DIVERSITY OF THE MASHUP ECOSYSTEM

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Abstract: Mashups allow users to develop applications from a variety of open APIs. The creation of mashups is supported by a complex ecosystem of interconnected data providers, mashup platforms, and users. A sign of a healthy ecosystem is that the number and diversity of APIs and mashups in the ecosystem increases continuously. In this paper, we describe a model of the evolution of the mashup ecosystem that allows us to estimate the diversification of the mashup ecosystem over time. In this model we show the evolutionary relationships between mashups as branches in a phylogenetic tree. We discuss how the diversification rate of the mashup ecosystem can be estimated by fitting this tree to a birth-death process model. The results of our research show that the diversity of the mashup ecosystem is increasing with time, however, not monotonically.

1 INTRODUCTION

Mashups allow users to develop applications from a variety of open APIs (Yu et al., 2008). For example, the Google Maps API generates maps for a given location, and its output can be combined with other open APIs and user-supplied data. The creation of mashups is supported by a complex ecosystem of interconnected data providers, mashup platforms, and users (withheld). It is a sign of a healthy ecosystem that the number and diversity of APIs and mashups in the ecosystem increases continuously. The growth of the mashup ecosystem has been attributed to preferential attachment, whereby users select the APIs to include in a mashup by their popularity (Yu and Woodard, 2008). Furthermore, there is evidence that many mashups are created by copying or imitating existing mashups (Weiss and Sari, 2010).

Previous work does not explain the evolution at the microlevel. *Is the ecosystem evolving to greater levels of diversity? What type of changes are introduced during this process?* In this paper, we model the evolution of mashups as a replication process with duplication and mutation. The changes introduced in this process lead to the diversification of the ecosystem. In this evolutionary process, new types or species of mashups are created by combining APIs in novel ways. We refer to this step as *speciation*. Speciation occurs when new species keep traits from their ancestors, otherwise we say that a species has become extinct. To picture this, let us think about the first mashups created. It was common to have mashups with only one API, such as Flickr or Google Maps. Later on, APIs were combined. Mashups that combine both APIs gave origin to the new Flickr and Google Maps species. Thus, Google Maps is considered extinct in the Flickr clade, and vice versa.

From this perspective, we define the diversification of the mashup ecosystem as the creation of a greater variety of mashups. Diversification can be modeled as a birth and death process, from which we can estimate the rate of diversification as the difference between speciation and extinction rate. The evolution of the mashup ecosystem can be reconstructed as a phylogenetic tree by tracing lineages that have given rise to at least one contemporary descendant.

This article investigates the patterns of evolution of the mashup ecosystem and estimates the rate of diversification of the ecosystem using phylogenetic analysis. Section 2 reviews related work. Section 3 describes the model we use to reconstruct the evolution of the mashup ecosystem. Section 4 presents our research method, and Section 5 our results. Section 6 closes with a discussion of the results.

2 RELATED WORK

2.1 Mashup Ecosystem

The structure of the mashup ecosystem and its growth over time has been examined in (Yu and Woodard, 2008) and (Weiss and Sari, 2010). The authors of the first study (Yu and Woodard, 2008) characterize the mashup ecosystem as a three-tier structure: a central tier around the Google Maps API, an intermediate tier of the most popular APIs, and a peripheral tier of less popular APIs that are, nonetheless, important for the rich network structure of the ecosystem to emerge.

In our own work (Weiss and Sari, 2010), we develop techniques for obtaining characteristics of the ecosystem and identifying significant ecosystem members and their relationships. The research suggests that the position of a data provider in the mashup ecosystem affects the likelihood of their API to be incorporated into a mashup. The number of mashups using a given API indicates how likely an API will be selected as the basis of a new mashup, and the frequency with which APIs are combined in a mashup indicates how likely they will be combined in future mashups. The research also shows that the complexity of mashups (where complexity is measured as the number of APIs used) increases with time and suggests that complexity drives the development of mashup platforms.

2.2 Recombinant Innovation

(Hargadon, 2002) highlights the recombinant nature of the innovation process. From this perspective, innovation can be described as the construction of new ideas from existing ones. Benefits include shortening the learning curve by combining known elements, sharing of past experience, and the diversity of problem solving frames. Recombinant innovation emphasizes the highly collaborative nature of innovation, and the role of brokers to bridge between domains and reinterpret existing ideas in new contexts.

