- [PI Desk Reference](#): Key resources from the UCSF Office of Sponsored Research for grant submission
- [DPBS Intranet](#)

Journal Club

Journal clubs serve as a critical cornerstone in the ongoing education and professional development of researchers, clinicians, and students alike. They provide a structured yet collaborative environment for dissecting and discussing current research papers in depth. Not only do these sessions enhance critical thinking and appraisal skills, but they also keep participants abreast of the latest advancements and methodologies in their field. Furthermore, journal clubs foster a culture of collective learning and interdisciplinary dialogue, enabling the exchange of diverse perspectives and insights. This enriches the understanding of complex topics and often sparks innovative ideas for future research endeavors.

How to find papers

Shea has established an RSS feed to stay updated on newly published papers. Utilizing [Feedly](#), he follows approximately 40 journals, receiving daily updates. Each morning, Shea skims through paper titles to identify articles of interest. He then reviews selected abstracts and fully reads a few of the more compelling papers. Additionally, he uses X (formerly Twitter) to discover papers that are being discussed or shared by other researchers in the field.

Shea follows all the journals in which he has published, as they are presumably relevant to his research. He also keeps tabs on other high-impact journals in the field, as well as the Pre-print servers BioRxiv (Genetics) and MedRxiv (Genetic And Genomic Medicine).

Some suggested journals are:

- Nature
- Science
- Alzheimer's & Dementia
- JAMA Neurology
- Lancet Neurology
- Nature Genetics
- The American Journal of Human Genetics

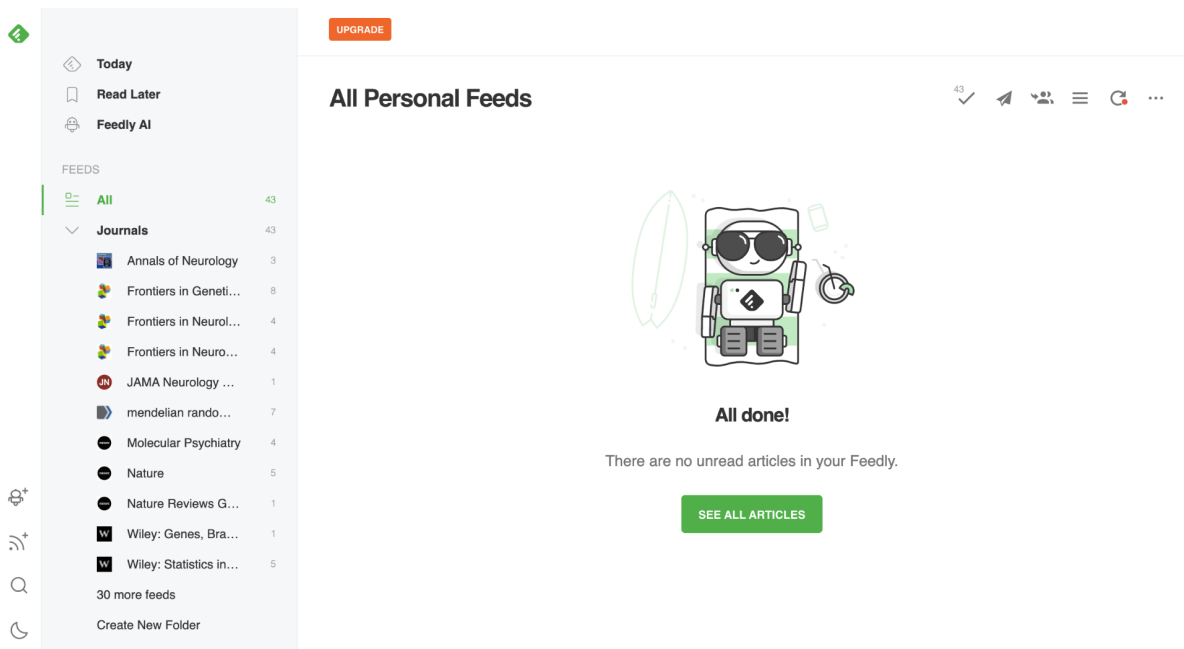


Figure 3: Shea Feedly

Structure

This is a suggested structure for Journal Club presentations. Presenters should aim for a presentation length of about 30 minutes, followed by a discussion period.

