

# Writing the NAR Paper

Thoughts and experiences

# Tip 1: Follow Cath's Tips

## TIPS

1. Start ASAP. It all takes more time than you think. I think so anyway!
2. Negotiate more "NAR time" with your manager if needed
3. Read other browser's NAR updates, like Ensembl
4. If it's not new, don't include it. This refers to a long introduction or summaries of categories.
5. Forget about the past "template" and shorten the NAR
6. Supplemental data are a great way to include tables & images without counting against your allotted page count.
7. Have boundaries with internal reviews, do these in stages with small groups.
8. Make a calendar and work backward.
9. Start with a clear outline
10. Keep it simple





## Takeaways from writing it.

- ***Give Yourself Time:*** schedule a calendar backward.
- ***Think Small:*** maybe start your paper in the NAR MS word template to avoid bloat.
- ***Let [newsarch.html](https://www.nar.org/newsarch.html) guide you:*** it may help limit yourself to newsworthy items.
- ***Visit the NAR site earlier:*** no harm seeing the submission steps before the end.

# Read previous NAR papers

- 2021 <http://www.ncbi.nlm.nih.gov/pmc/articles/PMC7779060>
- 2020 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC7145642>
- 2019 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6323953>
- 2018 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5753355>
- 2017 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5210591>
- 2016 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4702902>
- 2015 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4383971>
- 2014 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3964947>
- 2013 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3531082>
- 2012 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3245018>
- 2011 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3242726>
- 2010 <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2808870>

Just read them, avoid spending too much time on this step.



# Possible Outline Model (not req.)

**ABSTRACT**

**INTRODUCTION**

**NEW DATA IN THE GENOME BROWSER**

- -subsection 1
- -subsection 2
- -subsection 3 - as makes sense

**NEW SOFTWARE FEATURES IN THE GENOME BROWSER**

- -subsection 1
- -subsection 2
- -subsection 3 - as makes sense

**FUTURE PLANS**

**OUTREACH AND CONTACT INFORMATION**

**ACKNOWLEDGEMENTS**

**FUNDING**

**REFERENCES**

# Make a REAL Outline of the MEATY Section

Let [newsarch.html](#) guide you

## ANNOTATIONS AND VISUALIZATIONS (new data)

-Some Title 1

Put list of overview thoughts here

-Some Title 2

Put list of overview thoughts here

-Some Title 3

Put list of overview thoughts here

## SOFTWARE AND TOOL IMPROVEMENTS (new software)

-Some Title 1

Put list of overview thoughts here

-Some Title 2

Put list of overview thoughts here

-Some Title 3

Put list of overview thoughts here

# COMMIT TO A SUMMER SCHEDULE >>>MEMORIAL DAY TO LABOR DAY<<<

Reverse Order Schedule starting with September Due Date

Week end 9/Z: (9/15 Due)

Week end 9/Z: (Labor Day Holiday)

Week end 9/Z:

Week end 8/Y: FINALIZED DRAFT TO ENTIRE TEAM

Week end 8/Y:

Week end 8/Y: DRAFT2 REVIEW TEAM\_2

Week end 8/Y: (Vacation\_2 if planned 8/A-8/B)

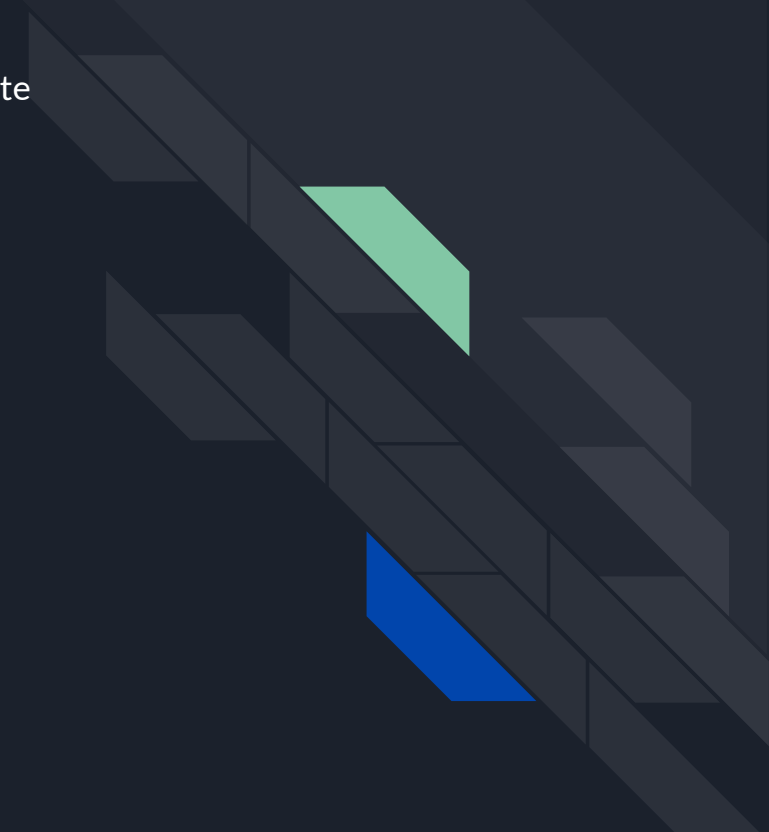
Week end 7/X:

Week end 7/X: DRAFT1 REVIEW TEAM\_1

Week end 7/X: (Vacation\_1 if planned 7/A-7/B)

Week end 7/X: (4th July Holiday)

Week end 7/X: (Memorial Day Holiday)





MID JULY:

Share Schedule with Review Teams

Share your complete outline - and revisions

People have summer vacations so your schedule has to also meet your REVIEW TEAM\_1 and REVIEW TEAM\_2 plans.

