Neo-functional Analysis: Phylogenetical Restrictions on Causal Role Functions

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The most recent resurgence of philosophical attention to the so-called 'functional talk' in the sciences can be summarized in terms of the following questions: (Q1) What kind of *restrictions*, and in particular, what kind of *evolutionary restrictions* as well as to what extent, is involved in functional ascriptions? (Q2) How can we account for the *explanatory import* of function-ascribing statements? This paper addresses these questions through a modified version of Cummins' functional analysis. The modification in question is concerned with phylogenetical restrictions on causal role functions, and it stems from an analysis of some primary areas in molecular biology. I examine how evolutionary consideration affects the so-called 'function-analytical explanatory strategy' (Cummins [1975] 1998, 2002). Finally, I argue that the neo-functional analysis here proposed accounts for a certain convergence between the main rival theories of biological function.

1. Introduction. The most recent resurgence of philosophical attention to the so-called 'functional talk' in the sciences can be summarized in terms of the following questions: (Q1) what kind of *restrictions*, and in particular, what kind of *evolutionary restrictions* as well as to what extent, is involved in functional ascriptions? (Q2) How can we account for the *explanatory import* of function-ascribing statements?

The plurality of answers has been recently summarized by Perlman's categories of philosophical theories of functions (Perlman 2004, 5–7). Despite its detailed structure, Perlman's taxonomy of functions does not track affinities through which some theories are interconnected in the proposed classification. In fact, the function debate also shows a certain *convergence* between the two main accounts within the 'naturalistic-reductionist' category, that is, the so-called 'backward-looking' and 'forward-looking' accounts of functions. Thus, contrary to the taxonomy

suggested by Perlman, the convergence between these influential philosophical theories has been proclaimed as the correct strategy (Kitcher [1993] 2003), or even considered as a detailed solution (see, e.g., Godfrey-Smith [1994] 1998). Both proposals, however, are biased towards the backward-looking group, regardless of how 'modern' or 'recent' the appealed evolutionary history is. However, can we attain to the 'convergence ideal' from an independent theoretical proposal? More specifically, what is an adequate strategy for attaining the right explanatory match between evolutionary considerations, drawing in a determined sense on the backward-looking theories, and dispositional views of the forward-looking group?

Cummins' 'function-analytical explanatory strategy' and his corresponding 'functional analysis' related to a specific class of statements in biology and psychology (Cummins [1975] 1998, 1983) appear to be solid contenders in that respect. This account, in its basic claims, is not biased towards either of the two competing groups of theories. Moreover, Cummins' functional analysis emphasizes its complete neutrality with regard to evolutionary considerations (Cummins 2002). In this paper, I will argue that the account of functional analysis only rejects an erroneous employment of the Darwinian theory of evolution in addressing questions (Q1)–(Q2). Thereby it frees up space for different kinds of evolutionary considerations. Thus, in Section 3, *evolutionary restrictions* on functional ascriptions will be introduced, which are needed for the viability of the function-analytical explanatory strategy in sciences such as molecular biology. The new element in the functional analysis will encourage more clearly a different account of functional explanation: in Section 4 of this paper, I will argue in favor of a three-level function-analytical explanatory strategy, which fares better with the debate's main questions (Q1) and (Q2) than Cummins' two-level account.[1] Finally, the proposed account of a *neo-functional analysis* will also secure the acclaimed convergence ideal and, as I will try to show, base this ideal in the scientific practice of some of the primary areas in molecular biology.

However, in the next section, I will examine first the main elements of Cummins' functional analysis.

2. Functional Analysis and the Convergence Ideal. Cummins advances his

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1. Similar views on the three-level extension of Cummins' original account of functional explanation are proposed in more detail especially in Craver 2001, and Bechtel 1986. In Section 3 and, in particular, in Section 4, I will more directly distinguish my proposal with respect to the one endorsed in Craver's paper. In distinguishing these two emendations of function-analytical explanation, it will be also made clear in what way the kind of evolutionary restriction here at issue differs from the one put forward in Bechtel's paper.

account by refuting the main assumptions employed by major philosophical theories of functions: the so-called 'assumptions (A) and (B)' (Cummins [1975] 1998). His account states a new assumption, which I shall call *Assumption (C)*.

