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Subject Section

Xenolog Classification

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Abstract

Motivation: Orthology analysis is a fundamental tool in comparative genomics. Sophisticated methods have been developed to distinguish between orthologs and paralogs and to classify paralogs into subtypes depending on the duplication mechanism and timing, relative to speciation. However, no comparable framework exists for xenologs: gene pairs whose history, since their divergence, includes a horizontal transfer. Further, the diversity of gene pairs that meet this broad definition calls for classification of xenologs with similar properties into subtypes.

Results: We present a xenolog classification that uses phylogenetic reconciliation to assign each pair of genes to a class based on the event responsible for their divergence and the historical association between genes and species. Our classes distinguish between genes related through transfer alone and genes related through duplication and transfer. Further, they separate closely-related genes in distantly-related species from distantly-related genes in closely-related species. We present formal rules that assign gene pairs to specific xenolog classes, given a reconciled gene tree with an arbitrary number of duplications and transfers. The xenology classification rules have been implemented in software and tested on a collection of ~13,000 prokaryotic gene families. In addition, we present a case study demonstrating the connection between xenolog classification and gene function prediction.


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to infer the specific duplication process that gave rise to a given set of paralogs (Durand and Hoberman, 2006; Van de Peer, 2004; Simillion et al., 2004).

Homology identification is a highly active research area, comprising methodological approaches ranging from sequence comparison to phylogenetic reconciliation. More recent innovations include the exploitation of shared synteny (Shi et al., 2011) and specialized methods for identifying multidomain homologs (Song et al., 2007, 2008; Ali et al., 2016).

Most work on homology analysis to date has not considered genes related through horizontal transfer. Studies of horizontal transfer commonly use approaches that seek to identify genes of foreign origin in a given genome, rather than homologous gene pairs that are related through horizontal transfer (reviewed in Azad and Lawrence, 2012). A few methods, such as gene tree - species tree reconciliation, do infer gene pairs that correspond to the donor and recipient of a transfer. Reconciliation algorithms that account for transfer events are relatively new (reviewed by Nakliie, 2010, 2013; Huson and Scornavacca, 2011), computationally more complex, and are only recently coming into use for genomic analyses (e.g., David and Alm, 2011; Richards et al., 2014).

Appropriate terminology for describing gene pairs related through horizontal transfer is a fundamental requirement for extending the homology analysis framework to include this evolutionary process. The term “xenolog”, proposed by Gray and Fitch (1983) to describe horizontally transferred genes, is in use, but not widely, and there is no consensus on a precise definition. Further, there has been little discussion of differentiating xenologs to convey distinctions between horizontally transferred genes with different properties (see Koonin et al., 2001, for a notable exception). Such xenolog classes would be analogous to paralog subtypes proposed to convey the relative timing of duplications and speciations (e.g., in-paralogs versus out-paralogs, Sommerhammer and Koonin, 2002) or distinguish between different mechanisms of duplication (e.g., ohnologs and tandem duplications, reviewed by Durand and Hoberman, 2006; Ramos and Ferrier, 2012).

**Background:** Fitch (1970) introduced the terms orthology (“homology [that] is the result of speciation”) and paralogy (“homology [that] is the result of gene duplication”) and proposed that “foreign genes...since they are neither orthologous nor paralogous but are clearly homologous...should be called xenologous” (Gray and Fitch, 1983). These definitions, which are framed in terms of the event that caused the divergence, have been widely adopted. In 2000, Fitch proposed more precise definitions of orthology and xenology. Orthology includes the requirement that the “common ancestor lies in the cenancestor of the taxa from which the two sequences were obtained,” where a cenancestor is the “most recent common ancestor of the [species] taxa under consideration,” and xenology is the “relationship of any two homologous characters whose history, since their common ancestor, involves an interspecies (horizontal) transfer of the genetic material for at least one of those characters.” In other words, a pair of genes, $g_1$ and $g_2$, are xenologs, if there is a transfer on the path connecting $g_1$ and $g_2$ in the gene tree.

In this updated definition, orthology is defined not just in terms of a speciation event, but in terms of the association of nodes in the gene and species trees. Under a duplication-loss event model, the earlier, event-based definition of orthology and this definition are equivalent. However, when transfers are included in the event model, the sets of orthologs predicted using the two definitions are not identical. Moreover, the event-based definition leads to predicted orthologs that have properties that are not usually associated with orthologs.