Sharing your Skeleton Outline, at least to REVIEW TEAM\_1 can save you a ton of pain.

Reworking your paper is way easier before you have written a full draft that may need to be entirely reconstructed.



Listen to the input you get from your review team on your outline.

Consider it a blessing to get this input before you've spent too much time writing. If need be, resubmit outline several times.

It is worthwhile to do a meeting with your review team to talk about the outline after they have looked at it.



# WRITING: Knock out easy sections first

**AUTHOR LIST:** ask management to verify your proposed list.

## **FUTURE PLANS**

- anything that won't be out by Sep 15th NAR deadline
- check with Project Manager to get sign-off on text early

## **OUTREACH AND CONTACT INFORMATION**

- model from previous versions

## **ACKNOWLEDGEMENTS**

- model from previous versions

## **FUNDING**

- contact finance early (was Rochelle Fuller)
- get spreadsheet matrix of funding per person
- use it to map onto previous versions of this section

# WRITING: avoid explaining the site

## ABSTRACT

-Do this last, it will be clearest when the paper is done.

## INTRODUCTION

-This has the potential to be the biggest pitfall

*Don't try to explain or introduce the site*

*Just introduce what your paper is about (new data & software)*

If need be, write a blog post so you can vent desires to explain how the site works. Then reference that blog post in your paper's introduction.

# WRITING: the MEAT

## NEW DATA

- Doing Images first can help you break this down
- Ask for help to get a Track List & Public Hubs List from the team  
(Progress Report author may know who did these tasks earlier)

## NEW SOFTWARE

- Doing Images first can help you break this down
- Write about what excites you, it probably will excite readers



Miscellaneous thoughts on breaking through  
procrastination and painful writer's block:

*Outdoor Exercise*

*Uplifting Music*

*Taking a Shower*

*Walk & Talk Meeting*

*Working Late Nights*

*Subsection Deadlines*

# WRITING: the abstract

Excerpts from abstracts of years past:

*New features released this past year...*

*New data tracks added...*

*This year's highlights include... Some release highlights of this year...*

*Highlights of the past year include the release of...*

*In the past year, we have, New datasets include, his year, we added a new tool that lets users...*

*We created browsers for... New software tools include...*

*Further, a large number of annotation tracks have been either added...*

*This year we have introduced...*

*Among the features released this year are... New display enhancements include...*

*We also describe updates to existing tracks... New data highlights this year include...*

# It's best to polish your draft

Before handing it off, and after revisions, reread your paper out loud, several times. This helps you spot troubled areas. 🚧 ⚠️ 🚧

Use Google Doc to collaborate your drafts with the team.

If you need more time talk with your review team, it is likely OK.

On the other hand, make your crunch time deadlines in the middle of the summer, not the end, to avoid excessive stress.

# FINAL STRETCH: submission

References: Don't use the "NAR Web Server Issue" in Zotero style that adds URLs (no URLs)

Images: You can use dev's "[convert](#)" tool or websites to ensure images are 300dpi.

Referees: Ask the team for list and add the names you finally use to the existing [Google Doc](#) (from Cath's Presentation).

# Responding to Referees

Share responses in Google Doc with top author team, include people as needed for topics (i.e., engineer of new tool for questions on tool).

Get internal team to sign off on your draft response.

One mode of responding is reply in **red text** with an opening paragraph thanking the reviewers for their assistance improving your manuscript. Then place their bullet point items inline in normal black text and respond to each one by one **in more red writing.**

## Dear Reviewers,

Thank you for your time reviewing this manuscript and for writing up your much appreciated comments. We have taken steps to address suggestions, making changes to the paper to increase clarity where applicable with some notes here to describe some background history and related future work. For context, we have placed our replies below your input and have noted where we revised the manuscript in response to your suggestions. Thank you again for your excellent review and your help improving this submission.

Brian Lee

## Specific comments

Referee: 1

### 1. GenArk support and display

When browsing the UCSC GenArk section, it was unclear that the lists of species being presented are overlapping. At first glance I assumed they were non-overlapping sets. I believe my confusion came from seeing both taxonomic groupings and projects in the same display. I am not sure if there's a way of making this clear to users when they come to use the site.

Thank you for this observation about the list of species being presented as having overlapping species, which is likely coming from visiting our current Genome Archive (GenArk) homepage (<https://hubsdownload.soe.ucsc.edu/hubs/>). We will be working to make this page more clear and informative in the future as we work towards a future manuscript to outline the specific software methods generating and supporting these GenArk hubs. For some history, the sets of hubs on this page are almost all non-overlapping, specifically all the hubs that reference NCBI, however, in working up to the current inclusion of the new NCBI labeled hubs, earlier previous hubs, notable the mouse strains hub and the Vertebrate Genomes Project hub, were created and placed at this 'hubs' page first. These previous public hubs, which account for some of the overlapping species you are noting, inspired the systems to generate the new NCBI-based public hubs separated into various taxonomic groups such as primates, mammals, and birds as described. Your comment is very helpful as it will aid us to clarify these details both on this GenArk homepage, and in our future paper describing the methodologies generating these assembly hubs.

### 2. Recommended track sets

Recommended track sets are an excellent idea and more browsers should have them. I did not read any plans for additional track sets UCSC would offer. Are the more clinical focussed sets the limits of what will be done? Are there other track sets the authors believe will be of interest to others?