# Writing exercise 04: Omit needless words

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### Excerpts from Strunk & White: Elementary Principles of Composition [4th ed., pg. 23-24]

**17. Omit needless words.**

Vigorous writing is concise. A sentence should contain no unnecessary words, a paragraph no unnecessary sentences, for the same reason that a drawing should have no unnecessary lines and a machine no unnecessary parts. This requires not that the writer make all his sentences short, or that he avoid all detail and treat his subjects only in outline, but that he make every word tell.

Many expressions in common use violate this principle.

|  |  |
| --- | --- |
| there is no doubt but thatthis is a subject thatthe reason why is that | no doubt (doubtless)this subjectbecause |

*The fact that* is an especially debilitating expression. It should be revised out of every sentence in which it occurs.

|  |  |
| --- | --- |
| owing to the fact that in spite of the fact that call your attention to the fact that  | since (because) though (although) remind you (notify you) |

### Words/phrases that can usually be omitted from scientific writing

* Figure 1/Table 1 shows that….

**Rationale:** By their nature, figures and tables show data. It is unnecessary to say so.

**Alternative:** Simply state the result and reference the appropriate figure/ (Figure 1).

* This result emphasizes/highlights/demonstrates that….

**Rationale:** These expressions are usually unnecessary. The result can stand on its own without editorializing.

**Alternative:** Simply state the result

* Interestingly, excitingly, fundamentally, surprisingly, etc.

**Rationale**: Adverbs are generally weak and do not add much to a sentence. It is better in academic writing to simply lay out the facts and let the reader evaluate whether a particular fact is interesting/exciting/surprising.

**Alternative:** Simply state the result/fact and remove any adverbs.

* So-and-so et. al (year) showed that; studies showed that…

**Rationale:** The emphasis should generally be on the findings themselves, not the authors who discovered them.

**Alternative:** Simply state the finding and cite the appropriate paper using an accepted citation style.

### Example1:

Interestingly, the phenomenon by which bacteria, in a remarkably intricate and multifaceted manner, develop resistance to bacteriophages, the viruses that specifically target and infect bacterial cells, can be attributed to a variety of mechanisms that have been extensively studied and meticulously documented in the scientific literature. These mechanisms, which are the result of both evolutionary pressures and selective forces, include, but are not limited to, the alteration of bacterial surface receptors, which bacteriophages utilize as essential docking sites for initiating the infection process. Studies have demonstrated that these receptors, through mutations or other genetic modifications, can undergo subtle or significant changes, thereby preventing the bacteriophage from effectively attaching and subsequently penetrating the bacterial cell. Additionally, it has been observed that bacteria can, quite fascinatingly, employ restriction-modification systems, which are essentially bacterial defense mechanisms that recognize and cleave foreign DNA, including that of bacteriophages, thus impeding the viral infection. Furthermore, CRISPR-Cas systems, which are adaptive immune systems found in bacteria, have been documented to provide a sophisticated and highly efficient means by which bacteria can remember and subsequently target and degrade the genetic material of invading bacteriophages. In conclusion, the resistance of bacteria to bacteriophages is, without doubt, a complex and dynamic process, involving a multitude of genetic and biochemical strategies that have been rigorously explored and continue to be an area of intense research interest in the field of microbiology.

Improved version:

Bacteria, develop resistance to bacteriophages, the viruses that specifically target and infect bacterial cells, using a variety of mechanisms. These mechanisms, which are the result of evolutionary pressures and selective forces, include, but are not limited to, the alteration of bacterial surface receptors, which bacteriophages utilize as essential docking sites for initiating the infection process. St These receptors, through mutations or other genetic modifications, can undergo subtle or significant changes, thereby preventing the bacteriophage from effectively attaching and subsequently penetrating the bacterial cell. Additionally, bacteria canemploy restriction-modification systems, which are bacterial defense mechanisms that recognize and cleave foreign DNA, including that of bacteriophages, thus impeding the viral infection. Furthermore, CRISPR-Cas systems, which are adaptive immune systems found in bacteriaprovide a efficient means by which bacteria can remember and subsequently target and degrade the genetic material of invading bacteriophages. The resistance of bacteria to bacteriophages isa complex and dynamic process, involving a multitude of genetic and biochemical strategies.

### Exercise 4A.

Read each sample of scientific writing and ask yourself: Are there any words which can be eliminated – either without changing the meaning, or strengthening the writing and making it clearer?