The Introduction: Start the presentation by introducing the paper, authors, and affiliations. Share what specifically attracted you to this paper. Was it the topic, the methodology, or something else? Briefly mention why this paper is important to the lab's work or the field in general.

The Problem: This section should clearly state the problem or the project that the research is addressing. It should be concise and to the point, providing enough context for the reader to understand the importance of the research. This section often includes a brief overview of the current state of knowledge or research in the field.

The Methods: Summarize the main methods and research techniques that are relevant to the results being presented. Briefly mention where the data comes from, if relevant.

The Results: This section should detail the main findings or observations of the research. It should explain what was discovered or observed and how it was done. This section often includes specific details about the methods used in the research.

Critical analysis: Discuss what the paper does well. This could be anything from innovative methods to significant findings. Point out areas where the paper falls short. This could be

limitations in the study design, data collection, or interpretation of results. Evaluate the validity of the results and the soundness of the methodology. Are the conclusions supported by the data?

The Implications: This section should discuss the implications of the research findings. It should explain how the findings contribute to the field and what they mean for future research. This section often includes speculation or predictions about future developments in the field based on the research findings.

Reading List

This curated list of references is an essential part of our shared knowledge base, designed to provide you with a solid foundation and a deeper understanding of the fields we are passionate about: genetic epidemiology and neurodegenerative disease. You will also find readings on other aspects of the scientific enterprise such as writing, presentations, and career development.

The references included here have been carefully selected for their relevance, clarity, and contribution to our field. They range from seminal papers that have shaped our understanding of genetic epidemiology and neurodegenerative disease, to the latest cutting-edge research that pushes the boundaries of what we know. You will also find comprehensive textbooks, insightful reviews, and practical guides that cover the methodologies, tools, and techniques we use in our lab.

Whether you are a new member seeking to familiarize yourself with our field, or an experienced researcher looking to stay abreast of the latest developments, this reading list is a valuable resource. We encourage you to delve into these materials and explore the fascinating world of genetic epidemiology and neurodegenerative disease.

Remember, learning is a lifelong journey, and science is continually evolving. This reading list is not static but will be updated periodically to reflect new discoveries and advancements in our field. We also welcome your suggestions for additions to the list, as we believe that everyone in our lab can contribute to our collective learning.

Alzheimer's disease

What is AD

- Knopman, D. S. et al. Alzheimer disease. *Nat Rev Dis Primers* 7, 33 (2021).
- Alzheimer's Association. 2023 Alzheimer's disease facts and figures. *Alzheimer's Dementia* (2023) doi:10.1002/alz.13016.
- Sirkis, D. W., et al. Dissecting the clinical heterogeneity of early-onset Alzheimer's disease. *Mol Psychiatr* 27, 2674–2688 (2022).
- Frisoni, G. B. et al. The probabilistic model of Alzheimer disease: the amyloid hypothesis revised. *Nat Rev Neurosci* 23, 53–66 (2022).

Health Disparities

- Kornblith, E. et al. Association of Race and Ethnicity With Incidence of Dementia Among Older Adults. *Jama* 327, 1488–1495 (2022).
- Adkins-Jackson, P. B. et al. The structural and social determinants of Alzheimer’s disease related dementias. *Alzheimer’s Dementia* (2023) doi:10.1002/alz.13027.

Genetics of AD

- Andrews, S. J. et al. The complex genetic architecture of Alzheimer’s disease: novel insights and future directions. *eBioMedicine* 90, 104511 (2023).
- Reitz, C., Pericak-Vance, M. A., Foroud, T. & Mayeux, R. A global view of the genetic basis of Alzheimer disease. *Nat Rev Neurol* 1–17 (2023) doi:10.1038/s41582-023-00789-z.
- Lambert, J.-C., Ramirez, A., Grenier-Boley, B. & Bellenguez, C. Step by step: towards a better understanding of the genetic architecture of Alzheimer’s disease. *Mol Psychiatr* 1–12 (2023) doi:10.1038/s41380-023-02076-1.
- Andrews, S. J., Fulton-Howard, B. & Goate, A. Interpretation of risk loci from genome-wide association studies of Alzheimer’s disease. *Lancet Neurology* 19, 326–335 (2020).
- Bellenguez, C. et al. New insights into the genetic etiology of Alzheimer’s disease and related dementias. *Nat Genet* 54, 412–436 (2022).
- [Alzheimer’s Disease Genetics Global Symposium](#). Webinar series with 40+ presentations and a Q&A discussion from global experts in the field of AD genetics.

