Explanatory standards in biology and physics textbooks: The case of polymers

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Abstract: Learning to construct good scientific explanations is an important aspect of learning science. To this end it is important to also consider that the detailed standards for good explanations differ across the sciences. Practitioners face these differences, for instance, when interdisciplinary work is attempted. This paper reports on a comparative qualitative study of exemplar explanations on polymers from molecular biology and polymer physics aiming to map the differences in standards for good explanations between the two domains. The study gives detail to the theoretical expectation that mechanistic explanations are the ideal in molecular biology whereas derivations play the central role in polymer physics. Mechanistic explanations in molecular biology focus on material objects with a function-determining structure. In polymer physics derivations are the preferred kind of explanation. Derivations focus on variables, particularly, physical quantities like energy and entropy, whereas the three dimensional structure of polymers is often ignored. Differences in the kinds of explanations-seeking questions deemed relevant within the two domains are also identified.

Keywords: Explanation, biology, physics, interdisciplinary research, empirical method, exemplars

1 Introduction

Explanations of natural phenomena, theoretical results and more are important products of scientific practice. What characterizes a good scientific explanation has puzzled philosophers for decades, and an exhaustive answer still eludes us. Still, in most cases, individual scientists and teachers are able to judge whether an explanation is good or bad even if they are not able to explicate the standards they use. These standards are often referred to as the individual's explanatory standards. Explanatory standards are not entirely idiosyncratic. Scientists from the same research domain tend to make very similar judgements about the quality of explanations on topics within their own research domain[1]. Explanatory standards are thus to a large extent shared *within* research domains[2]. However, they are not necessarily shared *across* research domains. In fact, it is widely recognized that different sciences have somewhat different explanatory standards (Woodward 2011). And yet, our knowledge about *how* explanatory standards differ across domains remains limited.

Why is this observation important? From an educational perspective there are two related reasons: 1) Learning to construct and evaluate explanations is an important part of any science education, and (at least) in higher education it is important that the student learns the explanatory standards of the research domain she is being

[1] I use the term 'research domain' to refer to any social unit of science, be it a discipline, sub-discipline or smaller social unit of science (Collins 2011).
[2] Following Kuhn (1996), one could say that the explanatory standards are part of the paradigm of the research domain.

enculturated into. Some argue that there should be more explicit discussion in the science classroom on what good explanations are (Peker, Wallace 2011; Chambliss, Christenson & Parker 2003; Unsworth 1997; Solomon 1995). If so, it will be important not to draw an overly generalized picture, but to be sensitive to the differences across scientific domains (Dagher, Erduran 2014). A mapping of these differences will be valuable for this purpose. 2) In interdisciplinary problem solving where explanations must be acceptable to all domains involved, the differences in explanatory standards can become an obstacle if they are not identified and addressed ((Lélé, Norgaard 2005; Love 2008; O'Rourke, Crowley 2013; Green, Fagan & Jaeger 2014) see also (Goddiksen 2014, introduction & ch. 3)). A person who has previously reflected on the explanatory standards of her domain and how they differ from those of other domains, perhaps guided by philosophical insights, will, other things being equal, be better prepared for this process than a person who has not (cf. (Goddiksen 2014, ch. 3). Thus, from an educational perspective, mappings of the existing differences in explanatory standards across scientific domains are relevant, both in relation to the aim of enabling the student to solve problems within her own domain and with respect to the aim of teaching the student to solve interdisciplinary problems. Unfortunately, philosophers have, with few exceptions[3], neglected to provide such mappings and instead focused on commonalities within various types of explanations.

Commonalities in explanatory standards across the sciences were very much in focus in the early studies of scientific explanations that aimed to find the shared characteristics of *scientific* explanations (e.g. (Hempel 1965; Friedman 1974; Van Fraassen 1980)). Specific types of scientific explanations have also been studied in great detail. Noticeably, *causal* explanations have been attempted characterized across all science domains (e.g. (Salmon 1998; Woodward 2003)), while recognizing that not all scientific explanations are causal. Others have attempted to characterize explanations *within particular domains* (see section 3). These studies are valuable, but do not in themselves provide a detailed picture of the differences in explanatory standards across domains (see the (Goddiksen 2014, introduction).

In this paper I therefore take a first step towards mapping the differences in explanatory standards across scientific domains. More specifically, I report on a comparative qualitative study of the explanatory standards of molecular biology and polymer physics, two domains that meet, for instance, in interdisciplinary nanoscience and biophysics. The aim of the study is to discover what types of explanation-seeking questions[4] are deemed relevant, and what standards exist for evaluating answers to such questions. I have specifically refrained, in this study, from asking about the detailed methods used in the two domains for *constructing* candidate explanations. I am merely interested in the types of questions asked and the standards for *evaluating* answers to such questions, however they may have been constructed.

2 Method

The study takes as its starting point the expectations that can be formulated based on the existing literature on explanations from (polymer) physics and molecular biology (presented in section 3). These expectations are

[3] Differences in explanatory standards within the biological sciences have received some attention (e.g. (Winther 2011)).
[4] For more details on explanation-seeking questions (see (Goddiksen 2014, introduction) and the appendix to this paper).

then tested and refined through an analysis of a substantial empirical material in the form of exemplar explanations from the two domains[5]. Given that explanatory standards are rarely discussed explicitly in the science classroom, an important way for students to learn to judge the relevance of explanation-seeking questions and the quality of answers to these is through examples of explanations given by authorities from the relevant domain. That is, students learn explanatory standards through *exemplars* (Woody 2003; Kuhn 1996, 1977). The explanatory standards of a given domain are embedded in the exemplar explanations that populate the pages of science textbooks and displayed to the students who internalize these by solving (theoretical and practical) problems similar to the exemplars. This means that the textbook exemplars used to educate future members of the community are a valuable source of knowledge about the explanatory standards of a given domain.

The methodological considerations on how to select a good textbook sample and how to identify explanations within it are discussed in detail in (Goddiksen, forthcoming). In (Goddiksen, forthcoming) I argue that identification of explanations can be done through a set of reliable linguistic indicators of the presence of explanations in a piece of text, in the form of keywords like 'why' and 'because'. A full list of the indicators used in this study is found in the appendix.

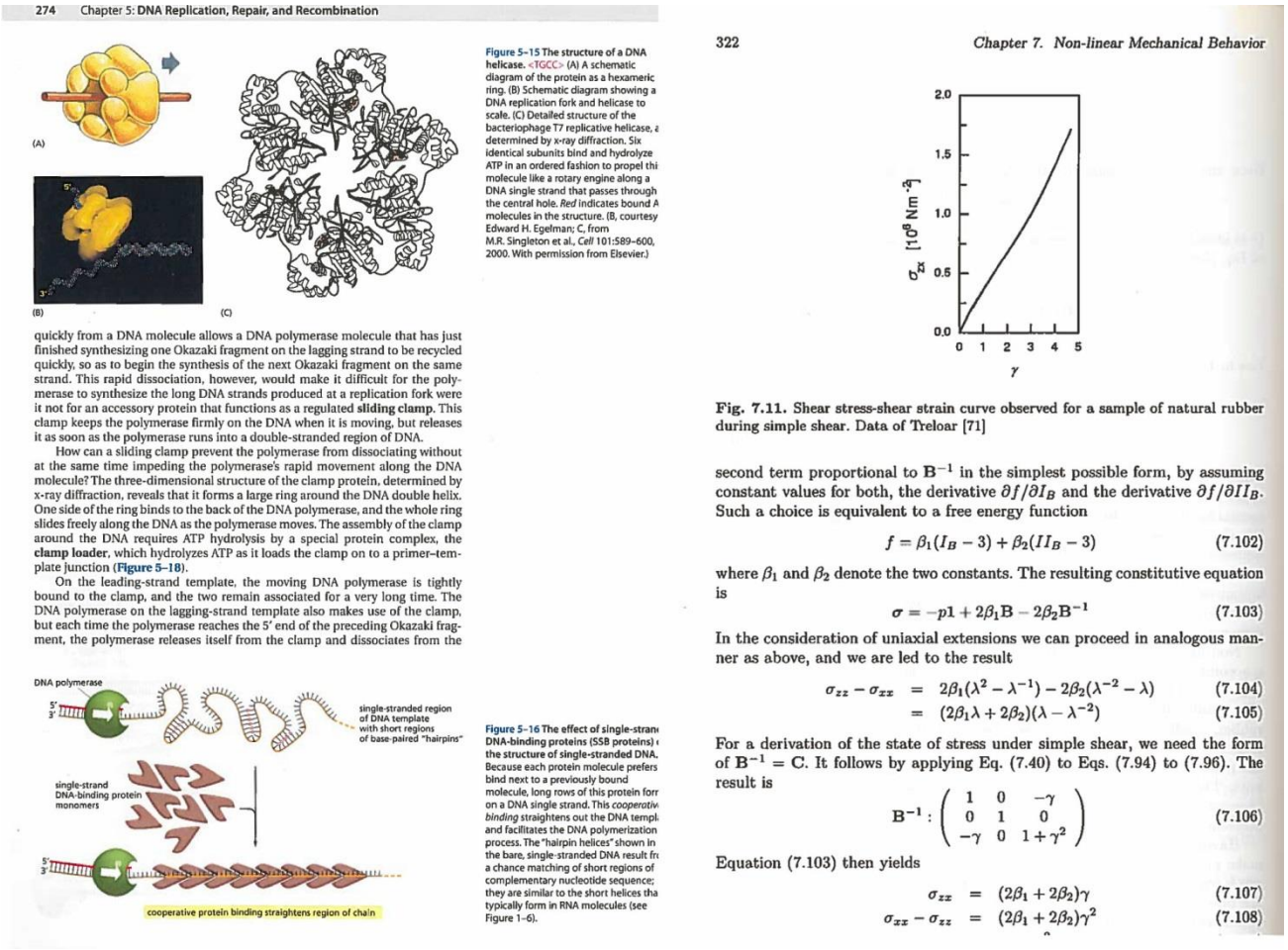
There are two types of explanations in science textbooks. Firstly, many explanations in textbooks are given as explanations of something that once puzzled researchers within the domain, which they have now explained. These explanations are exemplar explanations *par excellence*. They display the structure of a satisfactory explanation in the given domain and refer to the kinds of things and processes that can be referred to in explanations within the domain (although the details of explanations in introductory textbooks may be simplified relative to explanations aimed at practicing researchers). Secondly, some explanations explain tools that can be used to solve puzzles, for instance, the meaning of a technical term, or how to read a certain diagram. There are quite a few of these in introductory textbooks as well, but they are usually rather short, whereas the volume of genuine exemplar explanations is much bigger. The analysis presented in section 4 is based primarily on explanations of the first type.