For example, node $g_1$ and $g_2$ in Figure 1 are orthologs according to the event-based definition, because the event at their most recent common ancestor ($g_1$) is a speciation. Yet $g_1$ and $g_2$ are genes in the same-present-day species $X$, violating the assumption that genes in the same species cannot be orthologous. Gene pairs in species $X$ and $Z$ also exhibit surprising behavior according to the event-based definition. The most recent common ancestor of $g_1$ and $g_2$, denoted as $h_1$, is a speciation node, as is the most recent common ancestor of $g_1$ and $g_3$, implying that both pairs are orthologs in the species $X$ and $Z$. However, these pairs arose at very different times in the species tree, violating the assumption that orthologs drawn from the same pair of species are associated with the same species divergence and are roughly the same age (Goodman et al., 1979; Capra et al., 2013). Neither of these problems arises when the cenancestor-based definition is used, because neither $g_3$ nor $g_4$ are orthologs of $g_1$ under that definition. In both cases, the most recent common ancestor of the genes does not lie in their cenancestor.

More generally, the additional cenancestor requirement results in a restricted set of orthologs that excludes these problematic cases. However, a consequence of defining orthologs narrowly is that xenologs are defined broadly: the set of gene pairs whose history, since their divergence, includes a transfer is substantially larger than the set of genes that diverged through a transfer event at their most recent common ancestor. Xenologs, when broadly defined, exhibit diverse properties. First, not all xenologs have the same event at their most recent common ancestor in the gene tree. We observe xenologs where this divergence arose via transfer (e.g., $g_1$ and $g_2$), speciation (e.g., $g_3$ and $g_4$), and duplication (e.g., $g_5$ and $g_6$). Second, xenologs can occur in the same species (e.g., $g_3$ and $g_4$). Third, xenologs may vary greatly in how closely they are related, and the divergence of a pair of xenologs may pre- or post-date the divergence of their associated species. For example, genes $g_1$ and $g_2$ diverged more recently than species $X$ and species $Z$, whereas genes $g_3$ and $g_4$, diverged before species $X$ and species $W$.

**Our Contributions:** This broad definition of xenologs does not convey important distinctions between the diverse and complex xenologous relationships that arise due to horizontal gene transfer. To address this, we propose xenolog classes that reflect the events associated with the divergence of a xenologous gene pair, and the relative timing of transfer and speciation events. We present formal definitions of these classes in the context of a reconciled gene tree and rules to assign xenologous gene pairs to classes. Further, we show that these classes form a hierarchy, connecting the relationship of xenologs to their placement in the gene and species trees.

An algorithm implementing these rules has been integrated into the Notung 2.8 software package. An analysis of ~13,000 prokaryotic gene families demonstrates that all of the proposed classes arise in real gene tree data. We further present a case study that illustrates the potential functional implications of xenolog classification. Finally, we discuss how this framework could be used in future research to explore the evolutionary and functional fates of transferred genes.
2 Methods

Our classification takes as input a gene tree, $T_G = (V_G, E_G)$, that has been reconciled with a species tree, $T_S = (V_S, E_S)$, using a duplication-transfer model. The model may also include losses; losses have no impact on xenolog classification and we do not discuss them further. Reconciliation infers a mapping, $\sigma$, between genes and species, where $\sigma(g) = s$ indicates that gene $g \in V_G$ was present in the genome of species $s \in V_S$. Each internal node, $s$, is annotated with $\sigma(s)$, the event that caused the divergence of $s$, where $\sigma(s)$ is a duplication ($D$), a transfer ($T$), or a speciation ($V$). Transfer edges are denoted by $T_{ij}$, where $g_i$ is the recipient gene node, $g_j = \sigma(g_j)$ is the donor gene node, and $\sigma(g_j) = \tau$. We say transfer $T_{ij}$ is on the path from $g_i$ to $g_j$, if the path from $g_i$ to $g_j$ passes through both $g_i$ and $g_j$.

The output of our classification scheme is a homology table $H(g_i, g_j, \sigma, D, V)$. In this classification, which is based on the definitions introduced by Fitch (2000), genes $g_i$ and $g_j$ are:

- **orthologs** iff $\sigma \in \{\text{MCA}(g_i, g_j)\} = \sigma$ and there is no transfer on the path from $g_i$ to $g_j$;
- **paralogs** iff $\sigma \in \{\text{MCA}(g_i, g_j)\} = \delta$ and there is no transfer on the path from $g_i$ to $g_j$;
- **xenologs** iff there is at least one transfer on the path from $g_i$ to $g_j$.

Note that by explicitly defining orthologs to be genes that are not connected by a transfer, this definition of ortholog ensures that the ancestor of orthologous genes lie in their common ancestor; i.e., $\sigma = \{\text{MCA}(g_i, g_j)\} = \{\text{MCA}(g_i, g_j)\}$.

If $g_i$ and $g_j$ are orthologs, then $H(g_i, g_j) = H(g_j, g_i) = \Omega$. If they are paralogs, $H(g_i, g_j) = H(g_j, g_i) = \Omega$. If $g_i$ and $g_j$ are xenologs, then $H(g_i, g_j) = H(g_j, g_i)$, where $X(g_i, g_j)$ is the xenolog class of genes $g_i$ and $g_j$. In contrast to orthology and paralogy, xenology is not symmetric, due to the directional nature of horizontal transfer.