**Sample 4.1** 2

Gene regulatory networks allow bacteria to respond to changes in their environment by activating or repressing target genes ([1](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6851279/)). In this way, cells can exhibit phenotypes that balance the demands of expressing necessary genes while minimizing the diverse costs associated with the expression of genes that are not necessary ([2](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6851279/),[–8](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6851279/)). Regulatory networks must respond to a diverse array of signals, for example, integrating information regarding the availability of multiple resources that the organism uses with different preference ([9](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6851279/)). For a particular group of coregulated genes, the integration of these signals defines its regulatory input function. Knowledge of this function aids in the prediction of gene responses, understanding of the mechanistic basis of regulation, and understanding of the potential for regulation to evolve, and it is likely to be helpful in the pursuit of engineering of specific responses in artificial circuits ([10](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC6851279/)). Despite the importance of regulatory input functions, the understanding of their variation within a species is limited. This variation is important, as it reflects the potential for evolutionary changes in regulatory function and might reveal differences in selection pressures affecting different subpopulations.

**Sample 4.2.** 3

Tuberculosis (TB) caused by Mycobacterium tuberculosis infection remains a serious worldwide health concern in terms of infection incidence and associated mortality (Kone et al., 2022), despite the significant improvement in the situation; for example, the global mortality of TB considerably reduced by 47% from 1990 to 2015 through the global efforts of many countries, including China (Wang et al., 2014; World Health Organization, 2015). However, the incidence of tuberculosis is on the rise again; for instance, its global incidence rate in 2021 increased by 3.6% compared with that in 2020 (Ding et al., 2020; World Health Organization, 2022). Although approximately 70% of new tuberculosis cases are diagnosed predominantly in developing countries, especially in regions such as Southeast Asia and Africa, which have become heavy burdens for these countries (World Health Organization, 2022), the incidence rates in developed nations are increasing significantly as well, especially for vulnerable populations, such as children and AIDS patients (Dheda et al., 2016; Tomà et al., 2017).

**Sample 4.3.** 4

### Petroleum reservoirs are extreme environments with high pressure, high salinity, and high temperature ([Youssef et al., 2009](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1305731/full#B93)). Recent studies have shown that various microbes colonize these unique habitats and that they have a significant influence on the quality and recovery of oil ([Van Hamme et al., 2003](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1305731/full#B82); [Li et al., 2017](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1305731/full#B46); [Varjani and Gnansounou, 2017](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1305731/full%22%20%5Cl%20%22B84)). On the positive side, the microbes in petroleum reservoirs produce various metabolites (gases, acids, biopolymers, and biosurfactants) that may enhance oil recovery ([Bachmann et al., 2014](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1305731/full#B1)). However, negatively, some organisms may degrade hydrocarbons, altering oil components, and resulting in the production of heavy oil ([Head et al., 2003](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2023.1305731/full#B26)). Therefore, it is important to understand the metabolism and functions of microbial communities in petroleum reservoirs.

### Exercise 4B.

Look at your introduction thus far (or any other piece of your own writing)

Go through it, word by word, and cross out/delete any word that isn’t ~~absolutely~~ necessary

You may find it helpful to print out your work and cross out sentences physically, or to use Track Changes in Word (or a similar version control approach)

### References

1. ChatGPT, 4.0
2. Phillips KN, Widmann S, Lai HY, et al. Diversity in *lac* Operon Regulation among Diverse *Escherichia coli* Isolates Depends on the Broader Genetic Background but Is Not Explained by Genetic Relatedness. mBio. 2019;10(6):e02232-19. Published 2019 Nov 12. doi:10.1128/mBio.02232-19
3. Fu, X., Wan, X., Memon, A. A., Fan, X. Y., Sun, Q., Chen, H., Yao, Y., Deng, Z., Ma, J., & Ma, W. (2024). Regulatory role of *Mycobacterium tuberculosis* MtrA on dormancy/resuscitation revealed by a novel target gene-mining strategy. Frontiers in Microbiology, 15. https://doi.org/10.3389/fmicb.2024.1415554
4. Xu, J., Wang, L., Lv, W., Song, X., Nie, Y., & Wu, X. L. (2023). Metabolic profiling of petroleum-degrading microbial communities incubated under high-pressure conditions. *Frontiers in Microbiology*, *14*. https://doi.org/10.3389/fmicb.2023.1305731