Once identified, the exemplar explanations from the two domains can be compared in order to identify interesting differences using the theoretical expectations as a guide. Using expectations generated from the existing literature which often draws on case studies from scientific practice, as a starting point for the empirical analysis, rather than making the study completely bottom-up, counters the possible objection that results on differences in explanatory standards obtained from textbook material say little about the standards in actual practice. This possible objection would carry some weight if the aim of the investigation was to identify detailed methods for constructing good explanations. My aim here is to identify standards for evaluating explanations. Arguably, these standards are elaborated rather than changed during the course of a higher education, and textbook studies can thus give useful insights about the explanatory standards at play in scientific practice (cf. (Kuhn 1996, pp. 177ff)).

[5] Studies of explanations based on diverse samples of explanations are relatively rare. For some inspiring exceptions, see (Waskan et al. 2014; Overton 2013; Woody 2004; Ogborn et al. 1996; Dagher, Cossman 1992).

Differences in the standards displayed by the exemplar explanations in the two sets of textbooks will be easiest to detect when comparing explanations on similar topics. Occasionally scientists from two or more domains will be interested in similar objects although they ask different questions about them, and perhaps even conceptualize them in different ways; what Star and Griesemer (1989) called a boundary object. When comparing explanations across domains it is thus helpful to focus on explanations concerning a shared boundary object. This study aims to compare the explanatory standards of molecular biology and polymer physics. Polymers – large molecules composed of a few different monomers combined in large numbers - are one example of a class of objects that are of interest to both of these research domains (as well as others). Bio-polymers such as DNA, RNA and proteins play important and diverse roles in living organisms and are of fundamental interest to biologists. Polymer materials, such as rubbers and plastics, have been of major interest to chemists and physicists for many years both because of their commercial potential, and because they can have unusual physical properties[6]. Furthermore, polymers are a central topic in crossdisciplinary fields like biophysics and nanoscience that draw on both biological and physical sciences. Polymers are thus a topic where there is a potential need to negotiate explanatory standards in actual interdisciplinary practice.

[6] For instance, anyone who has left a rubber band from an open pack of frozen peas on the kitchen table for a while will know that, contrary to most other materials, rubber contracts when heated.



274 Chapter 5: DNA Replication, Repair, and Recombination

(A) (B) (C)

Figure 5–15 The structure of a DNA helicase. <TGCC> (A) A schematic diagram of the protein as a hexameric ring. (B) Schematic diagram showing a DNA replication fork and helicase to scale. (C) Detailed structure of the bacteriophage T7 replicative helicase, determined by x-ray diffraction. Six identical subunits bind and hydrolyze ATP in an ordered fashion to propel the molecule like a rotary engine along a DNA single strand that passes through the central hole. *Red* indicates bound ATP molecules in the structure. (B, courtesy Edward H. Egelman; C, from M.R. Singleton et al., *Cell* 101:589–600, 2000. With permission from Elsevier.)

quickly from a DNA molecule allows a DNA polymerase molecule that has just finished synthesizing one Okazaki fragment on the lagging strand to be recycled quickly, so as to begin the synthesis of the next Okazaki fragment on the same strand. This rapid dissociation, however, would make it difficult for the polymerase to synthesize the long DNA strands produced at a replication fork were it not for an accessory protein that functions as a regulated **sliding clamp**. This clamp keeps the polymerase firmly on the DNA when it is moving, but releases it as soon as the polymerase runs into a double-stranded region of DNA.

How can a sliding clamp prevent the polymerase from dissociating without at the same time impeding the polymerase's rapid movement along the DNA molecule? The three-dimensional structure of the clamp protein, determined by x-ray diffraction, reveals that it forms a large ring around the DNA double helix. One side of the ring binds to the back of the DNA polymerase, and the whole ring slides freely along the DNA as the polymerase moves. The assembly of the clamp around the DNA requires ATP hydrolysis by a special protein complex, the **clamp loader**, which hydrolyzes ATP as it loads the clamp on to a primer–template junction (**Figure 5–18**).

On the leading-strand template, the moving DNA polymerase is tightly bound to the clamp, and the two remain associated for a very long time. The DNA polymerase on the lagging-strand template also makes use of the clamp, but each time the polymerase reaches the 5′ end of the preceding Okazaki fragment, the polymerase releases itself from the clamp and dissociates from the

DNA polymerase
single-stranded region of DNA template with short regions of base-paired "hairpins"
single-strand DNA-binding protein monomers
cooperative protein binding straightens region of chain

Figure 5–16 The effect of single-strand DNA-binding proteins (SSB proteins) on the structure of single-stranded DNA. Because each protein molecule prefers to bind next to a previously bound molecule, long rows of this protein form on a DNA single strand. This *cooperative binding* straightens out the DNA template and facilitates the DNA polymerization process. The "hairpin helices" shown in the bare, single-stranded DNA result from a chance matching of short regions of complementary nucleotide sequence; they are similar to the short helices that typically form in RNA molecules (see Figure 1–6).

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σ_{zx} [10^6 Nm^{-2}]
2.0
1.5
1.0
0.5
0.0
0 1 2 3 4 5
γ

Fig. 7.11. Shear stress-shear strain curve observed for a sample of natural rubber during simple shear. Data of Treloar [71]

second term proportional to $\mathbf{B}^{-1}$ in the simplest possible form, by assuming constant values for both, the derivative $\partial f/\partial I_B$ and the derivative $\partial f/\partial II_B$. Such a choice is equivalent to a free energy function

$$f = \beta_1(I_B - 3) + \beta_2(II_B - 3) \tag{7.102}$$

where β_1 and β_2 denote the two constants. The resulting constitutive equation is

$$\boldsymbol{\sigma} = -p\mathbf{1} + 2\beta_1\mathbf{B} - 2\beta_2\mathbf{B}^{-1} \tag{7.103}$$

In the consideration of uniaxial extensions we can proceed in analogous manner as above, and we are led to the result

$$\sigma_{zz} - \sigma_{xx} = 2\beta_1(\lambda^2 - \lambda^{-1}) - 2\beta_2(\lambda^{-2} - \lambda) \tag{7.104}$$
$$= (2\beta_1\lambda + 2\beta_2)(\lambda - \lambda^{-2}) \tag{7.105}$$

For a derivation of the state of stress under simple shear, we need the form of $\mathbf{B}^{-1} = \mathbf{C}$. It follows by applying Eq. (7.40) to Eqs. (7.94) to (7.96). The result is

$$\mathbf{B}^{-1} : \begin{pmatrix} 1 & 0 & -\gamma \\ 0 & 1 & 0 \\ -\gamma & 0 & 1+\gamma^2 \end{pmatrix} \tag{7.106}$$

Equation (7.103) then yields

$$\sigma_{zz} = (2\beta_1 + 2\beta_2)\gamma \tag{7.107}$$
$$\sigma_{xx} - \sigma_{zz} = (2\beta_1 + 2\beta_2)\gamma^2 \tag{7.108}$$

Figure 1: Visually the books from the two domains look very different. Left: Page 274 from Alberts et al. (2006) with typical diagrams showing the structure of an important polymer (top), and a mechanism schema (bottom). Right: Page 322 from Strobl (1997) showing parts of a derivation and a graph of the relation among two variables.