In the remainder of this section, we define new xenolog classes and give formal rules for determining the xenolog class, $x(g_i, g_j)$, for a given gene pair $g_i$ and $g_j$. In Section 2.1, we consider the case where there is a single transfer on the path from $g_i$ to $g_j$ and they did not diverge by duplication (i.e., $\sigma = \{\text{MCA}(g_i, g_j)\} = \Omega$). In Section 2.2, we provide xenolog classification rules for the case where the common ancestor of $g_i$ and $g_j$ is a duplication and introduce a subclass of xenologs, called paraxenologs, for designating genes that are related through both duplication and transfer. We extend these definitions to allow an arbitrary number of transfers on the path from $g_i$ to $g_j$ in Section 2.3.

2.1 Xenolog classification with a single transfer

Consider a gene tree with a single transfer $T_{ij} = (g_i, g_j)$ from donor species $g_i \in \{g_i(g_j)\}$ to recipient species $g_j \in \{g_j\}$. Let $\sigma = \text{MCA}(g_i, g_j)$ be the common ancestor of $g_i$ and $g_j$ and let $T$ be the set of nodes in the subtree of $T_G$ rooted at $\sigma$. Transfer $T_{ij}$ defines three, non-overlapping sets of species tree nodes: $D = \{s \in V_S \mid \text{MCA}(s, s) \leq \sigma\}$, i.e. the species that are more closely related to the donor than the recipient; $R = \{s \in V_S \mid \text{MCA}(s, s) < \sigma\}$, i.e. the species that are more closely related to the recipient than the donor; $V = V_G \setminus T$, i.e. the nodes in the species tree equitably related to the donor and recipient.

We define four, mutually exclusive xenolog classes based on these sets. Xenolog classes are defined with respect to a reference gene $\bar{g} \in L(T_G)$ that is a descendant of the recipient of the transfer, i.e., $\bar{g} \in \Delta(g_j)$. For every $g \in \{L(T_G) \setminus \Delta(g_j)\}$, $g$ is on the path from $\bar{g}$ to $g$ and $g$ is a

- **Primary xenolog** iff $g \in \Delta(g_j)$;
- **Primary Recipient xenolog** iff $g \in D$ and $g \not\in \Delta(g_j)$;
- **Sibling Recipient xenolog** iff $\bar{g} \in R$;
- **Outgroup xenolog** iff $g \in O$.

Xenologs are classified relative to a reference gene; therefore, xenolog class assignments are not symmetrical. In the homology table, $H(\bar{g}, g) = \bar{g}(\bar{g})$, $H(\bar{g}, g) = \bar{g}$ is used to indicate that $g$ is the xenolog of the reference gene, $\bar{g}$, and that its class is given by $H(\bar{g}, g)$.

In Figure 1, all genes are xenologous to $\bar{g}$. Both $g_2$ and $g_3$ are in set $D$: $g_2$ is a Primary xenolog ($x(g_2, g_2) = \text{PX}$) and $g_2$ is a Sibling Donor xenolog ($x(g_2, g_2) = \text{SDX}$), because $g_2$ is a descendant of the donor (i.e., $g_2 \in \Delta(g_1)$ and $g_2$ is not. Genes $g_2$ and $g_3$ are in set $R$ and are Sibling Recipient xenologs ($x(g_2, g_2) = \text{SRX}$). Gene $g_4$ is an Outgroup xenolog ($x(g_4, g_2) = \text{OX}$) because $g_4$ is in set $O$. Genes $h_1$ and $h_2$ are paraxenologs and will be discussed in Section 2.2.

A xenologic gene pair can be further annotated to indicate cases where the genes are found in the same species: $g$ is an **autaxonolog** of $\bar{g}$, iff $\sigma = \sigma(g)$ (we designate this $x(\bar{g}, g) = X^\sigma$). Autaxonologs will also be assigned to a subclass. In Figure 1, $g_2$ and $g_3$ are both in species $X$; $g_4$ is a Sibling Recipient autaxonolog ($x(\bar{g}, g_4) = \text{SRX}^\sigma$).

Xenolog class hierarchies: The xenolog classes form a hierarchy that can elucidate how xenologs are related in both the gene and species trees. Primary xenologs are closest in the xenolog hierarchy and Outgroup xenologs are most distant. We denote this hierarchy by $\text{PX} < \text{SDX} < \text{SRX} < \text{OX}$, where $x(\bar{g}, g_1) < x(\bar{g}, g_2)$, if $g_1$ and $g_2$ are closer in the hierarchy than $\bar{g}$ and $g_1$.

