Mining and Modeling Web Trajectories from Passive Traces

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Abstract-In modern web, users contact lots of services, identified by the domain name of the server. The temporal sequence and transitions of visited domains form a trajectory of the user on the web. In this work, we analyze 4 weeks of such trajectories, extracted from logs collected in our university network, and mine them via big data and machine learning methodologies to extract the interests of users. Our goal is to create a model of such trajectories and find similarities so to observe peculiarity of users' browsing. Thanks to the model, we propose a methodology to automatically group together the trajectories of single users and/or communities into highly descriptive environments which in turn allow the analyst to identify the topic of interest. We propose an automatic way to highlight differences in terms of popularity and content of environments. Lastly, we analyze the transition among environments, showing how people in smaller communities, e.g., in the same department, have a much more homogeneous behaviour than people at large, e.g., in the university.

I. INTRODUCTION

Understanding how people move within websites has been always a important problem [1] for a variety of purposes like recommending content [2], comparing rankings in the web [3], or increasing privacy and security [4]. Users' browsing activities can be described by means of the paths that they follow when navigating through websites. The evolution of the web, obviously, changes how users interact with it.

Even with nowadays widespread encryption at the application layer, a passive observer of the network can still obtain valuable information about the trajectory a user follows in the web. For instance, the domains, or more precisely the Fully Qualified Domain Names (FQDN), of the websites contacted during browsing are still not encrypted and easily accessible from passive probes. Indeed, domains are exchanged in clear text, i.e., when resolving a domain via DNS queries [5].

In this work we refer to the sequence of domains visited by a user as the user *trajectory*. Both user's circumstances and preferences affect such trajectories. Here, we consider only the domains intentionally visited. Finding those in the stream of all contacted domains requires ingenuity: we propose a machine learning methodology to solve this problem.

Armed with the sequences of visited domains, i.e., user's trajectories, we analyze them using TribeFlow [6], [7], a

methodology we proposed to model each user as a random surfer over latent environments. User trajectories are the outcome of a combination of latent user preferences and the latent environment that users are exposed to in their browsing.

We build this model and analyze its results using a large dataset containing traffic summaries of ≈ 2500 anonymized users in our university campus in Torino during 4 weeks in 2017. A big data approach must be considered for retrieving, processing and managing such amount of data.

Thanks to the model, we show how to automatically group together the interests and browsing patterns of single users and/or communities into so-called environments. We propose an automatic way to highlight differences in terms of popularity and content. Lastly, we analyze the transition among environments, showing how the single department has a much more homogeneous behaviour than the whole university.

Our analysis shows that it is possible to:

- model accurately the users trajectories, by simply considering domains names, without the need of the whole packet traces;
- extract environments with similar or likely connected websites;
- highlight differences in terms of popularity and content of environment;
- extract the interests of communities of people.

The workflow of our system is the one sketched in Figure 1. Users are connected to the Internet and we monitor the network at a point of presence where we collect and log information about each TCP connection (Section II). From this log, we extract all the domains, for each user. Next we design a methodology (Section III-A) that, thanks to some active measurements, get the subset of domains related to services intentionally visited by users. We (i) focus on those domains, and (ii) reconstruct meaningful trajectories over time (Section III-B). At this point, we learn the possibly best fitting TribeFlow model on such data (Section IV) and we analyze results (Section V).

To foster new studies and permit results reproducibility, we contribute our dataset and model to the community. Anonymized trajectories of domains and their models are available to the public at http://bigdata.polito.it/content/ domains-web-users, while TribeFlow code is available at https://github.com/flaviovdf/tribeflow.

This research has been partially founded by SmartData@PoliTO center (https://smartdata.polito.it/).