Assumption (A). The assumption in question deals specifically with the question concerning the explanatory import of function-ascribing statements in science:

 A. The point of functional characterization in science is to explain *the presence* of the item (organ, mechanism, process, or whatever) that is functionally characterized. (Cummins [1975] 1998, 169; emphasis added)

Furthermore, (A) stays at the core of any backward-looking or *etiological* account of functions.[2] According to such an account, functional ascriptions *explain* the presence or existence of items in certain domains in science. The following pair of statements, as usually stressed in the debate, illustrates the influence of Assumption (A) on the explanatory strategy of etiological accounts:

(1)   The function of the heart is to pump blood into peripheral organs.
(1*) The function of the heart is to produce sound of a determined frequency.

Now, only statement (1) can be considered as a legitimate function ascription. According to (A), the main reason for that lies in its explanatory import, that is, it explains the presence of the item in question.[3] Hence we may legitimately claim the functional characterization of statement (1) and discard statement (1*). When engaging with Assumption (B), we will see a more comprehensive story behind the backward-looking group of theories, but as far as their answer to (Q2) is concerned, that is, the question of explanatory import, this is the basic strategy of any, in Cummins' terms, 'teleological explanation' (Cummins 2002). However, what is essentially wrong with the assumption here at issue?

2. As commonly stated, the official philosophical formulation of this influential strand in the function debate is traced back to Wright 1973 (see also Wright 1976). Although the group of backward-looking or etiological accounts is exceptionally large, members of which differ in resiliency to a variety of counterexamples (see, for instance, Boorse's classical counterexample in his paper from 1976), Cummins deems that all of them substantially rely on the assumption in question. His assessment does not change even in Cummins 2002, in which the representatives of the corresponding approach to functional explanation are labeled as "neo-teleologists" (Cummins 2002, 161).

3. As I will argue in Section 4, the role of function-ascribing statements is not directly explanatory. Contrary to the etiological accounts, functional claims will be playing a particular role within a three-level explanatory strategy.

Functional analysis considers the misidentification of the explanandum as a first difficulty of an account based on (A). On that assumption, functional explanations are answers to the question of a type 'why is an item there?' In other words, Assumption (A) identifies the *presence* or *existence* of functionally characterized item as the correct kind of explanandum for scientific functional explanations. However, on Cummins' account, the actual scientific practice quite clearly suggests that functional claims have different explanatory targets. In the final part of this section, we shall see in what way that point breaks with the etiological tradition in the function debate by establishing a new kind of explanandum for the corresponding function-analytical explanatory strategy in the psychological and biological sciences.

However, the misidentification of the explanandum by itself would not represent the main difficulty for the accounts based on (A). A more serious difficulty is concerned with a certain 'teleological' stance of the aforementioned explanatory strategy. In other words, functional explanations in science mime the type of explanations given to the presence of items of *intentional design*. Thus, the answer to the question "why is that thing there (pointing to the gnomon of a sundial)?" (Cummins [1975] 1998, 174) exemplifies a general scheme for a valid functional explanation on the grounds of Assumption (A). Now, in order to avoid the objections reserved for traditional teleology (Cummins 2002), and to account for the explanatory import of function-ascribing statements in science, the backward-looking approach provides a determined *naturalization* of the appealed sources of design. This brings us to the second assumption.

Assumption (B). On Cummins' account of functional analysis, the assumption in question can be defined as follows:

B. For something to perform its function is for it to have *certain effects* on a containing system, which effects contribute to the performance of some activity of, or the maintenance of some condition in, that containing system. (Cummins [1975] 1998, 169; emphasis added)

Assumption (B) deals with function-ascribing statements. In particular, it refers to a group of *restrictions* required for legitimate functional characterizations in science. (B), thus, finds in the *selectionist* tenets of the Darwinian theory of evolution the right kind of restrictions. We can justify the claim 'the function of the heart is to pump blood into peripheral organs' in virtue of evolutionary selectionist restrictions. On that account, the *pumping of blood* is taken to be the heart's function, because that is the *effect* of the item, which was *selected* by certain evolutionary pressures in the past.

However, in Cummins' view, this appeal to evolutionary theory is a "cheap trick" (Cummins 2002, 170). In what follows, I will explicate the

motivation for such a negative assessment of the philosophical mainstream view on functions.