Genes that are more closely related in the hierarchy are also more closely related in the gene tree. Let genes $g_1$ and $g_2$ in $V_G \setminus \Delta(g_j)$ be xenologs of $\bar{g}$ such that there is no transfer ancestral to either $g_1$ or $g_2$. Then, $\text{MCA}(\bar{g}, g_1) < \text{MCA}(\bar{g}, g_2)$, if $x(\bar{g}, g_1) < x(\bar{g}, g_2)$. This hierarchy, which is illustrated in Figure 2, is stated formally as follows:

**Theorem 2.1.** (Xenolog class hierarchy in the gene tree) Given $\bar{g} \in \Delta(g_j)$, for any Primary xenolog $g_2$, Sibling Donor xenolog $g_2$, Sibling Recipient xenolog $g_2$, and Outgroup xenolog $g_2$, of $\bar{g}$

$$\text{MCA}(\bar{g}, g_2) < \text{MCA}(\bar{g}, g_2) < \text{MCA}(\bar{g}, g_2) < \text{MCA}(\bar{g}, g_2).$$

Proof. See Section S.1.

We sketch the basis of this theorem informally, here. For every xenolog $g_2 \in V_G \setminus \Delta(g_j)$ of $\bar{g}$, the common ancestor of $g_2$ and $\bar{g}$ is a node on the path from $g_2$ to the root of $T_G$; i.e., there exists $g_2 \in V_G$, such that $g_2 = \text{MCA}(\bar{g}, g_2)$ and $g_2 \geq g_2$ for. $g_2 = g_2$. Then $g_2 \in \Delta(g_j) \setminus \Delta(g_2)$ and is therefore a Primary xenolog.

For $g_2 > g_2$, the descendants of $g_2$, the child of $g_2$ that is incomparable to the transfer, must satisfy two requirements. First, since all xenologs in $\Delta(g_2)$ are equally related to $\bar{g}$, all xenologs in $\Delta(g_2)$ must be assigned to...
the time since their divergence (Capra et al. 2013). This is not true of paraxenologs, to avoid violating the hierarchy. A scenario where this occurs is shown in Figure S1.

Xenolog hierarchy with paraxenologs: The xenolog hierarchy in Theorem 2.1 holds for paraxenologs if we ignore the distinction between xenologs and paraxenologs of the same class and consider $X^*$ to be on a par with the OX class in the hierarchy. If $X^D$ and $X^O$ are a Sibling Donor xenolog and a Sibling Donor paraxenolog, respectively, of $g$, then MRCA($X^D, g$) may be either ancestral to or a descendant of MRCA($X^O, g$) (Figure 3). Similarly, MRCA($X^D, g$) may be an ancestor or a descendant of MRCA($X^O, g$), where $g$ is an Outgroup xenolog of $g$.

The species hierarchy in Table S1 is also preserved, with the additional observations that Sibling Donor paraxenologs behave like Sibling Donor xenologs and MRCA($h, g$) $\geq h \geq$ MRCA($X^D, g$). We will reexamine the hierarchical properties of xenolog classes in trees with more complex event histories in the following sections.

2.2 Xenolog classification with transfers and duplications

We next consider the classification of genes $g_1$ and $g_2$ when there is a single transfer on the path from $g_1$ to $g_2$, and they diverge by duplication (i.e., $g \in$ (MRCA($g_1, g_2$), $g$) $\neq \emptyset$). Such gene pairs satisfy both the paralog and the xenolog criteria proposed by Fitch (2000), leading to potential terminological confusion. To avoid this confusion, we introduce the explicit designation par xenolog

Formally, let $g_{\text{DUP}} \in V_2$ be a duplication node in the gene tree with a transfer, $\tau = (g, e)$, in one of its two subtrees, and let $g \in$ (MRCA($g_1$), $g$) be a descendant of that transfer. Then, every gene in the second subtree of $g_{\text{DUP}}$ is a paraxenolog of $g$, to be denoted $X^D$. The key issue in extending the framework to multiple transfers is how to obtain a single $D, R$, and $O$ given multiple donor and recipient species. We first
intermediate species are represented by xenologous pairs that only pass through a subset of the k transfers, namely, g ∈ Δ(g_1^k), Δ(g_2^k). Information about where ancestral forms of g spent time as g traveled from s_1^k to s_2^k is captured by the complete set of g.

**Incomparable transfers:** We first consider the special case where k = 2 and the transfers are incomparable. Given a pair of genes, g_1 and g_2, connected by two incomparable transfers, r^1 and r^2 (Figure 5), one gene is a descendant of one transfer recipient (g_1 ∈ Δ(g_2^k)), and the other gene is a descendant of the other transfer recipient (g_2 ∈ Δ(g_2^k)). Since g_1 and g_2 are both descendants of a transfer recipient, xenolog g_2 can be classified with respect to g_1 = g_1 and vice versa.