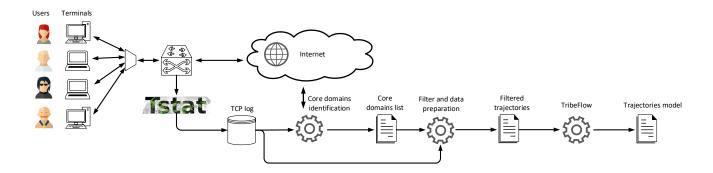


Fig. 1. Workflow of the followed process.

II. DATASET

Our analysis relies on a dataset collected in our university campus. In the dataset, users' terminals (usually PCs) are directly connected to the Internet via campus network (wired Ethernet) and uniquely identified by a statically assigned IP address, that is associated with one and only one user.

We rely on Tstat [8] to collect data. Tstat monitors each TCP connection, exposing information about more than 100 metrics, from IP addresses and port numbers, to fields coming from a DPI module. Here, we are interested in retrieving the domain name of the server being contacted. Tstat implements three techniques to get it. For HTTP flows, the Host header is extracted from HTTP request. In case of TLS, the DPI module provides the Server Name Indication (SNI) field in Client Hello message. SNI is a TLS extension by which the client indicates the domain of the server that is trying to contact. At last, Tstat reports the domain name clients resolved via DNS queries prior to flows [5]. We combine these three sources to label each flow with the server name, giving higher priority to Host and SNI fields where more than one is present.

Our data contains traffic of approximately 2 500 terminals, collected at our university Campus in Torino during 4 weeks between January and February 2017. The dataset includes 691 millions flows and 404 k unique domains, corresponding to more than 136 k unique second level domains. No holidays or festivities occurred during this period. In total we monitored 113 TB of traffic, logging 229 GB of data.

Here, for each TCP connection we just consider: (i) the anonymized client IP address as terminal identifier, (ii) its department inside the Campus, (iii) the starting time and (iv) the end time of the connection, and (v) the server domain name.

A. Ethical and privacy risk mitigations

Both the data collection process and the collected data have been discussed, reviewed and approved by the ethical board of our University. We took all possible actions to protect leakages of private information from users. In particular, we anonymized the IP addresses of terminals using a technique based on irreversible hash function and only retained the data that is strictly needed for our study. We further anonymized the server name in the datasets that we contribute to the community.

III. TRAJECTORIES EXTRACTION

A. Identification of Core domains

When visiting a web-page, the browser application first downloads the main HTML document and then fetches all the objects of the page (images, scripts, advertisements, etc.). These are often hosted on external servers (e.g., CDNs) having different domains. We call *Core domain* a domain originally contacted to download the main HTML document of a page. Core domains are important since they are intentionally visited by users, like www.facebook.com and en.wikipedia.org. We call *Support domains* those domains automatically contacted by visiting a Core domain, or by background applications, like static.10.fbcdn.net and dl-client.dropbox.com. Support domains do not contain useful information about user intention.

In the literature, previous works tackled the problem of identifying intentionally visited Core domains, also called *user actions*. Authors of [9] exploit the *referer* field in HTTP requests to reconstruct web-page structures from HTTP traces, while machine learning techniques are used by authors of [10] using the HTTP header. However, an important fraction of traffic is becoming encrypted, making the above approaches ineffective. Few efforts have been put in identifying user actions from encrypted traffic [11], [12]. These works aim at identifying user actions from flow level measurements examining traffic at runtime. Here, we aim at building a list of domains that typically contain user actions since they host actual web services.

We build on our previous work [13]. Given a domain, we visit the home-page it hosts. Based on the response, we classify it as a Core or Support domain. This is a classification problem, that we solve with a machine learning approach using a decision tree classifier. We consider an extensive list of features guided by domain knowledge, and let the classifier choose the ones that better allow it to separate Core and Support domains. Features include the length and the content type of the main HTML document (if present); the number of objects of the page and domains contacted by the browser to fetch all objects; HTTP response code (e.g., 2xx, 3xx and 4xx); and whether the browser has been redirected to an external domain. We use active crawling, and visit the home page of each domain by means of Selenium automatic browser to extract page features.¹