The line of attack on Assumption (B), on which Cummins insists most persistently, concerns the fact that "functions just do not track the factors driving selection" (Cummins 2002, 166). In other words, functions are out of reach of natural selection. What is targeted by that type of evolutionary pressure is concerned with the *survival value* (Tinbergen 1963) or *advantage value* (Wouters 2003) of functionally characterized item, not with the functional role itself. The point is exemplified by saying that "the better and worse wings have the same *function*, but only the former *spreads*" (Cummins 2002, 167; emphasis added). Therefore, the evolutionary pressures of natural selection track only the item that functions better in a given range of environmental circumstances than the item-competitors. According to the present objection to (B), the notion of function cannot be reduced to a corresponding selected effect. Thus, the approach of functional analysis loosens the dependence of function-ascribing statements on evolutionary considerations to the extent that they seem to be entirely neutral to restrictions in the latter sense. But, if the etiological basic strategy for reduction comes to a 'cheap trick' and, in addition, amounts to a misleading view on the Darwinian theory, on what grounds can we nevertheless legitimately retain functional talk in science? Furthermore, how can we account more adequately for its explanatory import? Cummins' answers are given by a cluster of claims in Assumption (C).

Assumption (C). The assumption according to which the approach of functional analysis addresses the issue of legitimate functional claims in science is stated as follows:

> x functions as a ϕ in s (or: the function of x in s is to ϕ) relative to an *analytical account A* of s's capacity to ψ just in case x is capable of ϕ-ing in s and A appropriately and adequately accounts for s's capacity to ψ by, in part, appealing to the capacity of x to ϕ in s. (Cummins [1975] 1998, 190; emphasis added)

However, rather than constituting the basic assumption of Cummins' theory of functions, the quoted formulation represents an implication of the explanatory strategy related to the *analytical account A*. Functional ascriptions in science are, thus, in a determined sense derivative upon a corresponding explanatory strategy. In other words, we are entitled to claim that 'the function of the heart is to pump blood into peripheral organs' on the grounds of the explanatory scheme, established by functional analysis. The explanatory strategy of this analytical account, as the basic claim related to Cummins' Assumption (C), "proceeds by analyzing a disposition d of a into a number of other dispositions $d1, . . ., dn$ had

by *a* or components of *a* such that programmed manifestation of the *di* results in or amounts to a manifestation of *d*" (Cummins [1975] 1998, 187). In the remainder of this section, I will single out the main elements of this explanatory strategy, by which Cummins traces the most significant distinction from the teleological explanatory strategy of etiological or backward-looking accounts.[4]

First, functional analysis has a different type of explanandum than teleological explanation. Rather than the presence or existence of a functionally characterized item, the new type of explananda is concerned with "the behavior of a containing system" (Cummins [1975] 1998, 176). Thus, referring to the aforementioned formulation of the analytical explanatory strategy, a *containing system* is indicated by the variable '*a*', and its *behavior* by the variables '*d*' or, according to Assumption (C), 'ψ', both indicating the corresponding disposition or capacity. The latter group of variables indicates the type of explananda targeted by Cummins' account of functional explanation.

Second, the account in question also has different elements within its explanans: (Es1) *Functions as Causal Contributions*. Since a certain higher-order disposition *d*, or a capacity ψ, requires explanation, the analytical account *A* decomposes it into a determined group of lower-order dispositions. In that explanatory framework, *functions* are only those *analyzing capacities ϕi* or *dispositions di,* which *causally contribute* in a specific, 'programmed', way to the manifestation of the analyzed capacity ψ or disposition *d* of *a*, that is, of a containing system *s*.[5] However, this causal reduction gains an explanatory import if and only if the explanans of functional analysis satisfies certain conditions; (Es2) *The Applicability Conditions*. The conditions in question are determined purely on the grounds of our "explanatory interest" in a related scientific domain (Cummins [1975] 1998, 191–192). Cummins' applicability conditions are concerned with the degree and typological difference between the analyzed and analyzing dispositions and, finally, with the relative complexity of organization of the analyzing capacities. Thus, a function-analytical ex-

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4. Although functional analysis abundantly employs the dispositionalist terminology, it should be distinguished from a forward-looking theory of functions, as already specified by Perlman's taxonomy. For an evaluation of the theories in the latter sense, such as Bigelow and Pargetter 1987 and Horan 1989, see Mitchell 2003, 103–108. Cummins' account of explanation in the psychological and biological sciences does appeal to a dispositional approach, but, as we shall see later on, does so only in a determined sense within the general function-analytical explanatory strategy. In my view, this point constitutes a major difference from a forward-looking or dispositional account.

