# Writing exercise 02: Paragraph Structure

## Dr. Morgan Feeney, AY 2024-25

### Excerpts from Strunk & White: Elementary Principles of Composition [4th ed., pgs. 15-17]

**13. Make the paragraph the unit of composition.**

The paragraph is a convenient unit; it serves all forms of literary work. As long as it holds together, a paragraph may be of any length — a single, short sentence or a passage of great duration.

If the subject on which you are writing is of slight extent, or if you intend to treat it briefly, there may be no need to divide it into topics. Thus, a brief description, a brief book review, a brief account of a single incident, a narrative merely outlining an action, the setting forth of a single idea — any one of these is best written in a single paragraph. After the paragraph has been written, examine it to see whether division will improve it.

Ordinarily, however, a subject requires division into topics, each of which should be dealt with in a paragraph. The object of treating each topic in a paragraph by itself is, of course, to aid the reader. The beginning of each paragraph is a signal that a new step in the development of the subject has been reached.

As a rule, begin each paragraph either with a sentence that suggests the topic or with a sentence that helps the transition. If a paragraph forms part of a larger composition, its relation to what precedes, or its function as a part of the whole, may need to be expressed. This can sometimes be done by a mere word or phrase (again, therefore, for the same reason) in the first sentence. Sometimes, however, it is expedient to get into the topic slowly, by way of a sentence or two of introduction or transition.

Enormous blocks of print look formidable to readers, who are often reluctant to tackle them. Therefore, breaking long paragraphs in two, even if it is not necessary to do so for sense, meaning, or logical development, is often a visual help. But remember, too, that firing off many short paragraphs in quick succession can be distracting. Paragraph breaks used only for show read like the writing of commerce or of display advertising. Moderation and a sense of order should be the main considerations in paragraphing.

### Example from a published paper1:

In gram-negative microbes, OMPs are assembled into the OM by the heteropentomeric β-barrel assembly machine (BAM complex). The BAM complex is composed of two essential proteins—BamA and D—and three nonessential proteins—BamB, C, and E. BamA is conserved in all diderm bacteria, and homologs can be found in the OM of mitochondria and chloroplasts (3–6). BamD is not conserved in organelles; however, it is ubiquitous in diderm bacteria, including endosymbionts with a greatly reduced genome (7). Due to this conservation, BamA and BamD have been proposed to be the ancestral BAM complex of proteobacteria, which represents the most phenotypically diverse phylum of prokaryotes (8).

* The first sentence introduces the topic (what do you expect this paragraph to be about?
* The succeeding sentences explain/establish/develop the statement made in the topic sentence
* The final sentence either emphasizes the thought of the topic sentence or states some important consequence.

### Exercise 2A.

Read each sample of scientific writing and ask yourself 3 questions:

1. For each paragraph, can you identify the topic sentence/topic of the paragraph?
2. Do the subsequent sentences logically flow and lead to a sensible, well-supported conclusion?
3. Could the structure/logical order of the paragraph be improved (if so, how?)?

**Sample 2.1** 2

To overcome oxidative stress induced challenges, bacteria have developed multiple strategies to combat ROS. O2- can be transformed by superoxide dismutases into O2 and H2O2, which can be further neutralized by catalases into H2O and O2. Furthermore, H2O2 is scavenged by alkyl hydroperoxide reductases [[3](https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1010669)]. ROS often oxidize a variety of proteins containing cysteine residues. This results in non-native disulfide bond formation, which often causes a loss of function. Antioxidants, such as thioredoxins and glutathione-dependent glutaredoxins reduce these disulfide bonds in the cytoplasm and restore protein function [[6](https://journals.plos.org/plosgenetics/article?id=10.1371/journal.pgen.1010669)].