We build a labeled dataset that we use for training and testing, considering a list of 500 Core and 500 Support domains. More in detail, we picked the list of domains found in the Campus trace, sorted by number of visits. Then, we manually visited each home page corresponding to the domain name. We manually label such domain as a Core or a Support domain by looking at the rendered web page. We stop the labeling process when we reach 500 items for each class. We obtain a balanced labeled dataset that we make publicly available.² For the decision tree, we opt for the J48 implementation of the C4.5 algorithm offered by Weka.³

Interestingly, the final decision tree results in a simple, efficient, and descriptive model which reads as: a) the main HTML document size must be bigger than 3357B and b) the browser must not be redirected to an external domain. Intuitively, support domains typically lack of real home page. When directly contacted, the server reply with short error messages. In some cases, Support domains redirect visitors to the service home page (e.g., fbcdn.net redirects on www.facebook.com). Despite its simplicity, overall accuracy is higher than 96% when tested against 1000 labeled domains, using 10–fold cross validations.

B. User trajectories reconstruction and characterization

First, we characterize the trajectories in our dataset. These results will support the credibility of trajectories and therefore the model assumptions, as we will describe in Section IV.

Applying the classifier to our dataset, we get that among the 404K domains, only 44K results Core. Figure 2 depicts two curves of domain popularity, where we rank each domain according to the fraction of visits directed towards it, for both all and Core domains. Notice the loglog scale. The pattern is similar for both the curves, even if the number of domain is quite different: a small portion of domains are popular and get the great majority of visits, with a long queue of domain getting few visits. Among the top 1 000 most popular domains (all), only 61 are Core domains. For Core domains, the popular domains are basically the ones with most pageviews, according to Alexa⁴, i.e., Google, Facebook, Youtube, etc. These bring little information on the specific interests of a user. On the contrary, we expect the less popular domains to give specific information about user interests.

It is also interesting to analyse the connection length and inter-arrival time distributions. Both measures are important given that we want to reconstruct meaningful trajectories based on relative arrival time of the visit. Figure 3(a) reports the empirical Cumulative Distribution Function (CDF) of the

³http://www.cs.waikato.ac.nz/ml/weka/

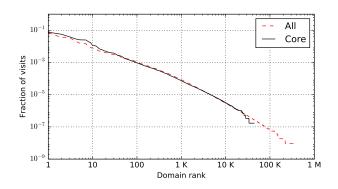


Fig. 2. Popularity of domains, considering all of them or just Core ones.

connection duration. Core connections are in general longer. 80% of the connections last less than 3 minutes. The interarrival between two consecutive connections is shown in Figure 3(a). It is in general shorter than the duration of a connection. This means that is not uncommon to have multiple contemporary connections. This could imply that there are contemporary connections towards multiple sites and therefore could be complex to estimate the sequence of visits of the user. Moreover we see that many connections have a very small inter-arrival time (≤ 0.01 s). This is due to the fact that browsers open multiple connections when visiting a web page. These connections could be towards many servers (Support domains), or even multiple connections towards the same domain.⁵ We analyze this aspect by showing the number of overlapping connections. Figure 3(b) shows the probability of number of overlapping connections. X axis is limited to 6 for ease of visualization. Analyzing all the domains, multiple contemporary connections are usual, and even tens of them are not rare. Even when limiting to Core domains, the probability of having no contemporary connections is only 26%.

When building the user trajectory, multiple contemporary connections towards the same domain would artificially create sequences of visit to the same domain. To filter this artifact, we group together such overlapping trajectories towards the same Core domain. Specifically, we group visits to the same domain happening in the same time window of duration equal to the duration of the first connection. We then recompute the number of concurrent connections, showed by the curve labeled *Core - filtered* in Figure 3(b). Almost no connection is now contemporary to others (less than 9%).