5. In Sections 3 and 4, I will point out this type of causal contribution as one of the major intrinsic difficulties of functional analysis.

planation A 'appropriately and adequately' accounts for an explanandum, provided the conditions at issue secure a sufficiently wide gap between the analyzed and analyzing capacities. Since there is no all-or-nothing situation in such a case, the applicability of this explanatory strategy, through which we state functional characterizations, is ultimately a *pragmatic* issue of choosing the right account for a given explanandum.

The production of proteins, as analyzed in molecular biology, may illustrate what Cummins has in mind by his peculiar explanatory strategy, which may be represented as an 'assembly-line production' (Cummins [1975] 1998). However, before we venture any further into the viability of the function-analytical explanatory strategy in molecular biology, we should explore the most frequently highlighted difficulty of Cummins' theory, namely, its *too liberal character* (see, e.g., Kitcher [1993] 2003; Weber 2004). As we shall see in the next section, functional analysis admits into science unacceptable functional characterizations. This difficulty brings the discussion of (Q1) back to the starting-point: on what grounds can we single out legitimate functional claims? Accordingly, what other kind of restrictions must be added to the already existing applicability conditions in order to make fully operative the function-analytical explanation in the corresponding scientific domains?

3. Neo-functional Analysis and Evolutionary Restrictions. Consider the following two situations, usually deployed against Cummins' account (Kitcher [1993] 2003, 169): (s1) an arrangement of rocks a makes partial causal contribution $Ca1$ to the widening of a river delta D. (s2) a mutation of the type a makes partial causal contribution $Ca1$ to the formation of a determined tumor D. Both situations satisfy the applicability conditions required by Cummins' version of functional analysis. However, we cannot identify the partial causal contributions $Ca1$ in (s1) and (s2) as *functions*, that is, legitimate scientific functional ascriptions to the items in question. Briefly, that point constitutes the aforementioned objection of a 'too liberal character' of functional analysis.[6]

Nevertheless, Cummins' original paper contains an explicit reply to that kind of objection. On this account, we can rule out the corresponding counterexamples purely on the grounds of the three pragmatic applica-

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6. The two situations, as it will be highlighted, including a third one, are not identical in their respective main features. For instance, (s2) is concerned with the normative side of functional characterizations, rather than with their overly liberal attributions in the strict sense (for a defense of functional analysis from this type of criticisms, see in particular Amundson and Lauder 1994, 452–453). Nevertheless, I will argue that having a 'too liberal character' reveals the most troubling difficulty in Cummins' account, which cannot be dismissed by simply switching functional analysis to science-based cases, as claimed by Amundson and Lauder (1994, 452).

bility conditions (Cummins [1975] 1998, 191). However, this proposal does not solve the problem, because the width of the gap, as posited by the applicability conditions, is equivalent in unacceptable and legitimate functional characterizations.[7] Thus, although these situations are not of the same kind, they all locate with sufficient precision the most vulnerable part in the account of functional analysis. A plausible solution to that kind of difficulty might consider the capacity of 'pumping of blood' as somehow amounting to a *biologically significant* capacity. Its significance, however, cannot be accounted for in the way pursued by the selected-effect theories of functions: as already shown, Cummins' functional analysis argues for a complete independence of evolutionary considerations in that sense (Cummins 2002).

In what follows, I will argue that in order to resolve its main difficulty, the approach of functional analysis should be integrated in a certain way with evolutionary considerations. In that respect, it is important to make clear: (i) what kind of evolutionary considerations may fit into the account in question; (ii) what role that kind of considerations can play in an account of functional ascriptions and of function-analytical explanation, which then can bring us closer to the proclaimed convergence ideal.

The scientific practice of molecular biology, in particular its efforts in discovering the complexity of protein synthesis, suggests an application of the Darwinian evolutionary theory, which seems to steer away from the 'cheap tricks' of the selectionist reductionism on functions. Moreover, the application in question also eschews an appeal to evolutionary considerations as a background or contextual knowledge in a general sense (Kitcher [1993] 2003, 173). The discovery and explanation of the main causal mechanisms in the overall process of protein synthesis also offer an important insight into how evolutionary theory takes part in the scientific field that appears to fit well into the function-analytical account described above.