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| What is the topic?  | Do the subsequent sentences logically flow to a conclusion?Yes  No  |
| Could the structure/logical order of the paragraph be improved (how)? |

**Sample 2.2.** 3

BldD sits at the top of the regulatory cascade controlling development, serving to repress expression of sporulation genes during vegetative growth (den Hengst et al., 2010). In *Streptomyces coelicolor*, BldD controls the expression of at least 167 genes, including 42 genes (∼25% of the regulon) that encode regulatory proteins (Elliot et al., 2001, den Hengst et al., 2010). Among these BldD targets are many genes known to play critical roles in *Streptomyces* development, including other bld regulators (e.g., *bldA, bldC, bldH/adpA, bldM*, and *bldN*), several whi (white) regulators required for the differentiation of aerial hyphae into spores (e.g., *whiG* and *whiB*), and genes encoding critical components of the cell division and chromosome segregation machineries such as FtsZ, SsgA, SsgB, and the DNA translocase SffA (den Hengst et al., 2010, McCormick, 2009). How BldD activity is regulated, however, has been unknown.

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| What is the topic?  | Do the subsequent sentences logically flow to a conclusion?Yes  No  |
| Could the structure/logical order of the paragraph be improved (how)? |

**Sample 2.3.** 4

Fungal plant pathogens present a significant threat to global food security and biofuel production. Soil-borne pathogens such as *Verticillium* and *Fusarium* fungi can cause destructive vascular wilt diseases in plants ([Berg et al., 2000](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full); [Ruiz-Roldán et al., 2008](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full)). Verticillium wilt is characterized by fungal hyphae colonizing and clogging the plant’s vascular tissues, leading to wilting and eventual death of affected leaves ([Klosterman et al., 2009](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full); [Prieto et al., 2009](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full)). The presence of micronuclei in necrotic plant tissues can promote the survival of pathogenic bacteria in the soil, creating a significant challenge for disease management in agriculture ([Klimes et al., 2015](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full)). *V. dahliae* demonstrates notable variability and co-evolutionary abilities with its host, and its pathogenic mechanism is intricate ([Depotter et al., 2019](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full); [Lv et al., 2022](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full); [Zhang et al., 2022](https://www.frontiersin.org/journals/microbiology/articles/10.3389/fmicb.2024.1377713/full)). The specific interaction between the pathogen and the host remains incompletely understood. Nonetheless, unraveling the molecular pathogenic mechanism of *V. dahliae* holds promise for effectively combating yellow wilt disease in cotton.

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| What is the topic?  | Do the subsequent sentences logically flow to a conclusion?Yes  No  |
| Could the structure/logical order of the paragraph be improved (how)? |

### Exercise 2B.

The following paragraph has had its topic sentence removed. Read the paragraph and suggest an appropriate first sentence that would introduce the topic.

**Sample 2.4.** 5

…..The dietary component phytate (myo-inositol-1,2,3,4,5,6-hexakisphosphate or InsP6) is widely distributed in the plant kingdom and especially abundant in wheat, rice and nuts3. The daily intake of this phytochemical is on average ~2.5 g phytate per person3,4,5. Phytate has been regarded as an anti-nutrient in animal feed6 owing to its strong metal-chelating properties. Yet, so far there is no evidence that phytate intake in humans might be problematic due to reduced bioavailability of minerals and other food components. In contrast, health benefits have been reported for the consumption of plant-based diets, including phytate-rich products, such as nuts, seeds and unprocessed whole grains2,7,8. Dietary phytate supplementation reportedly promoted epithelial repair resulting in improved barrier function9, reduced serum levels of glycated haemoglobin HbA1c and advanced glycation end products10, improved glucose metabolism11, reduced inflammation12 and exerted protective effects against colon cancer13. Nevertheless, the molecular mechanism by which dietary phytate confers these health benefits is largely unknown.

### Exercise 2C.

The following writing sample has had all paragraph breaks removed. Read the sample and decide where it would be best to insert paragraph breaks, and then compare your version to the published one.