IV. MODELING USER TRAJECTORIES WITH TRIBEFLOW

We want to model user habits focusing on how they move in the web from domain to domain. To achieve this goal, we rely on our recently proposed model called TribeFlow [6]. Here we provide a brief and simplified description of the methodology and invite to refer to [6] for all details.

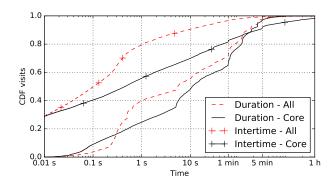
Let us represent the trajectory of each user $u \in U$ as a sequence of requests to domains. U is the set of users in the

¹http://www.seleniumhq.org/

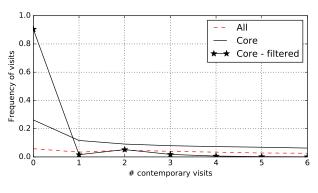
²http://bigdata.polito.it/content/domains-web-users

⁴https://www.alexa.com/topsites/countries/IT

⁵http://www.browserscope.org/?category=network&v=top



(a) Duration and inter-arrival of connections



(b) Number of contemporary visits

Fig. 3. Characterization of connections.

whole trace \mathcal{V} . Similarly, $d \in \mathcal{D}$ represents a domain. We generalize the dataset \mathcal{V} from a single edge network as a set of visits $v \in \mathcal{V}$, with each visit being represented as a triple: v = (u, t, d). t represents a timestamp of the visit.

It is expected that real user behavior will be (i) nonstationary, and (ii) time heterogeneous [14]. In other words, user behavior change and evolve over time, and is different for each user. TribeFlow was designed to cope with the complex challenges of learning personalized predictive models of nonstationary, time heterogeneous, and transient (Markovian) user trajectories.

Let a trajectory from a users be comprised of the visits ordered by time. That is, the trajectory for user u is: $\mathcal{V}_u = \langle$ $(u, t_0, d_0), (u, t_1, d_1), \cdots, (u, t_n, d_n) >$. TribeFlow objective is to capture the overall set of trajectories as a set of ktransitions matrices of size $|\mathcal{D}|$ by $|\mathcal{D}|$. Each matrix represents a stationary and time homogeneous first order Markov chain and characterize a latent environment z. Therefore, each environment is associated with the first order Markov chain $P(d_{i+1} \mid d_i, z)$. The domain d_i is associated with time t_i , whereas d_{i+1} is the next immediate visit at time t_{i+1} . This chain captures the probability of going to d_{i+1} given that the last visit was to domain d_i , within environment z. The number of environments k can be automatically inferred from the data with different methods [7].

For each user u, let us define a probability of interest, or strength, that this user has in environment z, $P(z \mid u)$. That is,

when a user is browsing the web, she selects a random environment associated to her interests or needs (e.g., search engines, social networks, or e-commerce websites). This choice is done according to $P(z \mid u)$. After selecting an environment, the user selects a domain based on $P(d_{i+1} \mid d_i, z)$.

Based on the definitions above, the whole dataset of trajectories are captured as random walks over random environments. Each environment captures a latent factor that leads to a user visiting a domain.

Given that for each user the overall behavior is captured as mixture (based on $P(z \mid u)$) of stationary and time homogeneous matrices $(P(d_{i+1} \mid d_i, z))$, the overall behavior captures a non-stationary, time heterogeneous, and transient system. Finally, TribeFlow can non-parametrically incorporate the inter-arrival time to model $P(\tau \mid z)$, with $\tau = t_{i+1} - t_i$. The overall probability of a user transitioning between two domains within an environment is defined as:

$$P(d_{i+1} \mid d_i, u, z, \tau, \alpha, \beta, \lambda) = \frac{P(d_{i+1} \mid z, \beta)P(d_i \mid z, \beta)P(\tau \mid z, \lambda)P(z \mid u)}{1 - P(d_i \mid d_i, z, \beta)}$$

. .

