

The Social Media Genome: Modeling Individual Topic-Specific Behavior in Social Media

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Abstract—Information propagation in social media depends not only on the static follower structure but also on the topic-specific user behavior. Hence novel models incorporating dynamic user behavior are needed. To this end, we propose a model for individual social media users, termed a *genotype*. The genotype is a *per-topic* summary of a user's interest, activity and susceptibility to adopt new information. We demonstrate that user genotypes remain invariant within a topic by adopting them for classification of new information spread in large-scale real networks. Furthermore, we extract topic-specific influence backbone structures based on information adoption and show that they differ significantly from the static follower network. When employed for influence prediction of new content spread, our genotype model and influence backbones enable more than 20% improvement, compared to purely structural features. We also demonstrate that knowledge of user genotypes and influence backbones allow for the design of effective strategies for latency minimization of topic-specific information spread.

I. INTRODUCTION

Trends and influence in social media are mediated by the individual behavior of users and organizations embedded in a follower/subscription network. The social media network structure differs from a friendship network in that users are allowed to *follow* any other user and follower links are not necessarily bi-directional. While a link enables a possible influence channel, it is not always an active entity, since a follower is not necessarily interested in all of the content that a *followee* posts. Furthermore, two individuals are likely to regard the same token of information differently. Understanding how information spreads and which links are active requires characterizing the users' individual behavior, and thus going beyond the static network structure. A natural question then arises: *Are social media users consistent in their interest and susceptibility to certain topics?*

In this work, we answer the above question by demonstrating a persistent topic-specific behavior in real-world social media. We propose a user model, termed *genotype*, that summarizes a user's topic-specific footprint in the information dissemination process, based on empirical data. The social media genotype, similar to a biological genotype, captures unique user traits and variations in different genes (topics). Within the genotype model, a node becomes an individual represented by a set of unique invariant properties.

For our particular analysis, the genotypes summarize the propensity and activity level in adoption, transformation, and

propagation of information within the context of different topics. We propose a specific set of properties based on adopting topic-specific Twitter hashtags—tokens that annotate messages and allow users to participate in global discussions [1]. The model, however, applies to more general settings capturing, for example, dissemination of urls or sentiment-charged messages.

We construct the genome (collection of user genotypes) of a large social media dataset from Twitter, comprised of both follower structure and associated posts. The observation of stable genotypes (behavior) leads to natural further questions: *Can the consistent user behavior be employed to categorize novel information based on its spread pattern? Can one utilize the genotypes and the topic-specific influence backbone to (i) predict likely adopters/influencers for new information from a known topic and (ii) improve the network utility by reducing latency of disseminated information?* We explore the potential of the genotype model to answer the above questions within the context of Twitter.

To validate the consistency of genotypes, we show that combining genotype-based classifiers into a composite (network-wide) classifier achieves accuracy of 87% in predicting the topic of unobserved hashtags that spread in the network. We extract and analyze topic-specific influence backbone structures and show that they differ from the static follower network. We, then, turn to two important applications: influence prediction and topic-specific latency minimization. We achieve 20% improvement in predicting influencers/adopters for novel hashtags, based on our model, as compared to relying solely on the follower structure. We also demonstrate that knowledge of individual user genotypes allows for effective reduction in the average time for information dissemination (more than 40% reduction by modifying the behavior of 1% of the nodes).

Our contributions, in the order they are presented, include: (i) proposing a genotype model for social media users' behavior that enables a rich-network analysis; (ii) validating the consistency of the individual genotype model; (iii) quantifying the differences of behavior-based influence backbones from the static network structure in a large real-world network; and (iv) employing genotypes and backbone structure for adopter/influencer prediction and latency minimization of information spread.

II. RELATED WORK

The network structure has been central in studying influence and information dissemination in traditional social network research [2], [3]. Compared to them, large social

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media systems exhibit a relatively denser follower structure, non-homogeneous participation of nodes, and topic specialization/interest of individual users. Twitter, for example, is known to be structurally different from human social networks [4], and the intrinsic topics of circulated hashtags are central to their adoption [5].