3.1. Phylogenetical Entrenchment as a Restriction on Functional Ascriptions in Molecular Biology. Taking into account the translational component in the process of protein production in a determined biological system, we may single out the following function-ascribing statement:

 (F1)   The function of the translational mechanism in a determined biological system is to transfer genetic information from the mRNA molecule to the corresponding amino acid residues in the primary structure of proteins.

7. As far as Cummins' maneuvering on that point is concerned, especially with regard to the standard example of heart's function, see Cummins [1975] 1998, 191–192.

At this point, it should be made clear whether there is any other type of reasons for claiming (F1) apart from the type of so-called 'stereochemical reasons', as they are generally classified in molecular biology (Crick 1970, 562). Even though scientific practice involved with that aspect of protein synthesis is not completely explicit on this issue, it nevertheless brings forward a suggestion that determines more closely the type of *evolutionary restriction* on the scientific claims exemplified by (F1). Consider in that respect the case of so-called 'back translation', that is, the possibility of nucleic acids synthesis, both of RNA molecules and of DNA, on a certain polypeptide template. As made clear in the debate on the impact of the discovery of 'reverse transcriptase' (Baltimore 1970; Temin and Mizutani 1970) on the original version of the 'central dogma' of molecular biology (Crick 1958), the possibility of back translation is discarded on several distinct grounds, among which there are also evolutionary considerations. The latter, however, appear to be employed rather generally, because of (1) indistinct character of *evolutionary pressures* acting on the protein synthesis process, (2) no detailed assessment of *fitness* or related criteria (Wouters 2003) with regard to other translational scenarios, (3) a 'panglossian' view on the *adaptive function* in question. However, despite that, the actually employed evolutionary perspective has a different character than apparently suggested by the above coarse application of the Darwinian tenets.

We may determine this particular kind of evolutionary restriction as a sort of *entrenchment* condition. This condition states the extent to which a supposed causal mechanism in molecular biology would require rearrangements of a given level of biological organization. Consider again the overall process of protein synthesis. Although being classified as a 'special transfer' of genetic information, the reverse transcription can be accommodated into the already existing organization of the main processes in molecular biology, without calling their capacities into question. The back translation, on the contrary, would require a thorough re-arrangement of "the whole intellectual basis of molecular biology" (Crick 1970, 563). The entrenchment condition thus instantiates evolutionary considerations by determining the relationship to phylogenetically more conservative causal mechanisms.[8] Taking into account the aforementioned kind of evolution-

8. This kind of evolutionary considerations are operative within molecular phylogenetics (for an adequate illustration of this point, and a general overview of the history of the related debate, see, respectively, Alberts et al. 1989, 12–13, and Dietrich 1998). The condition of phylogenetical entrenchment is also presupposed by Crick's famous characterization of the genetic code as the most deeply 'frozen accident' of evolutionary history (Crick 1968). Given the aims of this paper, I will leave aside the intrinsic difficulties of Crick's characterization and the general debate on that issue (see, e.g., Sarkar 2005).

ary considerations presupposed by the basic processes in molecular biology, it should become apparent in what way that kind of considerations might act as a restriction on scientific functional characterizations. In my view, this will also show how the neo-functional analysis can address the difficulty of a 'too liberal character', avoiding at the same time the objections against the selectionist theories of functions.

3.2. Phylogenetical Entrenchment as an Identification Criterion in the Neo-functional Analysis. Recall Cummins' scheme of the function-analytical explanation. On this account, function-ascribing statements can provide a determined explanatory import with respect to a higher-order capacity ψ of a system s if and only if the applicability conditions are met. However, as already seen, Cummins' original account is vulnerable to the counterexamples which suggest that a determined employment of evolutionary considerations is a possible way out of that difficulty, and more in tune with actual scientific practice.[9]

Now, the condition of phylogenetical entrenchment may intervene into the function-analytical explanatory strategy at the level of explanandum, namely, by *identifying* a determined analyzed capacity ψ. More to the point, the identification in question concerns the fact that ψ is considered as a 'biologically significant capacity' (Cummins [1975] 1998; Schaffner 1993). The applicability conditions, however, by themselves cannot account for the latter feature, whereas the reductionist program of a 'selected effect' variety is not in that respect a viable option.[10]