With incomparable transfers, the xenolog classes do not satisfy the hierarchical properties of Theorem 2.1. As before, let g_1 = MRCA(g_1, g_2) and let c be the child of g_1 that is ancestral to r^2 but not r^1 (i.e., c_1 ⊆ g_2 and c_1 = g_2). Recall that the first condition for preservation of the hierarchy is that all xenologs in Δ(c_1) must be in the same species set. Satisfaction of this condition is not guaranteed for incomparable xenologs because Δ(c_1) contains a transfer, r^2, that can move g_2 to a species that is not in the same set as M(g_1). Suppose, for example, the donor of r^2 is in a species in O, but its recipient is in a species in D. Since both g_1^2 and g_2^2 are in Δ(c_1), more than one species set is represented in Δ(c_1), violating the first condition. Primary xenologs are the one exception to this problem. Primary xenologs are defined in terms of g_2 and not in terms of D, R, and O, and are therefore unaffected by incomparable transfers. Primary xenologs are always more closely related to g_1 than are xenologs of any other class, in both the comparable and incomparable cases.

To avoid a classification that violates the hierarchy, we do not assign xenologs separated by incomparable transfers to specific subclasses. Given two genes separated by incomparable transfers, r^1 and r^2, without loss of generality, let g_1 ∈ Δ(g_1^k) be the reference gene, g_2 ∈ Δ(g_2^k) be the xenolog under classification, and g_α = MRCA(g_1, g_2) be their common ancestor. Then g_2 is a

Primary xenolog iff g_2 ∈ Δ(g_2^k);

\[ \hat{x}(g_1, g_2) = \hat{x}(g_2, g_2) = PX \]

Incomparable xenolog iff g_2 ∉ Δ(g_2^k) and x(g_α) = σ;

\[ \hat{x}(g_1, g_2) = IX \]

Incomparable paraxenolog iff g_2 ∉ Δ(g_2^k) and x(g_α) = δ;

\[ \hat{x}(g_1, g_2) = IX^C \]

In the incomparable case, H[g_1, g_2] = \hat{x}(g_1, g_2) is the classification of g_2 with respect to g_1, and H[g_2, g_1] = \hat{x}(g_2, g_2) is the classification of g_1 with respect to g_2. Either \( X(g_1, g_2) = PX \) and \( X(g_2, g_1) = IX \) (or vice versa), or \( X(g_1, g_2) = X(g_1, g_2) = IX^P \).

We now address the case where k > 2 by reducing the problem to one involving two incomparable super-transfers and applying the protocol just described. Let r^1 → r^2 be the transfers, in descending order, on the path from MRCA(g_1, g_2) to g_1 and g_2^k+1, where r^1 and r^2 are the set of transfers on the path from MRCA(g_1, g_2) to g_1. Since r^1 → r^2 must be mutually comparable, they can be replaced with super-transfer r^1 = (g_2^1, g_2^2), where g_2^1 = g_2^1 and g_2^2 = g_2. Similarly, we replace r^1 → r^2 with super-transfer r^1 = (g_2^1, g_2^2), where g_2^1 = g_2^1 and g_2^2 = g_2.

**Gene tree hierarchy for multiple transfers:** With multiple comparable transfers, the hierarchical properties in Theorem 2.1 hold for xenologs that share the same super-transfer from MRCA(g_1, g_2) to g_2. For example, in Figure 4, the xenolog class hierarchy is preserved for nodes g_2 and g_4, which are xenologs of g_1 with respect to r^2 only. Similarly, xenologs 2, 3, and 4, which are all defined with respect to the super-transfer r^1, also obey the hierarchy. However, g_1 and g_2 do not share the super-transfer and thus, do not obey the hierarchy. MRCA(g_1, g_2) < c, MRCA(g_2, g_2), yet \( \hat{x}(g_2, g_2) = \hat{x}(g_1, g_2) = PX \).
sets, classes, but guarantees a classification in which relatedness in the gene closely related, or more distantly related, than a given pair of Sibling or Outgroup xenologs. Thus, the Incomparable xenolog class provides consistent with their relatedness in the gene tree (Theorem 2.1): MRCA.

In contrast, this super-transfer, are more or equally related in the species tree than in of the donor species (as in Figure S2), Primary xenologs, with respect to exception. When the recipient species of the super-transfer is a descendant multiple comparable transfers summarized by a super-transfer, with one of transfers due to phylogenetic error, weakly supported branches were rearranged using a species-tree aware method as described in Section S.5.1. The resulting rooted, rearranged trees were then reconciled with the species tree with default costs ($C_1 = 3, C_2 = 1.5, C_3 = 1$). These costs are consistent with costs used in other recent phylogenomic analyses (David and Alm, 2011; Richards et al., 2014), which were selected to minimize the total net change in genome content. The time required to reconcile the 13,623 trees, including generating all optimal reconciliations and testing them for temporal feasibility, was 7.25 minutes on an Intel Xeon 2.30GHz processor (128GB RAM). The computational complexity of calculating the homology table, once the gene tree has been reconciled, is negligible.