2.1 The textbook material

The study is based on exemplar explanations from six widely used textbooks aimed at university students, three from each domain. The sample from each domain consists of both textbooks used at the introductory and intermediate undergraduate level (for polymer physics (Bower 2002; Plischke, Bergersen 2006)[7] for molecular biology (Watson et al. 2004; Alberts 2008)) as well as textbooks used in advanced undergraduate and graduate courses (for polymer physics (Strobl 1997) for molecular biology (Liljas et al. 2009)). The textbooks were selected through various criteria indicating wide use. Watson et al. (2004) is among the bestselling introductory books in molecular biology from one of the major publishing houses[8]. Looking at the recommended readings for more advanced courses at various institutions I identified acknowledged, but more advanced, books (Alberts 2008; Liljas et al. 2009; Plischke, Bergersen 2006; Strobl 1997). For the physics books,

[7] (Plischke, Bergersen 2006) is not exclusively a textbook on polymer physics, but introduces the methods from statistical physics in general and uses polymer physics as an area where they can be applied.

[8] http://www.pearsoned.co.uk/bookshop/subject.asp?item=297 (accessed June 12th 2014)

I also relied on personal communication with colleagues from physics with extensive research and teaching experience to point out relevant titles[9].

The general topic of the molecular biology textbooks is the workings of the living cell, and the study of polymers is a means to explain these. Entities that happen to be (made of) polymers – DNA, proteins, chromosomes etc. - are in almost constant focus, but the models presented often abstract away from this specific feature because it is not important in the specific explanation. In these cases the entities are not treated *as* polymers. In the data collection I chose to focus mainly on exemplar explanations where at least one entity is treated as a polymer. For instance, I have included treatments of DNA replication because, even though the proteins involved in this process are often not described as polymers, the DNA itself is. Conversely, I have ignored explanations of the later stages in cell division, where the DNA is compacted together with protein material to form chromosomes and the polymer nature of the various materials is completely ignored. In the polymer physics books, the topic is polymer materials and their properties, but otherwise the story is the same, explanations treating polymers as polymers have been included in the comparison.

3 Theoretical expectations: Mechanisms vs. deductions

In this section I briefly discuss the most relevant parts of the existing literature on explanations in physics and biology in order to see what differences one would expect to find in the empirical material. I start with biology.

As illustrated, for instance, by Winter (2011), there is great diversity in the explanatory standards of the biological sciences. Focusing on molecular biology and closely related domains, the existing literature gives the impression that the main difference in explanations from physics in general, and molecular biology in particular, is that physics explanations rely heavily on mathematical deductions based on general principles (laws of nature), whereas it is often claimed that general laws similar to the laws of physics are not found in biology (Mitchell 2000). Instead, molecular biologists explain by describing (causal) *mechanisms*. Machamer and collaborators characterize mechanisms as follows:

> ***Mechanisms are entities and activities organized such that they are productive of regular changes from start or set-up to finish or termination conditions (Machamer, Darden & Craver 2000, p. 3)***

There are alternative definitions of mechanisms. Bechtel and Abrahamsen emphasise that biologists tend to talk about mechanisms as performing *functions* rather than being "productive of regular changes" (Bechtel, Abrahamsen 2005, p. 423)[10]. All definitions of mechanisms are intended to cover explanations from several domains within biology and are thus necessarily general. It will therefore be interesting to explore the further constraints that face the molecular biologist, in particular, in terms of the *kinds* of entities and activities that

[9] The final selection was partly based on what titles were available at the time of performing research.
[10] Illari and Williamson (2012) further argue that mechanisms are often cyclic so they do not necessarily have neither "set-up" nor "termination conditions".

can be referred to in explanations, and see whether these constraints are different from the ones facing the polymer physicist. This question is addressed in section 4.1.

Related to this topic is the question of whether there are differences in the use of diagrams in the two domains. Diagrams play diverse and important roles in scientific explanations. In the biological sciences, the function of diagrams is often to more or less abstractly represent the mechanisms described in explanations (Sheredos et al. 2013). Such diagrams are referred to as *mechanism schemas* (Darden, Tabery 2010). If the use of diagrams is tightly connected to the way of explaining that is prevalent in a given domain, then one would expect to find differences in the use of diagrams between two domains with differing explanatory standards. Section 4.1 discusses the differences that can be identified between molecular biology and polymer physics.

I return to some further details of the philosophical studies of explanations in molecular biology later, but for now I turn to what has been said about explanations in physics.

There are at the same time very many and very few studies of explanations in physics. There are very many because most of the studies that claim to deal with scientific explanations in general draw exclusively on physics as their source of scientific examples. However, the examples are often simplified and the pool of examples drawn upon is very limited. There are surprisingly few studies that aim to capture some of the diversity of explanations in physics and analyse specific authentic cases in detail[11].

In the general literature there are two influential accounts of what to expect when looking at explanations in physics. One states that explanations in physics are deductions involving general principles that we might call laws of nature. There are two general versions of this account: Hempel's (1965) D-N model and the unifacationist accounts (Friedman 1974; Kitcher 1989). The other influential account of explanations in physics is Salmon's causal mechanical account (Salmon 1998). Where Hempel and the unificationists focus on physics as a science of laws and deduction, Salmon's causal mechanical account reminds us that (classical) physics is often also a science of colliding billiard balls and interlocking gears. The two views of explanations in physics need not be mutually exclusive. According to Salmon, an explanation can be both causal mechanical and a deduction from general principles, although it need not be (Salmon 1998, ch. 4). Woodward (2003, pp. 355) argues that while Salmon is right to remind us of the causal nature of many explanations in (classical) physics, his account of what characterises these causal explanations does not capture the way physicists explain using statistical mechanics - which is exactly what polymer physicists often do. Salmon's detailed account is thus not particularly useful in this study. The main alternative to Salmon's account is Woodward's own account based on manipulability (Woodward 2003). Very roughly, Woodward argues that causal explanations show how the manipulation of the value of one variable effects a change in the value or probability distribution of another variable. In this way, causal explanations help us to answer questions about "what if things had been different?". Woodward's account is even more general than the various accounts of mechanistic explanations[12]. The generality of Woodward's account means that even if explanations in polymer physics are completely captured by this account there are still a lot of open questions. Which variables are considered the

[11] For one exception, see (Weatherall 2011).

[12] On Woodward's account, mechanistic explanations are simply one type of causal explanations.

most relevant and why? How is the dependence between the variables argued for in polymer physics – is it through deductions from general principles as Hempel argued or something else, and is it the same way as molecular biologists argue for causal dependencies? These questions are considered throughout section 4.

In short, the existing literature leads to the expectation that when comparing exemplar explanations from molecular biology and polymer physics differences will be found. Mechanistic explanations can be expected to be abundant in molecular biology books, but not necessarily in physics books, which are argued to rely more extensively on general principles and mathematical deduction in their explanations.

4 Empirical Results

The keyword searches in the textbooks identified hundreds of indicators and a large and diverse set of connected explanations to be compared, but since many of the explanations identified are parts of other explanations which are again interwoven with others, it would not be meaningful to state a specific number of explanations identified. Some explanations are short, for instance, explaining the appropriateness of a specific approximation. Others cover whole sections - chapters even - and contain multiple sub-explanations. For instance, the entire twelfth chapter of Watson et al. (2004) is framed as an answer to the explanation-seeking question of "how the series of bases in the DNA directs the production of RNAs and proteins that perform cellular functions and define cellular activities" (p. 347). The theoretical expectations presented above were to some extent confirmed through this substantial empirical material, while significant nuances are also added. As expected, mechanistic explanations are abundant in the molecular biology books, whereas derivations (not deductions) of dependencies among variables take centre stage in the polymer physics books. The comparison also reveals interesting differences in the kinds of explanation-seeking questions asked, the details of the ontology of the two domains as well as differences in the relations among the models used in the explanations. The details are presented and discussed below in relation to three different themes: The ontology of change (section 4.1), modes of reasoning (section 4.2) and questions and models (section 4.3). In the discussion I rely on a few illustrative examples, but the conclusions drawn do not hinge on these specific examples.