However, if we assume into the neo-functional analysis here proposed the kind of evolutionary consideration instantiated by the condition of phylogenetical entrenchment, then this condition accounts for the identification of a certain capacity in molecular biology as a biologically significant capacity, therefore, as the explanandum capacity ψ. In other words, without recognition of the differential phylogenetical entrenchment, Cummins' explanatory strategy remains a non-starter, because as

9. In the recent debate, there are different non-evolutionary proposals for amending functional analysis. Among them Craver's proposal (2001) excels for its most elaborate sympathetic reading of Cummins' account. Nevertheless, Craver's purely pragmatic approach to the condition of 'topping off' (Craver 2001, 67–73) displays, in that respect, the same difficulty as Cummins' original account. As I will argue in the remainder of this section, the emendation of the corresponding point in functional analysis, through the kind of evolutionary considerations here proposed, may also render less arbitrary the so-called 'perspectival' character of Craver's contextual explanation (see Craver 2001, 71).

10. For a similar remark, see Schaffner 1993, 400–401. Schaffner, however, is skeptical about restoring the validity of functional analysis by implementing any other kind of evolutionary considerations in their standard sense.

it stands it is unable to account for the explananda of interest in a related biological domain.[11]

In the next section, I will examine in what way the introduction of evolutionary condition affects Cummins' original explanatory scheme. Thus, I will further support a three-level extension (see Craver 2001) of Cummins' two-level scheme of the function-analytical explanatory strategy. However, contrary to Craver's account, I will try to show that the evolutionary restriction of phylogenetical entrenchment better accounts for a distinct explanatory role of functional ascriptions in molecular biology.

4. Functional Ascriptions as an Intermediate Explanatory Level in Molecular Biology. Rather than acting as a *direct explanans* of the manifestation of a higher-order capacity ψ in Cummins' analytical account A, function-ascribing statements are now considered as occupying an *intermediate* level within an extended explanatory scheme. The level in question mediates between an evolutionary bound explanandum capacity ψ and the basic explanatory level consisting of a determined set of causal mechanisms.[12] Now, particular causal descriptions acquire their explanatory import *within* that version of a three-level function-analytical explanatory strategy. In order to exemplify the point under consideration, we should examine again the production of proteins.

Consider a different expression of (F1):

(F2) tRNAs *function* as the 'adaptor' molecules between an mRNA template and side chains of amino acids in a determined biological system.[13]

The explanatory import of (F2) can be accounted for by considering a tRNA's function ϕ as a determined schematic characterization that calls for particular causal-mechanistic explanations, for instance, *how* the so-

11. With that, it is simply meant that the evolutionary considerations of this kind are playing an active role with other factors in identifying 'biologically significant capacities', as shown in the case of the discovery and explanation of the basic mechanisms in protein synthesis. Accordingly, this particular emendation of Cummins' account also deals with the arbitrariness of the 'topping off' condition in Craver's proposal (see note 9). For another emendation of functional analysis, which is less conciliatory to Craver's pragmatic, non-evolutionary solution, see Section 4.

12. For an analysis of the conception of causal mechanism, used in molecular genetics for instance, see Godfrey-Smith 2000. I will however limit the analysis to an exemplification of the conception here at stake through its relationship to the class of function-ascribing statements.

13. As far as the role of the so-called 'adaptor hypothesis' in the history of molecular biology is concerned, see Morange 2000.

called 'acceptor stem' of a certain tRNA molecule interacts with the corresponding amino acid side-chain, specific for that tRNA (see, e.g., Stryer 1988, 733–746). In other words, the function ϕ in question provides a partial explanatory import with regard to Cummins' higher-order capacity ψ in some biological system s if and only if ϕ represents the right kind of schematic characterization or a framework-statement (Wouters 2004) for the causal-mechanistic explanations. Yet, what prevents us from reducing the level of function-ascribing statements to the basic explanatory level of causal mechanisms (see, e.g., Ruse 2002)? Is there any further role that evolutionary considerations can play in that respect?

At this point Cummins' notion of 'programmed manifestation' should be recalled, which qualifies the causal activity of component-parts in the function-analytical explanation (Cummins [1975] 1998, 187). Now, although delicate issues arise about this point (see, e.g., Craver 2001; Tabery 2004), the notion in question raises again the issue of evolutionary neutrality associated with Cummins' account. If the selected effect reductionism is not a plausible way to deal with the 'programmed' causal activity of functionally characterized item, some other kind of evolutionary considerations, nevertheless, calls for an application (Cummins 2002, 170). Let's finally see how the condition of phylogenetical entrenchment may fit into the acknowledged gap in the original version of functional analysis.