**Sample 2.5.** 6

The arms race between bacteria and bacteriophages (phages) has led to the evolution of diverse antiphage elements[1](https://www.nature.com/articles/s41564-024-01719-5#ref-CR1),[2](https://www.nature.com/articles/s41564-024-01719-5#ref-CR2),[3](https://www.nature.com/articles/s41564-024-01719-5#ref-CR3), such as CRISPR-Cas systems and restriction-modification systems (RM)[4](https://www.nature.com/articles/s41564-024-01719-5#ref-CR4). Phages usually rely on diverse counterstrategies to evade these antiviral systems[5](https://www.nature.com/articles/s41564-024-01719-5#ref-CR5),[6](https://www.nature.com/articles/s41564-024-01719-5#ref-CR6), including anti-CRISPR proteins[7](https://www.nature.com/articles/s41564-024-01719-5#ref-CR7) and anti-restriction endonuclease proteins[8](https://www.nature.com/articles/s41564-024-01719-5#ref-CR8). Moreover, the prokaryotic antiphage defence mechanisms are much more complex than previously perceived, and many prokaryotic defence systems and antidefence mechanisms are still unknown[9](https://www.nature.com/articles/s41564-024-01719-5#ref-CR9). Thus, studies on phage and bacterial genes may reveal numerous biological mechanisms involved in phage–host interactions. Phage-resistance genes are diverse, comprising nucleases, helicases, proteases and kinases[10](https://www.nature.com/articles/s41564-024-01719-5#ref-CR10). The nucleases from the RM and CRISPR-Cas systems that cleave phage DNA have been investigated extensively[11](https://www.nature.com/articles/s41564-024-01719-5#ref-CR11). In contrast, the role of proteases in phage defence is poorly studied. Proteases are commonly identified in phage defence systems[12](https://www.nature.com/articles/s41564-024-01719-5#ref-CR12),[13](https://www.nature.com/articles/s41564-024-01719-5#ref-CR13),[14](https://www.nature.com/articles/s41564-024-01719-5#ref-CR14),[15](https://www.nature.com/articles/s41564-024-01719-5#ref-CR15),[16](https://www.nature.com/articles/s41564-024-01719-5#ref-CR16). However, whether these proteases directly cleave phage protein to defend against phage infection is yet to be determined. On the other hand, given that phages strictly rely on the host cell for propagation, they have evolved different strategies to redirect the bacterial metabolism to establish an efficient infection cycle[17](https://www.nature.com/articles/s41564-024-01719-5#ref-CR17),[18](https://www.nature.com/articles/s41564-024-01719-5#ref-CR18), such as interfering with RNA transcription, DNA replication, protein translation and cell division pathways in bacteria[19](https://www.nature.com/articles/s41564-024-01719-5#ref-CR19). The phage proteins that could manipulate host behaviour are mainly expressed in the early stages of infection, and studies of phage-inspired antibacterial strategies could provide new targets for developing antimicrobial drugs[18](https://www.nature.com/articles/s41564-024-01719-5#ref-CR18),[20](https://www.nature.com/articles/s41564-024-01719-5#ref-CR20). Tens of thousands of complete phage genomes have been sequenced, and over two-thirds of phage genes are functionally unknown, many of which could potentially encode important functions to manipulate the host and overcome bacterial defence mechanisms[21](https://www.nature.com/articles/s41564-024-01719-5#ref-CR21),[22](https://www.nature.com/articles/s41564-024-01719-5#ref-CR22),[23](https://www.nature.com/articles/s41564-024-01719-5#ref-CR23),[24](https://www.nature.com/articles/s41564-024-01719-5#ref-CR24). *Pseudomonas aeruginosa* phage PaoP5 has a linear double-stranded DNA (dsDNA) genome with 176 predicted protein-encoding genes, while the function of over 80.7% of these open reading frames (ORFs) is uncharacterized. Interestingly, many of these hypothetical proteins are relatively conserved and share over 90% identity with the corresponding genes in other PAK\_P1-like *P. aeruginosa* phages isolated from Asia, Europe and Africa[25](https://www.nature.com/articles/s41564-024-01719-5#ref-CR25). This finding suggests that these genes might be essential for phage survival under specific conditions and some of them may encode antidefence mechanisms or host-takeover strategies. In this study, we tried to systematically study the function of hypothetical proteins in *P. aeruginosa* phage PaoP5 and identified a dual-functional phage protein that simultaneously regulates bacterial virulence and protects phage from bacterial defence.

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