4.1 The ontology of change

Visually, the two sets of explanations identified are very different (see figure 1). As expected, colourful diagrams including mechanism schemas play a central role in the molecular biology books. Mechanism schemas provide an overview of the mechanisms considered and can serve as a starting point for detailed discussions of the different kinds of entities involved in the mechanism. Mechanism schemas in the molecular biology books commonly represent multiple steps in the process through which the given mechanism produces a certain outcome. Arrows are ubiquitous. The different kinds of entities that are part of the mechanism are

important and must be clearly recognizable: strong colours are used[13], and the individual entities in the mechanism are represented by distinct shapes (see figure 2).

Not all diagrams in the molecular biology books are mechanism schemas. These other diagrams often represent the detailed three-dimensional structure of a polymer that plays an important role in a mechanism of interest (see figure 3). Common to all the diagrams is thus the focus on the structure of the different types of polymers, be it the primary, secondary, tertiary or quarternary structure (see figure 4), and how polymers with different structures interact to perform a given function.

Diagrams are also abundant in the polymer physics books. Where the diagrams in the molecular biology books are often mechanism schemas, the most abundant kind of diagram in the polymer physics books is the graph depicting simultaneous values of (often no more than two) variables, or the development of the value of one variable over time (cf. figure 1). Mechanism schemas similar to those found in the molecular biology books are all but absent from the polymer physics books, but as in the molecular biology books, diagrams and pictures representing the instantaneous structure of individual polymers are found in the polymer physics books.

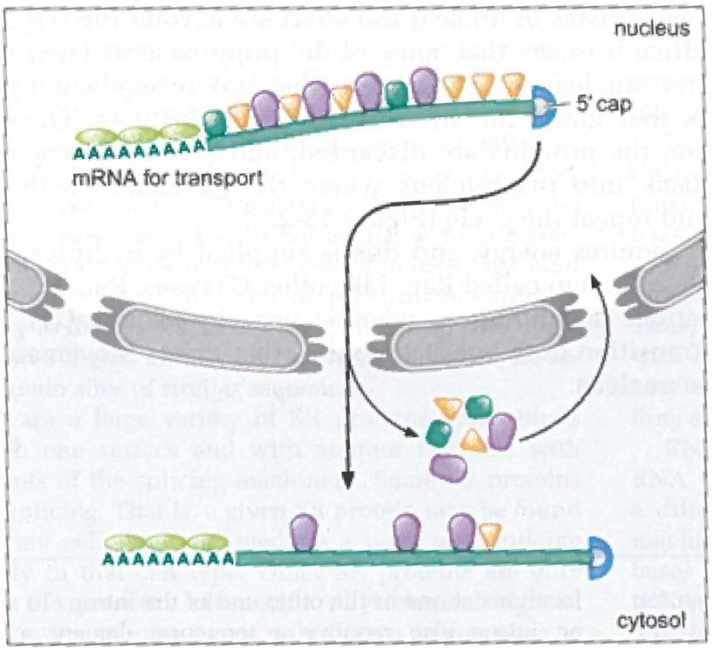

Figure 2: Transport of mRNA out of the cell nucleus. Only mRNAs with the right proteins attached will be transported. Note how the different proteins are represented by distinct colors and shapes. Figure 13.27 from Watson et al. (2004).

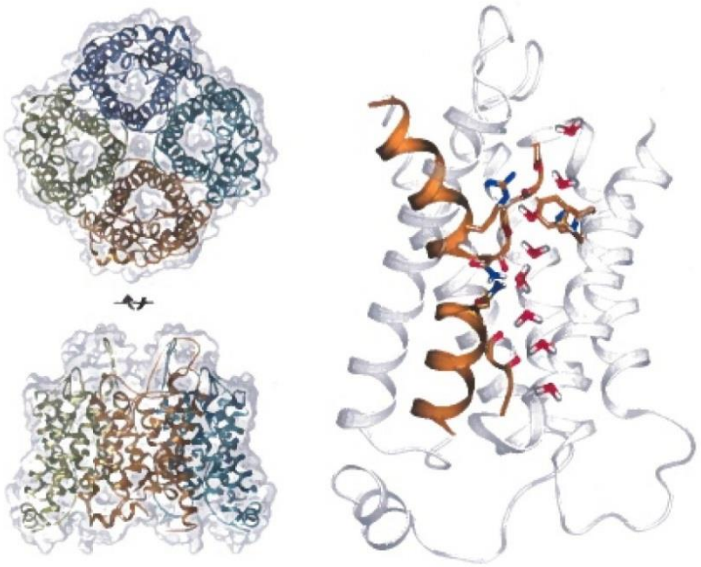

Figure 3: Left: The detailed structure of the protein aquaporin. Right: Water molecules passing though the pores in aquaporin. Figure 10.9 from Liljas et. al. (2009)

[13] The majority of the diagrams in all of the molecular biology books are in colour, whereas none of the polymer physics books have any illustrations in colour.

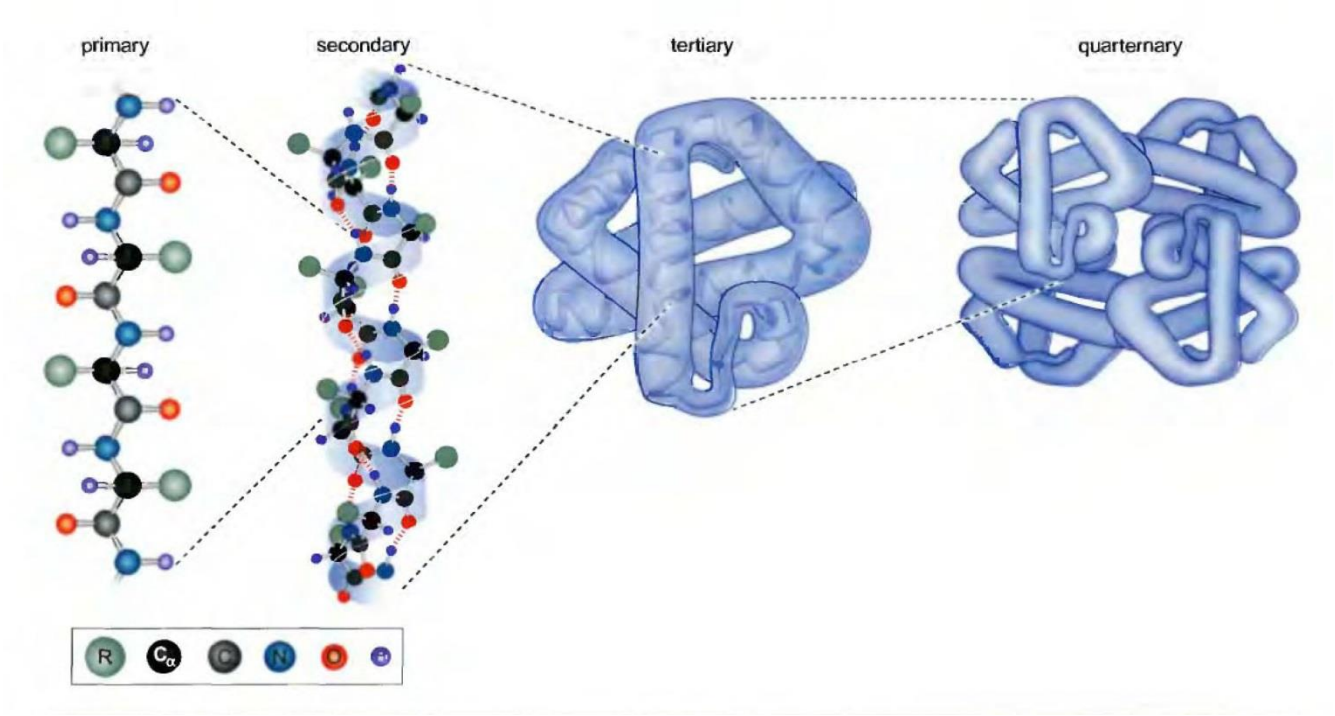

Figure 2: Four levels of polymer structure. Figure 5-7 from Watson et al. (2004).