The concept of recombinant innovation is closely linked to the concept of modularity, which works to accelerate innovation (Baldwin and Clark, 2000). Modularity allows relatively independent innovation within components, or localized adaptation, and the creation of new products by mixing and matching components, or recombination (Ethiraj and Levinthal, 2004). The increased modularity implied by open APIs is of great influence on the development of mashups. Open APIs are modules that can be combined and recombined in novel ways into mashups. Modularity is also the basis for imitating the design of a mashup, when a user clones an existing mashup. Work on the role of imitation in innovation (Ethiraj et al., 2008) leads us to conclude that modularity enables others to imitate the design of a system.

2.3 Growth Models

Many real networks such as citation networks (Price, 1965) and the Internet (Albert et al., 1999) have a degree distribution that observes a power law. A distribution is said to follow a power law, if it adheres to the form $P(x) \sim x^{-a}$. Networks with a power law distribution are also known as scale free networks (Albert et al., 1999). A growth model for scale-free networks has been proposed in (Barabasi and Albert, 1999) based based on two processes: growth (nodes are added continuously to the network) and preferential attachment (edges are added to nodes in proportion to the number of their existing edges).

The web growth model in (Kleinberg et al., 1999; Kumar et al., 2000) describes a copying process that gives rise to a scale free network. The main step to their model is that new nodes are created by copying a subset of the links of a randomly selected existing node. Others (Sole et al., 2002; Vazquez et al., 2003) also recognize that duplication mechanisms could explain the scale-free nature of biological networks. For example, the cell replication process has elaborate copying mechanisms to limit the number of replication errors. However, occasional errors are significant for creating the population diversity upon which selection acts to produce evolution.

2.4 Biological Diversity

Observing statistics of biological taxa, (Yule, 1925) detected that the distribution of the number of species per genus follows a long-tailed form, and proposed a stochastic model to fit this data. This model is widely used to estimate diversification rates. The growth process is reconstructed as a phylogenetic tree by tracing lineages that have given rise to at least one contemporary descendant (Nee et al., 1994). Following this approach, several methods have been proposed to estimate diversification rates, for instance maximum-likelihood estimators and method-of-moments estimator described in (Magallon and Sanderson, 2000). (Aldous, 2001) discusses stochastic modelling for phylogenetic trees and calls for statistic descriptive modelling. (Newman, 2005) states that the Yule process is one of the most convincing mechanisms for generating power laws.

3 MODEL

3.1 Mashup Ecosystem Structure

We model the mashup ecosystem as a network of mashups and APIs (withheld). Technically, the network is a bipartite graph $G = (M \cup A, E)$, where M is the of mashups, A the set of APIs, and E the set of edges or links between the two types of nodes. A link between a mashup $m \in M$ and an APIs $a \in A$ indicates that m uses a to provide its functionality.

As a shorthand, we can summarize the fact that mashup m combines a set of APIs a_1 to a_n as:

$$m = (a_1, a_2, \ldots, a_n) \quad (1)$$

To test how similar two mashups are, we use the the Jaccard similarity index (Paradis, 2006). It is defined as the number of APIs common to both mashups divided by the combined number of APIs:

$$sim_{jaccard} = \frac{|m_1 \cap m_2|}{|m_1 \cup m_2|} \quad (2)$$

Given two mashups $m_1 = (GoogleMaps, Flickr)$ and $m_2 = (Flickr, Amazon)$, the Jaccard similarity is $1/3 = 0.33$, as both mashups share $Flickr$, but are each combined with a different other API.

3.2 Birth-Death Models

Diversification is commonly modeled as a birth-death process (Nee, 2006). Speciation is assumed to occur at a constant rate b, and extinction at a constant rate d. The diversity of species in an ecosystem is expected to grow exponentially at the diversification rate:

$$r = b - d \quad (3)$$

The relative extinction rate is $e = d/b$ (Bailey, 1964).

4 RESEARCH METHOD

4.1 Mashup Alignment

The dataset is obtained from the ProgrammableWeb directory and over the period from Sep 2005 to Feb 2010.[1] The dataset has 4500 entries. Each entry consists of the name of a mashup and a list of APIs that compose the mashup. Mashups are aligned along two dimensions: first we sort the mashups chronologically, then we order them by their distance computed as the Jaccard similarity index (see Section 3).

