# Article information:

Pitfalls reconstructing the last common ancestor of chimpanzees and humans | PNAS  
<https://www.pnas.org/doi/full/10.1073/pnas.1524165113>

# Article summary:

1. The study by Young et al. attempted to reconstruct the last common ancestor of chimpanzees and humans using novel methodological approaches, focusing on scapular shape data.

2. Criticisms of the study include unclear biological meaning of the shape data, failure to consider allometric trends, biased conclusions favoring a Pan-like ancestor, and lack of testing alternative evolutionary models.

3. The complexity of reconstructing the mosaic anatomy of the last common ancestor is highlighted, emphasizing the need to consider gene regulation and the mosaic nature of ape and human evolution in understanding phenotypic differences despite genetic similarities.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

The article "Pitfalls reconstructing the last common ancestor of chimpanzees and humans" published in PNAS raises important criticisms of a study by Young et al. that attempts to reconstruct the anatomy of the last common ancestor (LCA) of chimpanzees/bonobos and humans. The author points out several key issues with the methodology and conclusions of the study, highlighting potential biases and shortcomings.

One major criticism is regarding the unclear biological meaning of the shape data used in the analysis by Young et al. The author argues that using allometric residuals without demonstrating a common allometric trend in the sample can lead to misleading results. Additionally, it is pointed out that Young et al. favor a Pan-like LCA despite evidence showing opposite evolutionary directions between Pan and Homo along major axes of shape variation.

Furthermore, the author questions the validity of using a simulated Australopithecus afarensis adult as an intermediate point in the evolutionary model, especially when actual A. afarensis adults fall within different variation groups. The lack of testing alternative models of evolution and assuming equal branch lengths in their phylogenetic trees are also highlighted as significant pitfalls in the study.

The article emphasizes that phylogenetic proximity does not necessarily predict phenotypic evolution, citing the remarkable phenotypic differences between Homo and Pan despite sharing 99% of their genes. This underscores the complexity and mosaic nature of ape and human evolution, cautioning against oversimplified interpretations based on single anatomical features.

Overall, this critical analysis provides valuable insights into potential biases, methodological flaws, and limitations in the study by Young et al., urging for more comprehensive approaches to reconstructing ancestral morphologies in human evolution. It serves as a reminder to consider multiple lines of evidence, avoid assumptions about evolutionary trajectories, and acknowledge the intricate nature of hominoid evolution when interpreting fossil data.

# Topics for further research:

* Evolutionary trends in Pan and Homo anatomy
* Allometric scaling in primate evolution
* Phylogenetic methods in reconstructing ancestral morphologies
* Phenotypic divergence in human and chimpanzee evolution
* Australopithecus afarensis variation and phylogenetic relationships
* Mosaic evolution in hominoids and its implications for human origins

# Report location:

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