As expected, there is thus some difference in the kinds of diagrams used, noticeably a difference in the way change is represented through diagrams. In the molecular biology books change is represented in steps, often towards a previously described function. The diagrams that are part of these explanations show how functions are served though change in the structure and distribution of specific polymers. More generally the explanations identified in the molecular biology textbooks are almost always spelled out in terms of reactions, movements, interactions and changing of shape of polymers. This is also illustrated from the kinds of explanation-seeking questions that are posed in the texts. Explanation-seeking questions about how a certain function is performed are common. For instance, Alberts and collaborators discuss the function of motor proteins and ponder the general question "How do these machines work?" (2008, p. 182). This question is obviously too broad to be answered in general, and must be rephrased to focus on the features of specific interest to the molecular biologist. The question now becomes: "[…] How do cells use shape changes in proteins to generate directed movements?" (ibid). In a similar vein, Liljas and collaborators discuss the structure of the membrane protein aquaporin (figure 3) as the answer to the question "How can the passage [through a membrane] of small ions or protons be avoided while permitting water to pass?" (2009, p. 346). These examples illustrate how explanation-seeking questions are phrased in terms of functions and answers are expected in terms of reactions, movements, interactions and changing of shape of polymers. The diagrams used in these explanations depict the polymers as they change shape, interact and react.

In the polymer physics books it is often a different kind of change that is represented and change is generally represented in a different way. Functions are less in focus, although polymer scientists are in practice often interested in identifying a polymer material that can serve a certain function. Change is represented through

continuous graphs depicting how a change in one variable affects a change in another variable without necessarily considering the reason for manipulating a variable in one way or another. In this sense they are simply answers to questions about "what if things had been different" (cf. section 3). This difference in the preferred way of representing change illustrates a more fundamental difference found in the textbooks from the two domains in thinking about *what it is that changes* when change occurs. They show that the two domains do not have the same ontology of change. The molecular biology books explain change as changes in the distribution, composition and interactions among *material objects*[14]. Explanations of this kind are sometimes sketched in the polymer physics books, but the detailed explanations, especially in the more advanced books, explicitly consider changes as change in the value of *variables*, often variables representing what we might call physical *quantities* such as entropy and different types of energy.

Although the polymer physics books conceptualise change as change in the value of variables, it does not mean that all explanations rely on abstract mathematical reasoning. More qualitative explanations of causal mechanisms are also found in the texts. However, the kinds of entities and activities that are described in these mechanistic explanations of polymer behaviour are different from those included in the molecular biology books. In the molecular biology books, material objects (polymers) encounter other material objects, and their interactions change and depend on the structure of these material objects. In the polymer physics books material objects commonly encounter entities like potential barriers or forces which are not easily interpreted as material objects. These encounters change not only the structure of the polymers, but also the value of variables like the entropy or internal energy of the polymer. I consider a detailed example below. Qualitative mechanistic explanations are thus displayed as valuable in both the polymer physics and molecular biology books. However, the polymer physics books will often indicate that these explanations are not as satisfying as derivations, at least if presented as the only explanation of a given phenomenon. Still, qualitative mechanistic explanations are included in the textbooks either because the explanation based on a derivation is too long or complicated to be discussed in the text (see e.g. (Strobl 1997, p. 139)), because they are the best of the available explanations, or because a qualitative mechanistic explanation supplements an explanation in the form of a derivation of mathematical relations among variables.

To illustrate the focus on variables and the importance of derivations in polymer physics, consider the problem of why rubber – a polymer material – is so elastic. This problem is treated in almost all textbooks on polymer physics, and all books give basically the same explanation: First a derivation showing that at constant temperature the force inside a stretched rubber sample pulling it back into shape depends only on the rate of change in the entropy of the sample. The next step is to derive the exact relation between these variables. To

[14] One important exception to the focus in molecular biology on material objects and their structure is the pervasive talk about *information*. Like energy, information is a quantity that can flow from one place to another (but unlike energy, information is not a conserved quantity). In physical theory, information is represented mathematically and has even been linked to other physical quantities. The heavy reliance by many molecular biologists on the concept information has struck some philosophers as controversial and unnecessary (Darden, Tabery 2010). It is controversial because the information concept used in molecular biology is clearly not the same as in other fields, noticeably it is not the same as physicists represent in their equations, and it has not been clearly defined. Looking at the textbooks, one notes that information is not treated mathematically as a quantity, but is used exclusively within the mechanistic framework described.

this end, a theoretical model of the rubber sample is constructed based on the, to the student, familiar Gaussian chain model[15]. It is derived that in this model the entropy of the sample decreases when the sample is stretched, and the resulting force inside the sample increases linearly as the sample is stretched. The explanation ends with considerations on how the results derived on the basis of the fairly simple model compare with experimental results. The specific material structure of the polymer chains in the rubber plays no role in this explanation. Versions of this explanations can be found in both Bower (2002, sec. 6.4) and Strobl (1997, sec. 7.1).

There are other ways of explaining the elasticity of rubber. An alternative mechanistic explanation – explicitly referring to the rubber polymers as material objects bumping increasingly into one another as they get stretched, forcing them to recoil - is sketched in the introductory book (Bower 2002, pp. 178-179). This approach is quickly abandoned however, in place of "developing an entropic, or statistical, theory of rubber elasticity in a quantitative way […]" (p. 179). The more advanced book does not explore alternative ways of explaining the phenomenon. Bower even provides reasons for preferring the quantitative, variable based explanation. Although the variable based explanation is in many cases only empirically accurate to the extent that it fits experimental data "to a first approximation" (p. 183), Bower lists three benefits of "the statistical theory" compared to "phenomological theories" (p. 183). One is that it relates the macroscopic properties of rubber to "the most important features of the molecular structure of real rubber" (ibid), the other two reasons point to specific examples of relations among variables that the model used in the explanation allows us to derive and thus "predict" (ibid). An additional virtue of the model which the explanation is based on is that it can be further developed to make it more empirically accurate. In fact, Bower proceeds to consider these extensions of the model in the section following the derivation just presented.

So, the explanation of the elasticity of rubber that relates it, in a quantitative way, to the entropy of the rubber while not directly considering the interactions among the polymers in the material is not just an explanation, it is a good explanation according to the polymer physicist. It is good because it refers to the variables – or "features" – that polymer physicists find most relevant when characterizing polymer materials, in this case not the material polymers themselves, but two physical quantities: the entropy and the internal force of the rubber sample. Furthermore, the explanation is good because it is based on a model and approach that allows exact mathematical relations between relevant variables to be derived. The model can even be further developed to become more precise with respect to specific systems (see section 4.3).

This explanation illustrates the more general point that the polymer physicist emphasises certain parts of his ontology in his explanations. Although he does not deny that polymer materials consist of material polymers with a specific structure, it is not the "most important feature" of the polymer material. Conversely, the molecular biologist does not deny that the energy and entropy of polymers change as they change shape, but physical quantities like these are rarely referred to in explanations. Instead the molecular biologist emphasises the material structure of polymers as the main explanatory features.

[15] The Gaussian chain is a very important model discussed further in section 4.3. It represents a single polymer chain that can change shape without energetic or geometrical constraints. The model can be extended in various ways, in this case by considering interactions between multiple Gaussian chains.

The observed differences in the ontology of change in the two domains are relevant when considering how cognitive resources from the two domains can be integrated. Within biology there is an increasing interest in developing models of living systems that have the quantitative character of physics and engineering models. This has, for instance, led to new interdisciplinary research fields like systems biology (Green, Wolkenhauer 2014). The discussion above illustrates that the transition to quantitative models often means significant changes in the way, and perhaps even the extent, to which these models are explanatory. As Weisberg (2007b) points out, one thing is to have a model that gives an accurate output compared to experimental data, what Weisberg calls dynamical fidelity, another is having a model that is accurate for the right reasons, what he calls representational fidelity. Changing from a typical molecular biology model based on material objects to a more physics inspired model not only means thinking about the same entities and activities in a quantitative way. In many cases it will mean adopting a different ontology of change and start thinking about different kinds of entities and activities, which in the eyes of some practitioners also means that these quantitative models have less explanatory power (see e.g. (Green, Fagan & Jaeger 2014; Morrison 2009)).

Integrating approaches from polymer physics into the study of polymers within molecular biology, or vice versa, thus implies not only that practitioners must learn something about the methods and language of the other domain, but also to engage in more fundamental reflections on what the important and interesting aspects of polymers are (cf. (Goddiksen 2014, ch. 3).