Risk factors

- Livingston, G. et al. Dementia prevention, intervention, and care: 2020 report of the Lancet Commission. *Lancet* 396, 413–446 (2020).
- Nianogo, R. A. et al. Risk Factors Associated With Alzheimer Disease and Related Dementias by Sex and Race and Ethnicity in the US. *Jama Neurol* 79, 584–591 (2022).

Dementia risk scores

- Anstey, K. J. et al. Dementia Risk Scores and Their Role in the Implementation of Risk Reduction Guidelines. *Front Neurol* 12, 765454 (2022).
- Huque, M. H. et al. CogDrisk, ANU-ADRI, CAIDE, and LIBRA Risk Scores for Estimating Dementia Risk. *JAMA Netw. Open* 6, e2331460 (2023).
- Walsh, S. et al. What would a population-level approach to dementia risk reduction look like, and how would it work? *Alzheimer’s Dement.* 19, 3203–3209 (2023).

Genetic Epidemiology

- [Psychiatric Genomics Consortium Online Textbook](#): YouTube series from the PGC highlighting different methods and tools used in genetic epidemiology.

Genome-wide association studies

- Uffelmann, E. et al. Genome-wide association studies. *Nat Rev Methods Primers* 1, 59 (2021).
- Marees, A. T. et al. A tutorial on conducting genome-wide association studies: Quality control and statistical analysis. *Int J Method Psych* 27, e1608 (2018).
- Balagué-Dobón, L., Cáceres, A. & González, J. R. Fully exploiting SNP arrays: a systematic review on the tools to extract underlying genomic structure. *Brief Bioinform* 23, bbac043 (2022).
- Abdellaoui, A., Yengo, L., Verweij, K. J. H. & Visscher, P. M. 15 years of GWAS discovery: Realizing the promise. *Am J Hum Genetics* (2023) doi:10.1016/j.ajhg.2022.12.011.
- Brandes, N., Weissbrod, O. & Linial, M. Open problems in human trait genetics. *Genome Biol* 23, 131 (2022).

Polygenic risk scores

- Choi, S. W., Mak, T. S.-H. & O'Reilly, P. F. Tutorial: a guide to performing polygenic risk score analyses. *Nat Protoc* 15, 2759–2772 (2020).
- Kachuri, L. et al. Principles and methods for transferring polygenic risk scores across global populations. *Nat. Rev. Genet.* 1–18 (2023) doi:10.1038/s41576-023-00637-2.
- Ding, Y. et al. Polygenic scoring accuracy varies across the genetic ancestry continuum. *Nature* 1–8 (2023) doi:10.1038/s41586-023-06079-4.
- Moorthie et al. Evaluation of polygenic score applications. [PHG Foundation \(2023\)](#)

Mendelian randomization

- Sanderson, E. et al. Mendelian randomization. *Nat Rev Methods Primers* 2, 6 (2022).
- Davies, N. M., Holmes, M. V. & Smith, G. D. Reading Mendelian randomisation studies: a guide, glossary, and checklist for clinicians. *Bmj* 362, k601 (2017).
- Hemani, G. et al. The MR-Base platform supports systematic causal inference across the human phenome. *Elife* 7, e34408 (2018).

Genetic correlations

- Rheenen, W. van, Peyrot, W. J., Schork, A. J., Lee, S. H. & Wray, N. R. Genetic correlations of polygenic disease traits: from theory to practice. *Nat Rev Genetics* 20, 567–581 (2019).

Heritability

- Barry, C.-J. S. et al. How to estimate heritability: a guide for genetic epidemiologists. *Int J Epidemiol* (2022) doi:10.1093/ije/dyac224.

Genetic ancestry

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Part IV

Conclusion

Signatures

As we conclude this handbook, we affirm our commitment to excellence, collaboration, and integrity. This document not only outlines our shared values and expectations but also serves as a testament to our collective dedication to advancing science and fostering a supportive, inclusive environment. Your signature below signifies your agreement to uphold these principles, contributing to our lab's success and the broader scientific community.

| Name | Role | Date |
|--------------|------|------------|
| Shea Andrews | PI | 2024-02-17 |

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