4.2 Tree Reconstruction

A phylogenetic tree captures the evolutionary relationships between species of mashups. Similar mashups are in related branches of the tree. To estimate the tree we use the neighbor-joining method (Gascuel, 1997), as implemented in the ape library in the statistics package R.[2] Neighbor-joining joins the two closest mashup species under a common node in the tree. The joined mashup species are then considered as a single species. The algorithm terminates when all pairs of mashup species have been considered. The estimated tree is subsequently calibrated by resolving multichotomies (more than two branches) and estimating node ages (Sanderson, 2002).

4.3 Experiments

We identify patterns of diversification at two levels. The first experiment analyses the dataset in time windows of 500 mashups, equivalent to six months each. The second experiment selects subtrees representing different clades or branches of the phylogenetic tree. For each tree and subtree diversification rates are computed according to the models in Section 3.

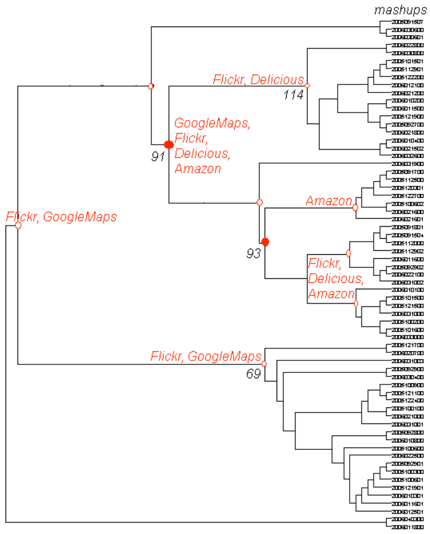
5 RESULTS

The experiments result in a total of 9 phylogenetic trees, one for each time window between September 2005 and February 2010. Each subset is filtered by excluding duplicates and selecting only mashups related to the top 5 APIs. Figures 1(a) and (b) describe mashups in two distinct snapshots. The windows W1 and W5 refer to the periods 09/2005-04/2006 and 07/2007-12/2007, respectively. Each tree node represents a specific API combination that gives rise to a clade of mashups which includes one or more APIs of this combination. A clade is a group of similar mashups sharing the same origin node. For example, in W1 node 91 represents the combination of GoogleMaps, Flickr, Delicious, and Amazon. Two large clades (node 93 and node 114) derive from it.

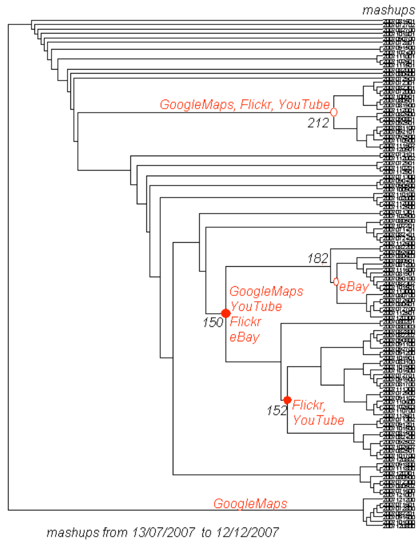
The tree structure changes when looking at different time intervals. Figure 2 includes all published mashups from 09/2005 to 02/2010 and highlights the

[1] http://www.programmableweb.com

[2] http://ape.mpl.ird.fr



(a) Tree W1, $[0,500)$



(b) Tree W5, $[2000,2500)$

Figure 1: Snapshots of the evolution of the mashup ecosystem two different periods of time.

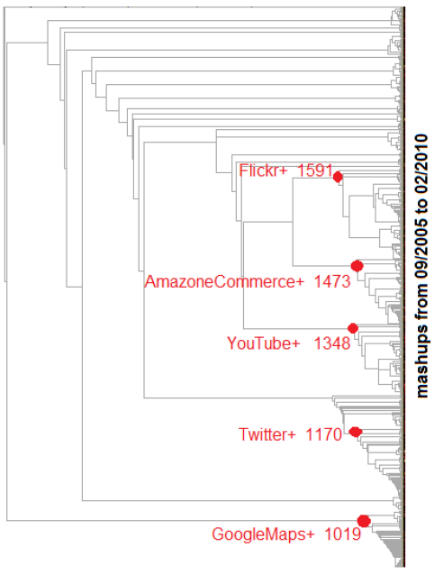


Figure 2: Phylogenetic tree for the evolution of the mashup ecosystem over the full observation period.

major niches created around the most popular APIs: GoogleMaps, Flickr, YouTube, Twitter, and AmazonCommerce. This visualization gives an idea of the number of different clades, or the diversity of the ecosystem. However, it does not establish a metric.