4.2 Derivations and structural reasoning

The rubber example presented above illustrates how the physics students are trained in explaining using derivations from early on, even if alternative strategies exist that, at the time, may be more intuitive to the student. Derivations allow physicists to answer some of the explanation-seeking questions they are most highly interested in: how the different variables depend on each other given certain conditions, and how the value of a specific variable can be computed. Physicists are well aware that they cannot answer every explanation-seeking question of interest through derivations. But, the textbooks from polymer physics tend to focus on questions that can be answered through derivations and to favour models and variables that allow for derivations. In this sense, explanatory standards not only constrain the possible answers to explanation-seeking questions, they also constrain what questions are considered in the first place (cf. (Kuhn 1996, pp. 36)). When explanation through derivation is not an option, qualitative mechanistic explanations are offered as an alternative. In this section, I look closer into what derivations are and compare them to the preferred way of theoretical reasoning in molecular biology, largely based on the construction of mechanism schemas and other diagrams from experimental results and, in turn, using these mechanism schemas to design new experiments.

Philosophers tended to equate derivations with deductions (cf. section 3). This implies that the quality (or soundness) of derivations is to be evaluated against the standards of deductive logic which dictate that quality depends on whether the assumptions that the deduction is based on are true, and whether the logical structure is valid. However, it has long since been observed that this move implies that very many explanations found in physics textbooks and in the most high-ranking physics journals are not up to the standards (see e.g. (Scriven 1962)). Derivations in physics are often based on assumptions that are known to be false (strictly speaking) and rely on general results that are known to be approximations (see also (Cartwright 1983)). This is

also true for the explanations identified in this study. For instance; in order to make the statistical treatment of individual polymer chains feasible, it is standardly assumed that the individual chains in a polymer material can be treated as infinitely long[16]. Plischke and Bergersen write:

> ***The degree of polymerization or the number N of [monomer] units is variable but can be of the order of 10^5 or more. This fact is what makes the use of statistical methods in the descriptions of even a single polymer chain possible, and we shall always assume that we may take the thermodynamical limit $N \to \infty$ for any quantity that we calculate. (2006, p. 384).***

The general results derived based on this assumption and used later on in other explanations are conditioned on the appropriateness of this and other assumptions and approximations made in the course of the derivation[17]. This is not a problem for the polymer physicists, but it is a problem for the philosopher who maintains that explanations based on unrealistic assumptions are always inadequate. Clearly, practitioners disagree with philosophers on this important issue, and if we aim to capture the explanatory standards of actual practice we need to nuance our view of what derivations are.

So, if derivations are not deductions what are they? Although they are often based on assumptions known to be false, derivations are often intended to have the structure of a mathematical deduction to the widest extent possible. So, parts of the structure of a derivation are analogous to a deduction. Often, it is not possible to construct an explanation of a given result solely through mathematical deduction from a set of assumptions, typically because it is not possible to solve the equations that can be deduced. To reach a result it is therefore necessary to make simplifying assumptions or approximations. Terms in equations may be simplified using familiar mathematical techniques and results, such as linear expansion or Stirling's formula. Properties of the system under consideration may be completely ignored or treated only in a simplified way, or the system may be considered only under very specific conditions that make it easier to handle mathematically. For instance, the system may be considered only under specific pressure or temperature conditions, where it can be argued that specific interactions can be ignored. This limits the scope of the explanation, but at least it enables a partial explanation rather than no explanation (example below). Treating derivations as something different than deductions thus points our attention to the use of false but reasonable assumptions as the basis for derivations, and the use of approximations and simplifying assumptions in the course of the derivation. This leads to the important question of what the standards are for using these. What, to the polymer physicist, is the difference between a good false assumption and a bad one?

[16] In some models, like the Rouse model, it is furthermore assumed that the individual chain can be divided into multiple sections that can all be treated as infinite (Strobl 1997, sec. 6.2).

[17] Morrison (2008, 2009) distinguishes abstract models from idealised models. The models in the polymer physics books are often abstract models because very unrealistic assumptions form the basis of the model: removing them would make the model useless. Morrison argues that biologists are often sceptic about the use of abstract models, and the molecular biology books contain mainly what Morrison calls idealized models. Idealized models may also rely on false and even unrealistic assumptions but these are made to ease the use of specific approaches not enable them, and they can thus be made more realistic without making the general approach infeasible.

Explanations based on theoretical models can be subverted by empirical evidence. So, of course it is important to consider whether an approximation compromises the empirical accuracy of the explanation. Thus, a common way of justifying simplifications of terms in equations is considerations on the size of the error introduced by this move. If the error is much smaller than what it is possible to measure in a feasible experiment, then the approximation is in many cases justified. Thus, a common trick when facing a difficult equation is to perform a linear expansion of it and disregard all but the first two terms in the expansion, since the remaining terms are insignificant under most circumstances. However, empirical accuracy is not the ultimate aim in every explanation. The rubber example shows that the physicist will sometimes prefer an explanation that is spelled out as a derivation of the relation among variables considered important, even if the explanation is not very accurate. In such explanations, approximations are sometimes justified simply through their fruitfulness. If explanation through derivation can be obtained by ignoring specific features of a given system, or by treating it only under very specific circumstances, then this can in some circumstances be enough to justify the approximation. To illustrate: To obtain a polymer material with a desired set of properties, it is often useful to mix two different polymers. Whether a mixture of two different polymers forms a homogenous phase or a two phase structure depends on a number of factors including the temperature and the molecular weight of the different polymers. Strobl (1997, sec. 3.2.1) explains the temperature and molecular weight dependence of the mixing properties of two polymers using a model due to Flory and Huggins. It is argued that a homogenous phase will occur if the mixing of the two types of polymers lowers the Gibbs free energy. An equation is set up dividing the change in the Gibbs free energy into two different contributions, one that is always negative and one that can be positive or negative depending on the specific conditions. The next step is to derive equations that enable calculations of the size of these two contributions. However, this is not possible in the model considered so far. So, to enable this next step, a mean field approximation is introduced into the model. This assumes that the complex interactions between an individual chain and the surrounding chains can be described as interactions between an individual chain and an external field. Using this approximation it is possible to derive approximate results that, although imprecise, provide "a basic understanding of the occurrence of different types of phase diagrams" (p. 83).

Compared to the polymer physics books, the molecular biology books display a different ideal for explaining from early on in the education. Molecular biologists usually learn some mathematics during their training, and the textbooks do contain a very limited number of equations including chemical equations. These few equations are mainly used as definitions (but only in the early "chemistry" chapters) or 'amount calculating devices'. No manipulations of the equations are performed, and the equations play no significant role in the explanations identified in the molecular biology texts. Thus, equations are not promoted as valuable tools for explaining dynamics, but only to determine specific quantities when necessary, for instance, in data analysis. Instead, the student is shown how to construct explanations through mechanistic thinking, focusing on the structures of polymers and the interactions that these different structures enable. The heuristic that structure determines function is prevalent, and affects the ways in which polymers are represented and reasoned about. As figure 2 illustrated, mechanism schemas often reduce complex polymers to simple shapes, abstracting away all other properties. Reasoning with mechanism schemas is thus a different challenge than reasoning with the more mathematical models used in polymer physics. Whereas a mathematical model requires mathematical

tools to be reasoned with, the mechanistic models rely on strong visualization skills and the ability to envision how results of mechanistic interactions can be detected in the laboratory, and vice versa, whether results of interventions on mechanisms in the laboratory affect the details of known mechanism schemas. Theoretical exercise questions ask students to explain, for instance, how interventions on the presented mechanisms would affect the mechanism, how the mechanisms explained in the chapters can be used to explain experimental results, and what experimental results reveal about the details of the mechanisms described.

4.3 A question of models

My aim in this paper is to identify differences between polymer physics and molecular biology, both in the kinds of explanation-seeking questions that are deemed relevant in the two domains, and the standards for good answers to such questions. So far, I have mainly focused on the standards for good answers. I argued that the explanations from molecular biology focus on mechanisms or parts of mechanisms, and that these are represented and reasoned with, for instance, through theoretical models such as mechanism schemas showing the specific activities and structure of the material objects that are part of the mechanism. The explanations from polymer physics, on the other hand, are either derivations of relations among variables based on mathematical models or qualitative mechanistic explanations based on the variable centred ontology of change of polymer physics. In this section, I consider more systematically some differences in the explanation-seeking questions that are asked within the two domains.