A diverse body of research has been dedicated to understanding influence and information spread on networks, from theories in sociology [6] and epidemiology [7], leading to empirical *large-scale* studies enabled by social web systems [5], [8], [9], [10]. Here, we postulate that the influence structure varies across topics [11] and is further personalized for individual node pairs. Lin and colleagues [12] also focus on topic-specific diffusion by co-learning latent topics and their evolution in online communities. The diffusion that the authors of [12] predict is implicit, meaning that nodes are part of the diffusion if they use language corresponding to the latent topics. In contrast, we focus on topic-specific user genotypes and influence structures concerned with passing of observable information tokens and their temporal adoption properties.

Earlier data-centered studies have shown that sentiment [8] and local network structure [5] have an effect on the spread of ideas. The novelty of our approach is the focus on content features to which users react. Previous content-based analyses of Tweets have adopted latent topic models [13], [14]. We tie both content and behavioral features to network individuals.

With regards to influence network structure and authoritative sources discovery, Rodriguez and colleagues [15] were able to infer the structure and dynamics of information (influence) pathways, based on the spread of memes or keywords. Bakshy et al. [16] focus on Twitter influencers who are roots of large cascades and have many followers, while Pal et al [17] adopt clustering and ranking based on structural and content characteristics to discover authoritative users. Although the above works are similar to ours in that they focus on influence structures and user summaries, our genotype targets capturing the invariant user behavior and information spread within topics as a whole, involving a collection of topically related information parcels.

III. GENOTYPE MODEL

Here we define our genotype model that captures the topic-specific behavior of a single user (node) within a social media network. Our main premise is that, based on observed network behavior, we can derive a unique signature of a user. Hence, the genotype model is a user model, by definition, in the sense that it is an abstract representation of a social network user. For our analysis, this signature captures adoption and reposting of new information, activity levels, and latency of reaction to new information and influential neighbors. Although other behavior traits can be incorporated as well, we seek to summarize user behavior with respect to a set of predefined topics.

A social media network $N(U, E)$ is a set of users (nodes) U and a set of follow links E . A directed follow link $e = (u, v), e \in E$ connects a source user u (*followee*) to a destination user v (*follower*). The network structure determines how users get exposed to information posted by their followees. The static network does not necessarily capture influence as users do not react to all information to which they

are exposed. To account for the latter, we model the behavior of individual users within the follower network within their genotypes.

In its most general form, a user's genotype G_u is an entity embedded in a multi-dimensional feature space that summarizes the *observable behavior* of user u with respect to different topics. It is up to the practitioner to define the different dimensions of the topic feature space, and an observable behavior in the network locality of a node. Each genotype value can be viewed as an allele that the user introduces to the process of message propagation through a network.

In our study, we focus on hashtag usage within Twitter, since hashtags are simple user-generated tokens that annotate tweets generated by either a social group or a specific social phenomenon, and are often "learned" from others on the social network [1]. In this context, a hashtag serves as a genetic parcel of cultural information, just like alleles of a gene within a biological context. Hashtags can be associated with topics such that an individual's response to a collection of hashtags within a topic indicates a user's propensity to respond to other hashtags within that same topic.

We consider a set of predefined hashtags $H = \{h\}$, each associated with a topic $T_i \in T$. To obtain the genotype, we analyze the social media message (tweet) stream produced by a user u , with respect to H . Let us define $m(\cdot)$ to be a function that maps each occurrence of (u, h) to a real value $m : \{(u, h)\} \mapsto \mathbf{R}$. Let $H_{(u, T_i)} := \{h\}_{T_i} \cap \{h\}_u$, then the i^{th} element of the user genotype G_u is the set of $\{m(u, h) \mid h \in H_{(u, T_i)}\}$ values. We remark that this set of values may also be reduced to their average value or some approximated distribution function if one wishes to have a coarser representation of the data.