Homology tables were computed for the 13,194 trees possessing at least one temporally feasible solution. From these, homologs of all categories were tabulated. For families with more than one optimal reconciliation, the number of pairs in each category was averaged over all reported, optimal event histories.

Upon reconciling a gene tree with a species tree, Notung 2.8 generates a homolog table, $H$, for all pairs of leaves in the gene tree. There may be more than one minimum-cost event history that reconciles the gene and species trees. A homology table is generated for each optimal, temporally feasible reconciliation reported. Transfers imply temporal constraints because the donor and recipient of a transfer must have co-existed; a reconciliation is temporally feasible if all temporal constraints imposed by the inferred transfers are mutually compatible. Notung 2.8 reports all optimal reconciliations that are temporally feasible, up to a user-specified limit (Stolzer, 2012).

Homology tables can be viewed in the graphical user interface or exported from the command line in a tab-delimited, CSV, or HTML format. Row $H[\hat{g}_i, \hat{g}_j]$ contains the homology relationships between reference gene, $\hat{g}_i$, and all other genes in $V_H$. For orthologs and paralogs, $H[\hat{g}_i, \hat{g}_j] = H[\hat{g}_j, \hat{g}_i]$. For xenologs, $H[\hat{g}_i, \hat{g}_j] = \mathbf{x}(\hat{g}_i, \hat{g}_j)$ gives the xenolog class of $g_i$ with respect to $\hat{g}_i$, a reference gene that is the recipient of at least one transfer on the path from MRCA($\hat{g}_i, \hat{g}_j$) to $\hat{g}_i$. If there is also a transfer on the path from MRCA($\hat{g}_i, \hat{g}_j$) to $g_j$, then $H[\hat{g}_j, \hat{g}_i] = \mathbf{x}(\hat{g}_i, \hat{g}_j)$ gives the xenolog class of $g_j$ with respect to reference $\hat{g}_i$. Otherwise, $H[\hat{g}_i, \hat{g}_j] = \ast$.

The classification procedure is generally applicable to reconciled gene trees and can be implemented in any reconciliation software package that enforces temporal consistency. When temporal consistency is not enforced, reconciliations with transfers between ancestor and descendant species can arise. Since this scenario is similar to super-transfers that form a loop (Figure S2), the classification proposed here could easily be adapted for programs that do not enforce consistency.

4 Empirical Results

Genomic Study: As a proof of principle, we analyzed 13,623 gene families from a dataset of 65 genomes of Proteobacteria and Cyanobacteria (Latysheva et al., 2012). To control for spurious inference of transfers due to phylogenetic error, weakly supported branches were rearranged using a species-tree aware method as described in Section S.5.1. The resulting rooted, rearranged trees were then reconciled with the species tree with default costs ($C_1 = 3, C_2 = 1.5, C_3 = 1$). These costs are consistent with costs used in other recent phylogenomic analyses (David and Alm, 2011; Richards et al., 2014), which were selected to minimize the total net change in genome content. The time required to reconcile the 13,623 trees, including generating all optimal reconciliations and testing them for temporal feasibility, was 7.25 minutes on an Intel Xeon 2.30GHz processor (128GB RAM). The computational complexity of calculating the homology table, once the gene tree has been reconciled, is negligible.

Homology tables were computed for the 13,194 trees possessing at least one temporally feasible solution. From these, homologs of all categories were tabulated. For families with more than one optimal reconciliation, the number of pairs in each category was averaged over all reported, optimal event histories.
Orthologs, paralogs, and xenologs are all represented in this dataset, and every xenolog class is also observed (Figure 6 and Table S2 – S6). More than a quarter of homologous gene pairs were xenologs. Of these pairs, 85.7% are xenologs with only one reference gene, where all transfers on the path from the reference to its xenolog are mutually comparable. Of these xenologs, 60.2% are either Primary or Sibling Donor (para)xenologs; thus, the majority of the inferred xenologs are closer to the donor than the recipient.

Gene pairs separated by incomparable transfers are fairly rare compared with all types of xenologs separated by any number of transfers. Such pairs have two xenologs, one for each reference gene; at most one member of each pair can be classified as a Primary xenolog (PX), otherwise they are untyped (IX). The fraction of incomparable xenologs for which the hierarchy provides no information is quite small: 72.0% of incomparable (para)xenologs are (PX, IX) pairs; the rest are (IX, IX) or (IX+, IX-).

Less than 1% of all xenologous pairs are aut xenologs, which could be due to preferential transfer of novel genes or a high incidence of xenologous recipient. Due to this preferential transfer, the majority of the inferred xenologs are (PX, IX) pairs, which are closer to the donor than the recipient. Of these xenologs, 60.2% are either Primary or Sibling Donor (para)xenologs; the rest are (IX, IX) or (IX+, IX-).