The molecular biology books display to the student that relevant explanation-seeking questions about polymers can be asked about the mechanisms they are part of and the functions these mechanisms serve, the structure of individual polymers, and experimental procedures for studying these mechanisms or parts of mechanisms. Substantial parts of the molecular biology books are devoted to answering questions about how mechanisms such as DNA replication or protein synthesis normally work in healthy cells. Important are also explanations of how perturbations to these mechanisms, for instance, through experimental manipulations or natural mutations, can affect the workings of the mechanism, potentially leading to diseases, but also to new knowledge about the details of the mechanism. Models, both theoretical and experimental, are important parts of the answers to the explanation-seeking questions posed in the molecular biology books. Experimental models, noticeably model organisms like the bacterium *Escherichia coli* or the yeast *Saccharomyces cerevisiae*, are important in the construction of the explanations, but they can also transform the explanation-seeking questions answered in the textbooks. To answer an explanation-seeking question, for instance, about the mechanism of DNA replication, initially formulated generally about cells, it is often necessary to transform it into a question about a model organism, such as yeast, and subsequently consider whether the answer can be extrapolated back to become an answer to the initial general question. Often, the diversity of living systems means that this is not entirely possible, and so parts of the explanation presented in the textbook applies only to systems reasonably similar to the model organism. To illustrate, consider the discussion in Alberts et. al. (2008, pp. 281-289) of how cells initiate DNA replication, specifically the answer to the explanation-seeking question: “how are replication forks created in a double stranded DNA molecule?” (p. 281). This question, posed about cells in general, is first broken down into two questions; one about bacteria, and one about eukaryotes (Archea are not considered). The question about bacteria is answered by presenting the relevant

mechanism identified in the model organism *E. coli*. Similarly, the question about eukaryotes is transformed into a question about yeast. After presenting the relevant mechanism in yeast, where a protein complex abbreviated ORC recognises specific sequences in the DNA and initiates the replication, the text goes on (p. 288) to consider whether the results obtained by studying yeast as a model organism can be extrapolated into an answer to the question about eukaryotes. Is the mechanism, for instance, the same in humans? Not quite. At least, it has been difficult to identify specific DNA sequences similar to the ones that the ORC complex binds to in yeast. The text concludes:

> ***Thus, as is true in many other areas of cell biology, the mechanism of DNA replication initiation in yeast may vividly highlight the core processes, while the situation in humans represents an elaborate variation on the theme (Alberts 2008, p. 288).***

So, the text set out to answer an explanation-seeking question about DNA replication initiation in cells in general, and did so by first transforming it into two questions about model organisms and providing a detailed answer. With these answers at hand, it was considered whether they could be extrapolated into an answer to the original question. It was concluded that the mechanisms in other cells are likely to be "similar in outline" (p. 288) to the mechanism described for the model organisms, but the details will differ.

Theoretical models in the form of diagrams are also indispensable parts of the textbook explanations, and an important tool of reasoning for the molecular biologist, but unlike the experimental models, explanation-seeking questions are not asked about the theoretical models. Furthermore, the questions which the theoretical models are used to answer are not about something defined through a theoretical model. Commonly they are about some mechanism, or part of a mechanism identified in the laboratory, which the theoretical model can provide some further understanding of.

Similar to the molecular biology books, the polymer physics books display to the student that relevant explanation-seeking questions about polymers can be asked about the properties of polymer materials or individual polymer chains that can be studied in the laboratory. As in the molecular biology books, general explanation-seeking questions may be answered by transforming them into a question about a specific experimental model material, e.g. polyethylene, and the explanation is noted to apply only to systems sufficiently similar to this experimental model (e.g. (Bower 2002, sec. 5.3.2)). However, the polymer physics books display an additional kind of explanation-seeking questions that can be relevant to ask within the domain; namely explanation-seeking questions about theoretical models. These questions fall in two different categories. One is the theoretical analogue to the questions about experimental models. A question initially posed about some kind of material thing, e.g. a piece of rubber, may be transformed into a question about a theoretical model of this thing. Once the question has been answered within the theoretical model, it is necessary to consider how accurate the model is when compared to actual data. The example considered in section 4.1, of what the exact relation between the decrease in the entropy of a rubber sample and the magnitude of the force inside the rubber pulling it back into shape as it is stretched, illustrates this approach. Here, the explanation-seeking question was initially asked about a familiar class of objects, rubbers. To answer the question, it was transformed into a question about a model constructed for the occasion. This model is

based on a more general model called the Gaussian chain model which has been introduced earlier in the book (see below). Within this model, an exact relation can be derived which can be compared to experimental results. As noted in section 4.1, this particular model is not very accurate, but has the virtues of being mathematically tractable and based on variables that figure prominently in the ontology of change of polymer physics.

The other category of explanation-seeking questions about theoretical models asked in the polymer physics books are initially formulated as questions about theoretical models. Unlike the molecular biology books, the polymer physics books introduce important theoretical models with characteristic names like the Rouse model or the Gaussian chain and initially explore them simply as interesting models[18]. Consider, for instance, the Gaussian chain or "feely jointed chain". This model is introduced in all the textbooks from polymer physics simply as an interesting model. It represents a single polymer molecule, alone in the universe, as a chain of N points jointed by one-dimensional links of equal length. Furthermore, it is assumed that the chain can change shape without geometric or energetic constraints. Because the model is so highly idealized, it is mathematically tractable, and interesting results can be derived within it quite easily if it is assumed that N is practically infinite (cf. the quote in section 4.2). After introducing a general model like the Gaussian chain, the books proceed to ask explanation-seeking questions about the model. How is the value of a given variable determined within the model? How does the model relate to other theoretical models? What is the effect of adding new assumptions to the basic model? Only subsequently is the question of how accurate the model is compared to particular systems considered. Once this is determined, the books may return to the model and ask how the accuracy can be improved. The answer is often to introduce further assumptions into the model which may make it less general and more difficult to handle mathematically. The Gaussian chain model, for instance, can be made more precise by adding self-avoidance to the model - i.e. the constraint that two segments of the chain cannot occupy the same position in space. This makes it more challenging to perform calculations within the model, but it improves the model's dynamical fidelity. Textbooks from other parts of physics will introduce general theoretical models in much the same way as the Gaussian chain is introduced in the polymer physics books. A general theoretical model like the harmonic oscillator is thus commonly introduced in this way in textbooks on classical or quantum mechanics (Giere 1988; Cartwright 1983). Importantly, such general theoretical models are not introduced as models of an interesting class of systems described independently of the model. Rather, the models define a new class of systems, namely the systems which the model can reasonably be applied to. Once the Gaussian chain model has been introduced, it is possible to divide polymer materials into those that have "Gaussian properties" (Strobl 1997 p. 304), i.e. materials where the behaviour of the individual polymers can be described though the Gaussian chain model, and those that do not have Gaussian properties. The results derived within the Gaussian model will, by definition, apply to any system that can be argued to have Gaussian properties. The next challenge is therefore to find out how many actual systems with Gaussian properties exist. Of course, if there were none, the model would not have ended up in the textbook.

The observation that additional types of explanation-seeking questions are asked in the polymer physics books compared to the molecular biology books raises two related questions: What does the polymer physicist gain

[18] The section on polymers from Pliscke and Bergesen (2006) consider only such general theoretical models.

by asking these additional questions? And, given that the physicist actually gains something: Why are questions about theoretical models not asked in the molecular biology books?

To answer the first question, consider the related question of which theoretical models a physicist gains something from introducing and exploring as general models. The following are important characteristics of the general models introduced in the polymer physics books:

1. The general models enable the polymer physicist to construct explanations as derivations referring to variables that figure prominently in the domain's ontology of change (representational fidelity), although these explanations are not always very precise compared to experimental results (dynamical fidelity).
2. If the dynamical fidelity of the basic model is low, it is important that it can be improved by adding assumptions to it. In this way, it can become a more precise model of the class of systems defined by the original model. The price is often that the model becomes less mathematically tractable.
3. The general models can be extended to become tractable models of particular experimental systems, as illustrated when the Gaussian chain model was extended to become a model of a piece of rubber (cf. section 4.1).