The transition between the snapshots is mirrored in the diversification rates. In this birth-and-death process, diversity is estimated in terms of diversification rate ($r = b - d$) and extinction fraction ($e = d/b$). Figure 3 shows the diversification rate (left axis) and extinction fraction (right axis) in the 9 phylogenetic trees representing the mashup ecosystem.

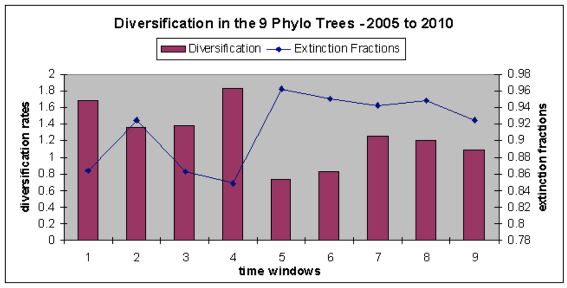


Figure 3: Diversification rate (left axis) and extinction fraction (right axis) in the mashup ecosystem.

We observe high speciation in the first four windows and high extinction rate in the remaining windows. In particular, W5 presents the lowest diversification rate and highest extinction fraction. Overall, the pattern we observe is one of initial high diversification (windows 1-4), which is followed by a period of decline (windows 4-5). Subsequently (windows 5-7), the diversification rate increases again, and has somewhat declined again since (windows 7-9).

Such an increase in diversity followed by a decline in diversity is expected by the dominant design paradigm (Utterback, 1996). According to this paradigm, innovation is expected to produce a great variety of solutions until a dominant design emerges. Innovation diversity will increase again when changes to the environment favor the evolution of a new dominant design. Tree reconstruction offers a new way of empirically measuring this phenomenon.

Further investigation of the major clades of each tree offers more information about diversity, as showed in Figure 4. The highest extinction fraction

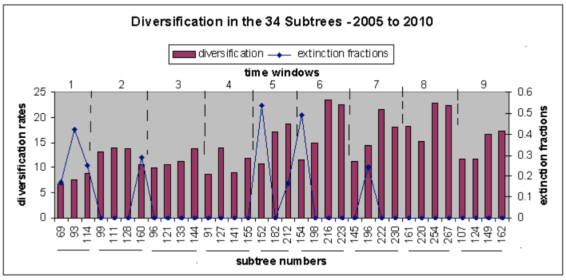


Figure 4: Evolution of the diversification rate by clade.

in the first time-window is the clade from 93-node, see Figure 1(a). As discussed before, the extinction event happens, because the Amazon clade tends to evolve independently, not preserving traits from its ancestors. Other outlier for extinction fraction is from 152-node of the W5 tree, see Figure 1(b). In this case, the Flickr and YouTube clades tends to evolve without the participation of GoogleMaps or eBay.

6 CONCLUSIONS

The results of our analysis indicate that the *diversity of the mashup ecosystem increases with time*. Growth of diversity indicates a healthy ecosystem. However, *diversity did not increase monotonically,* as one might have expected. The non-monotinicity of the growth of diversity signals that the mashup ecosystem was able to recover from a temporary decline in diversity.

The findings are relevant to the data providers and users. Diversity is important as it fosters innovation. By opening up APIs to users, data providers can leverage third-party innovation while maintaining control over what information is exposed. Users can create mashups that incorporate the APIs in novel ways not anticipated by the data providers. In exchange, data providers gain access to more ideas for applications of their APIs and API improvements than they could have discovered on their own.

In future work, we will further examine the reasons for the non-monotonic growth in diversity, as observed by the two periods of decline. From this, we want to build an understanding of the conditions for successful growth of the mashup ecosystem and other similar ecosystems. We would expect disruption to growth to result from the introduction of fundamentally new species of mashups. One such event would be the creation of the Twitter API. We leave a more thorough analysis of this effect to future work.

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