As in the case of (F2), when we functionally characterize a tRNA molecule, according to the function-analytical approach, this claim amounts to a partially *programmed* causal contribution to the manifestation of a higher-order biological capacity. Since the latter is *ultimately* identified as explanandum on the grounds of its phylogenetical entrenchment, this kind of evolutionary consideration puts certain constraints on the way a tRNA molecule can make a partial causal contribution to the overall process of poly-peptide production in a determined biological system.[14]

In order to illustrate more closely the point here at stake, let's examine the case of *adaptor hypothesis*. The function of a particular tRNA is

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14. Here again comes into focus the importance of an evolutionarily amended 'topping off' condition for the viability of functional analysis. Thus, even though the phylogenetical entrenchment of ψ provides just a basic determination for particular causal activity ϕi of a corresponding functionally characterized item, it nevertheless brings out the main boundaries for causal-mechanistic explanations. In that respect, Amundson and Lauder (1994, 465) rightly emphasize the role of the concept of morphospace in phylogenetical analyses as a suitable theoretical device for the interface of functional and evolutionary morphology. In what follows, I will limit my analysis to a historical case study in molecular biology, which shares the main features with the present scenario.

constrained by the rules of the genetic code and those of a Watson-Crick type of base-pairing. Given a deep phylogenetical entrenchment of these rules, a major evolutionary constraint, conceived in the aforementioned sense, limits to a large extent a range of possible programmed manifestations of a tRNA's partial causal contribution to the transfer of genetic information in the protein production process.[15] The examined case, thus, suggests that a specific employment of the Darwinian evolutionary theory in molecular biology plays no other role with regard to the overall strategy of function-analytical explanation than to establish a hierarchy of *limiting conditions*, which is expected to be binding most strictly for the programmed causal activity of a functionally characterized item.

We may now assess the results obtained by the neo-functional analysis here proposed by answering questions (Q1) and (Q2).

5. Concluding Remarks. As for (Q1), even functional ascriptions in sciences such as molecular biology are restricted by evolutionary histories. However, contrary to the general reductionist program of the backward-looking accounts, the function of a determined biological item is not singled out on the grounds of some supposed selective scenario from recent or, rather, remote evolutionary past. Following Cummins' approach, the neo-functional analysis identifies functions as particular causal contributions to the behavior of a containing system. Nevertheless, evolutionary restrictions in the sense of phylogenetical entrenchment introduce limitations into possible programmed causal activity of a functionally characterized item, without thereby reducing the causal contribution in question to a corresponding selected effect.

The proposed emendation of functional analysis through the notion of phylogenetical entrenchment, besides protecting it from the objection of being too liberal in the attribution of functional properties, also accounts more adequately for the function-analytical explanatory strategy in mo-

15. On the other hand, there is an important limitation to the phylogenetical entrenchment of the genetic code, expressed by the so-called 'wobble hypothesis'. The latter is concerned with a steric freedom in the tRNA's pairing of the third base of the mRNA codon. The 'wobble hypothesis' has some significant implications: (i) contrary to the predictions based on the rules of complementary base-pairing, some tRNA molecules recognize more than one mRNA codon; (ii) the so-called 'degeneracy' of the genetic code results partially from "imprecision (wobble) in the pairing of the third base of the codon" (Stryer 1988, 745). Arguably, we might conclude that the wobble hypothesis could to a certain degree encourage a revision of the Dobzhanskyan perspective (see Theodosius Dobzhansky's famous slogan "nothing makes sense in biology except in the light of evolution" in Dobzhansky 1964, 449). The revision can ultimately amount to the claim that "much of the received framework of evolution makes no sense in light of molecular biology" (Sarkar 2005, 5). However, as already suggested, I will consider the corresponding implications on different grounds.

lecular biology. Thus, as far as question (Q2) is concerned, on the account of the neo-functional analysis, a distinctive import of function-ascribing statements within that explanatory strategy does not simply consist in a compressed version of more detailed causal-mechanistic explanations. Their import to the overall function-analytical explanation in molecular biology rather consists in constituting the right kind of framework-statement for the basic explanatory level of causal mechanisms determination. It is exactly on this explanatory strategy that we can base the convergence ideal on biological functions.

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