Overview

Your abstract is usually a short paragraph of 200-300 words, or you can say 8-10 sentences, that helps your reader get a good sense of what your research is about, and helps them decide if your paper is something they will decide to read. If you say 8-10 sentences, I’ve found it useful to have 1-2 sentences on background and research question, 1-2 sentences on design and methods, 2-3 sentences on results, and 1-2 sentences on discussion and interpretation. It should encompass these basic things: the purpose of your study and brief background of the research question, the key design of your study and methods used, major findings, and key interpretations of the result (their significance). Here we have a checklist guide for before and after an abstract is drafted.

1. **Like your thesis, it should summarise and put forth the argument.**
   **(And it should be written last, after your paper is done.)**

   It would be impossible to try to write the abstract before you have figured out the flow of your research experiments, methodology, and explaining the significance of your data. Just like how you might revise your thesis statement multiple times throughout the process of writing any scholarly research paper, the scientific abstract (ideally) is the essence you have managed to obtain from your results to present the ‘so what’ of your research. It is often good practice to re-write the abstract multiple times in different ways, and see which one works best. Always re-read the abstract to check for any errors!

2. **Introduce the background and question or questions that your research tackles.**
   **(1-2 sentences)**

   Precisely because many hypotheses that require an entire research study to be conducted are highly complex and sophisticated, the abstract is challenging to write because it needs to summarise this particular problem. Or rewrite this sentence as: The abstract is challenging to write because oftentimes, your research study is highly specialized and complex. It is thus useful to think about how to best contextualise your study and its importance to the field and to highlight the specific question you have tackled in your paper. Giving a universal or vague description of your research will not encourage others chancing upon your paper in an online search to read the whole study.

3. **Outline research design and methodology (1-2 sentences)**

   Similarly, complex series of actions must be distilled into an overall method (with caveats if necessary) to explain the design of your research. What have you done in your experiment that is novel or different from what scholars before you have done? Depending on the complexity of your paper, you may also want to write for a target audience and use the ‘lingo’ of their field. This way, there is more detail at how you have arrived at your results, which directly segues into how and why they are significant the way they are.

4. **Summarise key results (2-3 sentences)**

   A key mistake made by junior scholars is over-excitement —and hence oversharin their results in the abstract. A good way to make sure that you are not reporting too much or too
little of your results and data is to evaluate the existing papers in the field and what may be the most valuable information that you have obtained through research, and this information should be necessary and sufficient to help someone begin to understand your overall ‘thesis’ or stance on the significance of your result. It would also be important then to check back into the field you are writing for as to how much detail would be sufficient to describe key findings, for example, reporting the numbers of significance testing (p-tests, t-test, z values).

5. **Summarize your interpretation of the results (1-2 sentences)**
The interpretation of your results should be a nuanced answer to your research question. There may be caveats and other lessons, but always find a way to put your results in context.

6. **Check for the style of abstract-writing in your specific discipline or journal.**
At this point, congratulations may be in order if your paper is being published in a journal! The word count, style, and format of the scientific abstract for publication in journals may differ. Check with your supervisor or editors to ensure that you have done everything correctly, while not compromising on the key points mentioned above. Electronic journals (and some professors) may allow for hyperlinks to be included in the abstract to allow the reader to click-through to the information that helps you explain your research. In that case, choose your hyperlinks carefully so as not to lead the reader through too many sites or other papers, to provide them with the most important information required to better understand your research at the level of the abstract.

**Example Abstract**

Lemurs and the other strepsirrhine primates are of great interest to the primate genomics community due to their phylogenetic placement as the sister lineage to all other primates. Previous attempts to resolve the phylogeny of lemurs employed limited mitochondrial or small nuclear data sets, with many relationships poorly supported or entirely unresolved. We used genomic resources to develop 11 novel markers from nine chromosomes, representing ~9 kb of nuclear sequence data. In combination with previously published nuclear and mitochondrial loci, this yields a data set of more than 16 kb and adds ~275 kb of DNA sequence to current databases. Our phylogenetic analyses confirm hypotheses of lemuriform monophyly and provide robust resolution of the phylogenetic relationships among the five lemuriform families. We verify that the genus *Daubentonia* is the sister lineage to all other lemuriform taxa. The Cheirogaleidae and Lepilemuridae are sister taxa and together form the sister lineage to the Indriidae; this clade is the sister lineage to the Lemuridae. Divergence time estimates indicate that lemurs are an ancient group, with their initial diversification occurring around the Cretaceous-Tertiary boundary. Given the power of this data set to resolve branches in a notoriously problematic area of primate phylogeny, we anticipate that our phylogenomic toolkit will be of value to other studies of primate phylogeny and diversification. Moreover, the methods applied will be broadly applicable to other taxonomic groups where phylogenetic relationships have been notoriously difficult to resolve.