 α, β , and λ are hyper parameters which are fixed to sensible defaults [6]. The goal of the model is to learn the matrices Θ (with k rows and $|\mathcal{U}|$ columns) and Φ (with $|\mathcal{D}|$ rows and k columns) that correspond to probabilities $P(z \mid u)$ and $P(d \mid z)$, respectively⁶. After the model is trained, the probability $P(d_{i+1} \mid d_i, z)$ is simply defined as: $P(d_{i+1} \mid d_i, z)$ $d_i, z) = P(d_{i+1} \mid z)P(d_i \mid z)$ The probability matrix for each environment, as well as the strength of each user in an environment is learned through Gibbs Sampling (see [6] for details).

Learning the model on our dataset: using TribeFlow, we are able to summarize our large dataset of trajectories in a succinct and interpretable manner. For training the model, the only parameter we have to tune is the number of environments k. More environments allows to better approximate the trace, but increase the complexity of the models. We therefore use a weighted version of the error, obtaining a best number of environment k = 30.

We train different models, each with 30 environments, by using: 1) the whole Campus trace, 2) the single Architecture department trace and 3) the Electronic department trace.

V. RESULTS

In this section, we analyze the model we created in Section IV and we show how it can be useful for studying the behaviour of the users.

A. Environments as clusters of common domains

Once we build the 30 environments, we manually inspect and analyse the most relevant domains inside them. We expect each domain d to be present in all the environments z, with a probability P(d|z). We can therefore sort the domains d

⁶In Θ each cell captures $P(z \mid u)$ for a given environment and user.

sublimetext.com amazon.it stackoverflow.com evernote.com researchast.net mozilla.org github.com microsoft.com altera.com



Vanityfair,it microsoft.com repubblica.it maisonsdumonde.com scribd.comimmobiliare.it instagram.com pimkie.it instagram.com academia.edu

(a) Electronic dept. with many (b) Electronic dept. environment with (c) Architecture dept. environment (d) Architecture dept. environment computer-science related domains many e-commerce domains with many travel related domains with many fashion related domains

subito.it

kijiji.it

edcoon.it

Fig. 4. Examples of top-10 domains in different environments of Electronic and Architecture departments, showed as word-clouds.

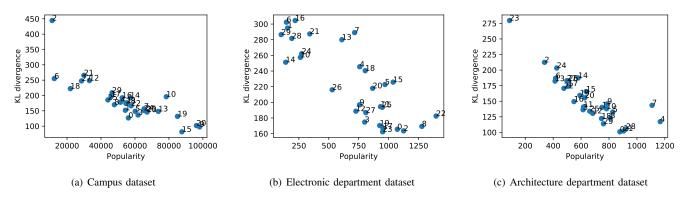


Fig. 5. Diversity and popularity of the environments for different datasets.

accordingly to the probability distribution $\Phi_z(d) = P(d|z)$ inside each environment, and then visually inspect the most probable domains. By construction, we expect to have domains that are usually sequential in time within the same environment. Results show that most of the environments contains the most popular and generic domains, e.g., search engines and social networks. However, we clearly see some specific domains to dominate in some environments, i.e., the model let domains with the same topic to emerge in some specific environment only. For instance, we observe news, weather forecast, engineering forums and science journals related website to dominate different environments. This reflects the user habits of browsing a sequence of domains with the same topic. To illustrate this, consider the models extracted from users within the Electronic and Architecture departments. Figure 4 illustrates the word-clouds of the top 10 domains of specific environments⁷. Observe how expressive are the word-cloud in describing the topic of each environment.

