

Reviews in Computational Biology

7. Effective Citations



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General rule

- **Put reference at the end, as evidence for your statement (concise, unobtrusive).**

“Curiously, viruses from one branch of Archaea resemble tailed phages in morphology and genome organization (Pfister et al., 1998).”

“When this cell is infected, the phage drives the replication of the plasmid, and no longer drives its own DNA replication (Brüssow, 2001).”

\citep{key1,
key2}

“Indeed, several authors have followed this route (Rocha and Danchin 2004; Agrafioti et al. 2005)”

- **Same thing with figures, tables, etc.**

“Myoviridae have a long contractile tail (Figure 1).”

Two Exceptions

\citet{key}

- **If the author name is part of the sentence, follow with date in parenthesis.**

“Techniques for summarizing multiple trees using split networks are described in Bandelt (1995), Holland et al. (2004), and Huson et al. (2004).”

- **If the citation only applies to part of the sentence, add at the end of that part.**

“[H]igher expressed genes have higher CAIs (Akashi 2001), are less dispensable (Gu et al. 2003), more abundant (Ghaemmaghami et al. 2003), and more likely to be found in protein-protein interaction experiments (Bloom and Adami 2003) than lower expressed genes.”

How about numbered citations?

- In general, no difference

“The Eulerian path strategy was inspired by early work on sequencing by hybridization (SBH) [35].

“These programs have been critical to the success of many recent genome projects including mammals [3], plants [10] and worms [11].”

- But explicit mention of author and/or date is sometimes appropriate

“Since the introduction of the chain termination sequencing method by Frederick Sanger in 1977 [1], the genomes of more than 800 bacteria and 100 eukaryotes have been sequenced, including the genomes of several human individuals [2–4].”

“Using previous data of Grainger et al. [17], who had determined ...”

Wright or Rong?

- “Under the correct model, ML is always consistent, while under over-simplistic models, this is not always true and has to be taken into account (see Yang, 1994).”
- “The idea of representing the history of evolution by a tree structure goes back to Darwin (Darwin, 1860).”
- “Another relevant tool is that of the BLAST-like alignment tool (Kent, 2002) which has reinvented some of the reconstructive aspects of the BLAST algorithm to be more sensitive and quicker.”
- “Also, Faith (Faith, 2006) pointed out that Helfenbein and others works (Faith, 2004, 1992; Faith and Trueman, 2001; De Queiroz and Poe, 2001) claim that both methods are Popperian (...)”
- “As shown in Figure 2 using this more empirical approach does not reduce the total error rate.”
- “For a more complete review of ChIP-seq technology, applications and software see Park (2009) and Pepke et al. (2009).”

Sources of the examples

- Brüssow and Hendrix. *Phage genomics: small is beautiful*. Cell (2002) vol. 108 (1) pp. 13-6
- Drummond et al. *A single determinant dominates the rate of yeast protein evolution*. Mol Biol Evol (2006) vol. 23 (2) pp. 327-37
- Huson and Bryant. *Application of phylogenetic networks in evolutionary studies*. Mol Biol Evol (2006) vol. 23 (2) pp. 254-67
- Martínez-Antonio et al. *Structural and functional map of a bacterial nucleoid*. Genome Biol (2009) vol. 10 (12) pp. 247
- Pop. *Genome assembly reborn: recent computational challenges*. Briefings in Bioinformatics (2009) vol. 10 (4) pp. 354-66
- ... and a few reviews written in this class.