Weisberg (2007a, 2007b) provides some useful distinctions for understanding the benefits of models with these characteristics from an epistemological perspective. The dynamical fidelity of the general models discussed in the polymer physics books may not be very good. But dynamical fidelity is not always the primary aim of explanatory models. The general theoretical models introduced in the polymer physics books can be categorized as what Weisberg (2007a) calls minimal models, i.e. models that attain a satisfactory degree of dynamical fidelity by including as few factors as possible. Because they attain some degree of dynamical fidelity and at the same time can be applied to a large and diverse set of systems, they arguably have a high degree of representational fidelity and can be used to identify the variables within the domain's ontology of change that are the most important. The representational fidelity of the general models is then inherited by more specific models constructed, based on the general models, although the additions made may of course spoil the representational fidelity of the more specific model.[19]

The benefits of introducing general models that define a new kind of entities can also be viewed from a more cognitive perspective. Giere (1988, ch 3) argued, based on studies of textbooks in classical mechanics, that the theoretical models introduced in textbooks are connected in families. What connects the families of models varies. The theoretical models in the molecular biology books are connected by being models of the whole of or parts of the same mechanism or models of interacting mechanisms. They are thus connected through the relations among the objects or mechanisms they represent, and these can be identified without reference to the theoretical models in the family. Models in the polymer physics books are also connected in this way. However, in line with Giere's observations from classical mechanics, I argue that the theoretical models in the polymer physics books are connected into an additional set of hierarchical families. Many of the theoretical models in the polymer physics books are in addition connected by representing systems of a kind defined by a

[19] Based on a historical argument, Morrison (2007) shows that having a model or mathematical framework that can be applied with modifications to a great many systems is no reliable indicator of the truth of the framework.

general model introduced in the textbooks and explored for its own sake. The model of a rubber sample discussed in section 4.1 is thus both part of a family of theoretical models of rubber, and part of a family of theoretical models of polymer materials with Gaussian properties. Similarly, in classical mechanics a model of a ball rolling in a bowl is part of a family of models of spheres rolling on a surface which also includes, for instance, the model of a ball rolling down an inclined plane, and the family of models that are extensions of the general model of the harmonic oscillator which also includes, for instance, the model of the pendulum. There is an important difference between these two families of models. While the models in the first family are models used in solutions to problems with similar surface features, but solved through rather different problem solving techniques, the models in latter family are used in solutions to problems that in spite significant differences in surface features are solved using very similar techniques including the techniques learned by exploring the general theoretical model that defines the family. So, while recognizing a theoretical problem, for instance, the problem of describing the motion of a ball rolling in a bowl, as a problem that can be modelled using a model in the spheres-on-a-surface family of models suggests a wide range of problem solving strategies that may or may not be useful, recognizing it as a version of the familiar harmonic oscillator problem, provides a fairly narrow set of techniques that are very likely to be useful for solving the problem.

Chi and collaborators (1981) showed that the families of models set up by introducing a general model and exploring it for its own sake are utilized by expert physicists when categorizing theoretical problems. They showed that expert physicists categorize classical mechanics problems according to the general heuristics relevant for solving the problem, whereas novices categorise largely according to the kinds of entities described in the problem. They argued (pp. 134-38) that a plausible interpretation of why experts and novices categorize differently is that they form different (mental) models when presented with a problem. The expert physicist first constructs a highly idealised model of the problem and then considers whether there are peculiarities of the specific system that need to be put back into the model. A benefit of this strategy is that it enables the expert to identify a known general model that is likely to apply with modifications to the specific problem. However, this is only valuable if the known general model has been explored previously, thus relating a problem solving strategy to it. Recognizing a specific problem as an instance of the more general type of problem thus allows the expert to go in at the top of a hierarchical family of theoretical models and use the general strategies for solving problems of that type. From here, the physicist can look down through levels of generality in the family of models for existing extensions of the general model that may be valuable in the concrete case. The physicist may not find a suitable existing model, but only inspiration on how to extend the general model to make it fit the specific case. If so, and if the problem is eventually solved, the novel solution can become an extension of the established family of models and the problem solving strategies associated with it.

There is thus a rationale for why the polymer physicist finds it relevant to ask explanation-seeking questions about theoretical models. So why do the molecular biology books refrain from asking this type of explanation-seeking question?[20] Finding a complete answer to this question would require a historical investigation that

[20]Explanation through mathematical models is common within other domains within biology, and there is some debate within the biological sciences over the explanatory value of these models (Winther 2011; Green, Fagan & Jaeger 2014).

goes well beyond the textbook material considered in this study. I therefore limit myself to some considerations on why the benefits gained from asking explanation-seeking questions about theoretical models in polymer physics would not necessarily be gained by starting to ask them in molecular biology.

The epistemological benefits from asking explanation-seeking questions about general but minimal models discussed above are conditioned on the possibility of constructing minimal models that have representational fidelity as well as some dynamical fidelity with respect to a diverse class of systems. This possibility depends both on the complexity of the systems of interest in a given domain and on the domain's ontology of change. I argued in section 4.1 that the ontology of change in molecular biology is different from that of polymer physics. So, even when the two domains are interested in similar systems, it is not obvious that it is possible to construct very general models with a sufficient degree of representational and dynamic fidelity relative to the ontology of change of molecular biology, i.e. models representing to the distribution, composition and interactions among material objects, just because it is possible relative to the ontology of change of polymer physics.

The cognitive benefits discussed above of using general models to establish additional families of models have only been documented for theoretical problem solving. Especially, the more advanced polymer physics books are aimed clearly at a theoretical audience, for whom these benefits will be substantial. The molecular biology books on the other hand present explanations that have been constructed through laboratory research on model organisms. The benefit demonstrated by Chi and collaborators of recognizing a problem as a variant of a problem solved using a theoretical model from a family of models connected through a general theoretical model is that it suggest a narrow set of theoretical strategies for solving the problem. It is not obvious that the same family of models will always suggest an equally narrow set of experimental strategies for investigating the problem. Only if this can be established can the cognitive part of the rationale for asking explanation-seeking questions about theoretical models in polymer physics be directly transferred to molecular biology.

So, although a rationale for asking explanation-seeking questions about theoretical models in polymer physics can be established, differences in ontology and research methods mean that this rationale does not necessarily transfer to molecular biology, or other research domains for that matter.

5 Conclusions

In the preceding pages I outlined the differences in explanatory standards displayed in exemplar explanations from molecular biology and polymer physics. The discussion partly confirmed the expectation that mechanistic explanations are promoted in molecular biology, whereas derivations are in focus in polymer physics. However, the empirical analysis also provided important nuances to these expectations. I showed that mechanistic explanations are also valued in polymer physics, although not as much as derivations. I showed that the specific entities and activities in focus in the molecular biology books are changes in the distribution, composition and interactions among material objects, whereas the ontology of change is different in polymer physics, which explains referring to variables, noticeably physical quantities like energy and entropy. I also showed that explanations as derivations are importantly different from explanations as deductions. To understand

explanations as derivations, it is important to pay attention to the approximations and simplifications used, and the details of how these are justified. Finally, I showed that only the polymer physics books display explanations-seeking questions about theoretical models as a relevant kind of explanation-seeking questions and considered possible rationales for this difference.

I argued in the introduction that mappings of differences in explanatory standards across science domains are not just of interest to philosophers; they are relevant to educators as well. Differences in explanatory standards can become an obstacle in interdisciplinary problem solving if they are not identified and addressed. They are thus part of the reasons why it can be surprisingly difficult to integrate cognitive resources from different domains. If the aim of future education is to increasingly enable the students to perform integration of cognitive resources from a number of domains, as many argue it should be (see e.g. (NAS 2004; Roco, Bainbridge 2003; European Commission 2008)), it will be important that the students learn not only science content from different domains, but also to discuss differences in fundamental standards for good research, including good explanations, across domains, and how these differences may be bridged (Öberg 2009; Eigenbrode et al. 2007). To this end, descriptive studies like the one presented in this paper will be of value.

6 Appendix: On the keywords used to identify explanations

The exemplar explanations that formed the empirical basis for this study were identified through a set of keywords that were taken to be reliable indicators of a passage being an explanation (for more details, see (Goddiksen, forthcoming). The keywords were:

- All version of 'explain' and 'explanation'
- Why
- 'How', except when used in questions about how much.
- All versions of 'understand' and 'understanding'
- Because

Explanations are generally conceptualized as answers to explanations-seeking questions (Goddiksen 2014, introduction). 'How' (except 'how much') and 'why' indicate explanation-seeking questions, and the answers to such questions can be considered explanations when found in textbooks. Explanations provide understanding, so identifying passages providing understanding will identify explanations. However, other kinds of discourse – including thought experiments - may also provide understanding. A list is found in (Lipton 2009). Passages that were judged as not being of a kind of discourse on this list were considered explanations.

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