Transfer is a greater source of genetic novelty than duplication (Treangen et al., 2001). Paralogs constitute 2.2% of all homologs, and xenologs are 4.8% of all xenologs. The low level of paralogy observed is consistent with prior reports that in prokaryotes the majority of the inferred xenologs are (PX, IX) pairs; the rest are (IX, IX) or (IX+, IX-) pairs.

Interestingly, the vast majority of par xenologs, 73.4%, areSibling Donor par xenologs. Recall that par xenologs that diverged after the cenancestor of the transfer can be unambiguously classified and are always more closely related to the donor than to the recipient of the transfer. Par xenologs that diverged before the cenancestor, i.e., closer to the root, cannot be assigned a specific class without breaking the hierarchy. As with incomparable xenologs, the low fraction of untyped par xenologs suggests that, at least for this data set, there are relatively few pairs for which it is impossible to extract some information from the xenolog classification.

Methodological factors may also contribute to the trends we observe. Gene families were inferred with OrthoMCL (Li et al., 2003), which tends to place paralogous subfamilies in separate clusters. This could be a factor in the low level of paralogy, par xenologs, and aut xenologs in this study. It could also contribute to the preponderance of SDX pairs, relative to X pairs, as the tendency to break up paralogous subfamilies would result in relatively few inferred duplications near the root of the gene tree. We considered to what extent the empirical parameters influenced the outcome of the analysis presented here. We investigated the impact of OrthoMCL on subsequent xenolog classification in a small set of curated families (Section S.5.5). In most cases, OrthoMCL clusters agreed with the curated family definitions. However, when OrthoMCL did split up paralogous subfamilies, the number and type of paralogous xenologs predicted changed dramatically.

In order to assess the impact of taxonomic breadth on our results, we also applied our classification procedure to two taxonomically-restricted subsets: families found only in the Cyanobacteria phylum (C: 49 species, 7,485 trees) and only in the Synchococcales class (S: 30 species, 1,429 trees). Respectively, Orthologs, paralogs, and all xenolog classes are present, and the observed trends are similar to those reported above for the full data set (Section S.5.4, Figures S8 and S9, and Tables S7 – S16). In summary, the agreement between the full and restricted datasets suggests that our method is not highly sensitive to taxon sampling.

Finally, to probe the impact of event costs on xenolog classes observed in this study, we repeated this analysis with an increased transfer cost, C = 4, as described in Section S.5.3. All xenolog classes were, again, observed. The higher transfer cost resulted in a moderate increase in the number of paralogs and par xenologs of all classes, and a decrease in the number of non-paralogous xenologs inferred. The change in the relative frequencies of the other various classes was generally small (less than 15%) with one exception: the proportion of Outgroup xenologs decreased by more than 50%. The increase in para(xeno)logs and decrease in Outgroup xenologs, taken together, suggests that more duplications may be inferred near the roots of gene trees with a higher transfer cost. Thus, in this analysis, the trade-off between duplications and transfers does not affect all xenolog classes equally.

**Bio4 Case Study** To explore the connection between xenolog classes and protein function, we applied our approach to the **Bio4** gene family; several **Bio4** genes have been horizontally transferred and have been characterized experimentally (Hall and Dietrich, 2007). The **Bio4** protein is an enzyme in the biosynthesis pathway (Figure S11). Plants and some fungi possess a **Bio4** homolog that encodes a bi-functional enzyme, which acts as both a 7,8-diaminopelargonic acid synthase (DAPAS) and a dethiobiotin synthetase (DTBS); steps 3 and 4 in the pathway, respectively. In bacteria, the **Bio4** homolog only performs the DTBS function; the 3rd step is carried out by an unrelated protein. Unlike other fungi, however, the **Bio4** homolog in yeast (Saccharomyces cerevisiae, and its close relatives) also encodes a **Bio4** homolog that encodes a bi-functional enzyme.

The hierarchical nature of the xenolog classification aids in the interpretation of the functional evolution of the family in this case study. The molecular function of yeast **Bio4** is closer to that of Sibling Donor xenologs, which encode the DTBS-only enzyme, than its Sibling Recipient xenologs, which encode bi-functional enzymes. In contrast, the **Bio4**

Recipient xenologs provide information about genomic context. The fact that the Sibling Recipient xenologs encode a bi-functional enzyme raises a red flag: the replacement of a bi-functional enzyme with a DTBS-only enzyme in yeast suggests loss of the DAPAS function. Either a different enzyme must be carrying out the DAPAS function or yeast no longer has a functional biotin synthesis pathway. In fact, the former is true; the DAPAS function is performed by an unrelated gene, that was also acquired horizontally (Hall and Dietrich, 2007).

