How to Read a Scientific Article

Don't try to read the entire article all at once, from start to finish. Instead, take a step-by-step approach.

- **Read the abstract.**
  The abstract is a brief summary of the article. It should give you an overview of what the paper is about and what the authors' research accomplished. If the content of the paper does not seem to meet your expectations and will not help you answer your questions, you may want to choose another article.

- **Skim the article.**
  Look at the section headings and any figures or tables, taking time to read the captions.

- **Go back and carefully read the entire article, section by section.**
  Write down any questions you have about the article while you're reading it; that way, you can see if the authors answer your questions later in the article. Focus on the Introduction, Results, and Conclusion, and don't get bogged down in the methods.

*Note:* Look up any words that you don't understand. Use a science dictionary or biology dictionary for scientific terms. If you still don't understand some concepts in the article, even after reading it several times, ask your instructor for help.

References:
Parts of a Scientific Article

Title/Author
The title of the article, the authors' names, and the authors' addresses are usually the first prominent parts of the article.

The authors' addresses are provided to show their affiliation with a particular research institution and allow other scientists to contact them regarding their research:

1 Max Planck Institute for Evolutionary Anthropology, Leipzig, Germany, 2 Laboratoire d'Anthropologie, Paris, France, 3 Laboratoire de Génétique et Biométrie, Université de Genève, Switzerland, 4 Institute of Anthropology, Natural History Museum, Vienna, Austria, 5 Institute of Quaternary Paleontology, Academy of Sciences and Arts, Zagreb, Croatia, 6 Ångström Laboratory, Uppsala University

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Abstract
The abstract is a paragraph summarizing the content of the article. Read the abstract first to see if the article will be useful to your research:

The retrieval of mitochondrial DNA (mtDNA) sequences from four Neandertal fossils from Germany, Russia, and Croatia has demonstrated that these individuals carried closely related mtDNAs that are not found among current humans. However, these results do not definitively resolve the question of a possible Neandertal contribution to the gene pool of modern humans since such a contribution might have been erased by genetic drift or by the continuous influx of modern human DNA into the Neandertal gene pool. A further concern is that if some Neandertals carried mtDNA sequences similar to contemporaneous humans, such sequences may be erroneously regarded as modern contaminations when retrieved from fossils. Here we address these issues by the analysis of 24 Neandertal and 40 early modern human remains. The biomolecular preservation of four Neandertals and of five early modern humans was good enough to suggest the preservation of DNA. All four Neandertals yielded mtDNA sequences similar to those previously determined from Neandertal individuals, whereas none of the five early modern humans contained such mtDNA sequences. In combination with current mtDNA data, this excludes any large genetic contribution by Neandertals to early modern humans, but does not rule out the possibility of a smaller contribution.

Introduction
The introduction presents the research question being asked. It explains the context of the research and often discusses previous work that was done on the topic:

Despite intense research efforts, no consensus has been reached on the genetic relationship between early modern humans and archaic human forms such as the Neandertals. While supporters of “multiregional evolution” argue for genetic exchange or even continuity between archaic and modern humans (Weidenreich 1943; Wolpoff et al. 1984, Wolpoff et al. 2000, Duarte et al. 1999, Hawley and Wolpoff 2001), proponents of a “single African origin” of contemporary humans claim that negligible genetic interaction took place (Cann et al. 1987; Stringer and Andrews 1988; Ingraham et al. 2000, Underhill et al. 2000, Stringer 2002). Mitochondrial DNA (mtDNA) sequences from early modern humans who lived in principle would be able to resolve the question of a contribution of Neandertal mtDNA to modern humans. However, human DNA is pervasive in paleontological and archaeological remains as well as in most laboratory environments (e.g., Krings et al. 2000; Hofreiter et al. 2001b, Waudler et al. 2003). It is therefore currently impossible to differentiate contaminating modern DNA sequences from endogenous human DNA in human remains. Thus, although mtDNA sequences have been reported from remains of early modern humans (Adcock et al. 2001; Caramelli et al. 2003), it is not possible to determine whether such DNA sequences indeed represent endogenous DNA sequences (Abbott 2003). A related problem is that if a Neandertal fossil yields modern human-like DNA sequences, those might be discarded as putative contaminations (Nordborg 1998, Trinkaus 2001), even if they may be endogenous and represent evidence for a closer genetic relationship or interbreeding between the two groups.
Methodology/Procedures

The methods section (sometimes called materials and methods) discusses how the research was conducted. It explains what materials were used and what procedures were followed to perform an experiment:

Materials and Methods

**Amino acid preservation** About 10 mg of bone were removed from each specimen and analyzed as in Schmitz et al. (2002) with minor modifications. In brief, proteins are hydrolyzed and amino acids labeled with p-phthaldehydride/N-acetyl-L-cysteine and analyzed by high-performance liquid chromatography (Shimadzu, Kyoto, Japan) under conditions that separate the different amino acids as well as their stereoisomers. Eight amino acids are analyzed and their respective concentration measured: D- and L-alanine, glycine, D- and L-aspartic acid, serine, glutamic acid, valine, D- and L-leucine, and isoleucine.

Results/Discussion

This section presents the results of the research. The information is often presented in a table or chart format and show statistical calculations performed on the data.

Results and Discussion

The preservation of endogenous DNA in fossils is correlated with the amount, composition, and chemical preservation of amino acids (Pomar et al. 1996). We find that endogenous DNA can be amplified from Pleistocene remains when the amino acid content is more than 30,000 parts per million (ppm), the ratio of glycine to aspartic acid between two and ten, and the aspartic acid racemization (i.e., the stereoisomeric D/L ratio) less than 0.10 (Pomar et al. 1996; Krings et al. 1997, 2000; Schmitz et al. 2002; data not shown). We analyzed the amino acid preservation of 24 Neandertal and 40 early modern human fossils (Table S1). Several important Neandertal fossils, such as La Ferrasie and Krapina, as well as important modern human fossils, such as Veternica, proved to be too poorly.
6. Conclusion
In the conclusion, the authors explain how their results of their research have addressed their research question. They may suggest where further research is needed:

Concluding Remarks
It is noteworthy that under the model of constant population size, about 50 early modern human remains would need to be studied to exclude a Neandertal mtDNA contribution of 10%. To exclude a 5% contribution, one would need to study more early modern human remains than have been discovered to date. Thus, definitive knowledge of the extent of a putative contribution of Neandertals to the modern human gene pool will not be possible, although extensive studies of variation in the current human gene pool may clarify this question (Wall 2000). It is, however, worthwhile to note that samples considered as anatomically “transitional” between modern humans and Neandertals, such as Vindija (Smith 1994; Wolpoff 1999) and Madeč (Frayer 1986, Frayer 1992; Wolpoff 1999), analyzed here, fail to show any evidence of mtDNA admixture between the two groups. Thus, while it cannot be excluded that Neandertals contributed variants at some genetic loci to contemporary humans, no positive evidence of any such contribution has yet been detected.

7. References
The references section presents publications that the author cited in his work. Read the articles the author has cited to find out more about your topic.

References

Source: Adapted from the CSUS Biology Library Research Tutorial