B. Analysis of diversity and popularity of environments

To quantify how the 30 environments are different among each other, we use as metric the Kullback-Leibler (KL) divergence [15]. KL divergence $D_{\text{KL}}(\Phi_{z_1} || \Phi_{z_2})$ measures how one probability distribution Φ_{z_1} diverges from a second, expected probability distribution Φ_{z_2} . It is defined as:

$$D_{\mathrm{KL}}(\boldsymbol{\Phi}_{z_1} \| \boldsymbol{\Phi}_{z_2}) = \sum_{d \in D} \boldsymbol{\Phi}_{z_1}(d) \log \frac{\boldsymbol{\Phi}_{z_1}(d)}{\boldsymbol{\Phi}_{z_2}(d)}$$

In our case, the expectation is taken using the probabilities of each domain $d \in D$. Φ_{z_1} and Φ_{z_2} are the domain probabilities for environments z_1 and z_2 ($\Phi_{z_1}(d) = P(d|z_1)$ and $\Phi_{z_2}(d) = P(d|z_2)$). Therefore, environments z quite different from all the others will have a large value of $D_{KL}(z) = \sum_{z_i} D_{KL}(\Phi_z || \Phi_{z_i})$, that we call KL divergence for environment z.

We further compute the mean expected number of visits for each environment, namely the *popularity* of the environments z, computed as $V(d) \cdot P(d|z)$, where V(d) is the number of visits towards domain d in the original dataset.

We plot $D_{KL}(z)$ versus $V(d) \cdot P(d|z)$ for each z. Figure 5 shows results for: (a) the whole Campus, (b) Electronic, and (c) Architecture departments. Each environment is labeled with a different number for ease of visualization. We see in all cases a clear trend: the most popular environments are also the one that are less diverse from each other. These environments are generic, and thus less interesting to inspect. On the other hand, environments with large KL divergence usually have a low number of expected visits. These environments are the most peculiar ones. For example, consider environment 2 in Campus traces. Analyzing its most popular domains, it appears related to users/devices that often go to visit *sony.com* and *sony.it*, possibly because they hosts home-pages automatically visited by software installed on those users' devices. Other

⁷We removed common domains, i.e., Google, Facebook, and Youtube because they are among the most popular in all the environments.

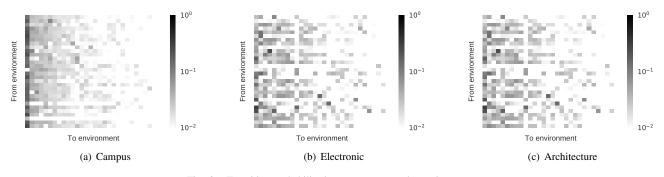


Fig. 6. Transition probability heat-maps among the environments.

examples of peculiar environments include domains related to torrents and movie streaming portals, and to popular bank accounts. This method of analysis offers the analyst an automatic way to highlight interesting environments.

C. Transitions in communities

In the previous subsections we showed how interests are different in communities of people. We now show how communities switch among environments. In Figure 6 we show the heat-maps of the transition probability matrix $P(z_1|z_2)$ from environment z_1 to another environment z_2 , in logarithmic scale. This matrix can be easily computed from the model parameters. By construction, elements of a row has to sum to 1, while the sum on the element of a column represents the probability of landing to that particular environment. We sort the columns by such (reversed) sum of probabilities. We see how for Campus datasets, transitions are usually towards a single popular environment that contains generic websites (on the foremost left in Figure 6(a)). On the other hand, transitions on Architecture and Electronic departments are spread towards many topics, some of which are specific of each department. Among all the possible 870 transitions, only 86 for the Campus are above the random probability, while this number increases to 129 for Electronic and 146 for Architecture department. This means that inside the departments people are much more homogeneous and tends to visit more evenly the peculiar environments. Even if very different between each others, these environments are in general more common within the same community of people.

VI. CONCLUSIONS AND FUTURE WORK

In this work, we described how to create from passive traces meaningful trajectories of users on the web, and then how to represent them in a succinct and interpretable manner. We showed that our model allows to automatically and easily inspect the interests of users and communities, and to highlights transitions and diversity is such clusters of domains. We plan to extend our work in order to: (i) study temporal evolution of trajectories and environments, (ii) apply our methodology to much bigger datasets coming from ISPs, and (iii) propose personalized recommendation systems for users browsing.

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