In this example, a closely related gene (a DTBS-only enzyme) in a distantly related (α-proteobacterial) species is a better predictor of **Bio4** enzymatic function than a distantly related gene (the dual function homolog) in a closely related species (Kerosoria lipopoitica). The distantly related homolog in a closely related species provides information about **Schematic of the Biolog gene family.** Dashed line indicates lineages that likely had a dual-function DTBS+DAPAS enzyme; solid line indicates DTBS-only function. With respect to the gene j in S. cerevisiae, set i is comprised of other fungi, and their genes are SRX. Set j includes all bacterial taxa; the descendents of the donor gene are PX and other genes are SDX.
the genetic background; i.e., the genome could be lacking a gene encoding the DAPAS function. These insights are linked to the hierarchical structure of xenolog classification could support large scale, automated analyses in comparative, evolutionary genomics.

5 Discussion

Distinguishing orthologs from paralogs, as well as the division of paralogs into subclasses based on the timing and nature of the events by which they arise, has proved to be a valuable analytical approach in molecular evolution, systematics, comparative genomics, and homology-based function prediction.

Here, we examine the challenges associated with the expansion of this framework to include horizontally transferred genes. The term “xenolog” has been introduced to describe gene pairs related through horizontal transfer (Gray and Fitch, 1983; Fitch, 2000). However, the set of genes that share a history with at least one transfer encompasses a very broad set of relationships.

In this work, we propose subtypes that provide a more nuanced classification of xenologs. We provide formal rules for classification, given a reconciled gene tree with an arbitrary number of transfers and duplications. These rules have been implemented in Notung 2.8, a freely available phylogenetic reconciliation software package.

Consistent with the framework Fitch first introduced in the 1970s, phylogenetic reconciliation captures information about the historical association between genes and species, as well as the divergence events that characterize the xenologs in each class. A potential limitation of this approach is that it requires that species evolution be modeled as a tree. While some have argued against tree-like models, given the prevalence of horizontal gene transfer in bacteria, a tree can provide a useful heuristic, despite the reticulate nature of prokaryotic evolution (Mindell, 2013, and work cited therein).

As with most theoretical work on reconciliation, our classification assumes that the gene tree and the inferred events are correct. In practice, errors in gene tree reconstruction or incongruence due to unrecognized incomplete lineage sorting could lead to downstream errors in xenolog classification. For example, the xenolog classification proposed here could be embedded in a probabilistic reconciliation framework (e.g., Akerborg et al., 2009), which would support an explicit and quantitative model of uncertainty. Methods that account for phylogenetic uncertainty offer an approach to bridging this gap, and are an important direction for future work.

Missing data is another potential source of error. If the data set does not contain at least one descendant of the donor, a transfer will be inferred from a putative donor that is actually an ancestor of the donor species. When temporal consistency is enforced, the sets D, R and O remain unchanged. Hence, the classification of Sibling Donor, Sibling Recipient, and Outgroup xenologs will be unaffected by this error. However, some genes that are actually Sibling Donor xenologs will be incorrectly classified as Primary xenologs. In this case, missing taxa can lead to errors in xenolog classification, but will not result in major changes in interpretation; these xenologs will still be correctly classified as being more closely related to the donor than to the recipient of the transfer.

Our classification is an extension of Fitch’s classic framework and is based solely on information that can be extracted from gene tree - species tree reconciliation. Just as information about the spatial organization of duplicated genes can be used to infer tandem or whole genome duplication, the incorporation of other sources of information, such as synteny, sequence alignments, or structural comparison, could be used to develop richer accounts of xenolog relationships. For example, Koonin et al. (2001) have proposed that horizontal gene transfer can result in the acquisition of a new gene family, expansion of an existing gene family, or allelic replacement without change in copy number.

Our classification provides a context for stating general hypotheses about the functional and evolutionary fates of different classes of xenologs. Since Sibling Donor xenologs are more closely related to the reference gene than Sibling Recipients, they may be more likely to share molecular functions than the reference gene. In contrast, the cellular environment of the reference gene may be more similar to that of Sibling Recipient xenologs. This could also convey information about the process of amelioration following transfer (Lawrence and Ochman, 1997). For example, the prokaryotic homologs of a fungal gene of prokaryotic origin are likely not informative with regard to the cellular compartment in which the encoded protein is active. The functional fates of genes that have experienced both duplication and transfer is a largely unexplored question. Selective pressures are likely to change following both gene duplication (Lynch, 2007, and work cited therein) and horizontal gene transfer (Treateng and Roche, 2011; Boto, 2010, 2016, and work cited therein). Little is known about the combined effect of these changes on rates of divergence and functional specialization.

Recent attempts to test the ortholog conjecture, which posits that orthologs are more functionally similar than paralogs, have demonstrated the challenges presented by confounding factors in high-throughput data, and especially in the use of ontologies (Nehrt et al., 2001; Chen and Zhang, 2012). Testing analogous xenolog conjectures will be even more challenging: probing all four xenolog classes would require large-scale, unbiased functional data sets for at least five species. Nevertheless, with the current pace of functional genomics, genomic-scale investigations of xenolog function are not far in the future.

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