To construct each user's topic-genotype from empirical data, we consider a variety of metrics $m(\cdot)$ for (u, h) pairs, listed in Table I. These metrics serve the purpose of quantifying a user's response to a hashtag by defining the data values that are used to estimate the topic distributions. While TIME and N-USES are intuitively obvious metric choices, LAT and LOG-LAT are novel to this manuscript. N-PAR and F-PAR have been previously studied in a different context [5], and are included here for comparison.

IV. DATASETS

We chose Twitter to analyze user behavior via our genotype model, since Twitter has millions of active users and messages have a known source, audience, time stamp, and content. Similar analysis can be performed in other social media networks with a known follower structure and knowledge of the shared content (memes, urls and buzz words) in time.

A. Twitter follower structure and messages

We use two datasets from Twitter: a large dataset *SNAP* [9] including a 20% sample of all tweets over a six-month period and the complete follower structure [4]; and a smaller *CRAWL* dataset containing all messages of included users that we collected using Twitter's public API in 2012, where we started from initial seed nodes (members of the authors' labs) and crawled the follower structure and related posts. *SNAP*

Metric	Function definition	Notes
Time	$\text{TIME}(u, h) = \min_{(u, h)}(t(u, h)) - \min_{v \in V_u}(t(v, h))$, where $t(u, h)$ is the time (u, h) occurs and V_u is the set of followees of u .	The absolute amount of time between a users first exposure to the given hashtag and his first use of that same hashtag.
Number of Uses	$\text{N-USSES}(u, h) = \{(u, h)\} $, where $ \cdot $ is the cardinality function.	The total number of occurrences of the (u, h) pair.
Number of Parents	$\text{N-PAR}(u, h) = \{v \in V_u \mid t(v, h) < t(u, h)\} $	The number of followees to adopt before the given user.
Fraction of Parents	$\text{F-PAR}(u, h) = \{v \in V_u \mid t(v, h) < t(u, h)\} / V_u $.	The fraction of a user's followees who have adopted the hashtag prior to the user.
Latency	$\text{LAT}(u, h) = (\{h_j \in H_{T_i} \mid H_{T_i} \ni h, \text{ and } t(u, h_j) < t(u, h)\})^{-1}$	The inverse of the number of same-topic hashtags posted to the user's time-line between his first exposure to the hashtag and his first use of the hashtag.
Log-latency	$\text{LOG-LAT}(u, h) = \log(\text{LAT}(u, h) / \text{Avg}(\text{LAT}(w, h) \text{ s.t. } w \in U))$.	The logarithm of each latency value after each latency value has been divided by the mean latency value for that hashtag.

TABLE I: Behavior-based metrics that are components of the topic-specific user genotype.

Topic	SNAP (users=42M,tweets=467M)			CRAWL (users=9K,tweets=14.5M)		
	Hashtags	Users	Uses/HT	Hashtags	Users	Uses/HT
Business	27	20k	1,155	19	1,493	88
Celebrities	32	26k	1,009	-	-	-
Politics	485	349k	2,020	121	5,480	49
Sci/Tech	33	415k	6,889	63	4,982	100
Sports	98	76k	3,274	24	320	14

TABLE II: Statistics of the SNAP and CRAWL data sets.

includes a network-wide view for a 6 month period, while CRAWL provides longitudinal completeness for a smaller sub-network of users. Statistics of the two datasets are summarized in Table II and further discussed in the Supplement [18].

B. Grouping hashtags into topics

While hashtags present a concise vocabulary to annotate content, they are free-text user-defined entities. Hence, we need to group them into topics in order to summarize user behavior at the topic level. In this work we assume a 1:1 mapping of topics to hashtags, while in a more general framework disseminated hastags (urls, memes, etc.) can be “softly” assigned to more than one topic. We work with five general topics as dimensions for our user genotypes: Sports, Politics, Celebrities, Business and Science/Technology. We obtain a set of 100 high-confidence hashtag annotations from a recent work by Romero and colleagues [5], further augmented by a set of curated business-related hashtags [19]. We combine this initial set of annotated hashtags with a larger set based on text classification.

To increase the number of considered hastags, we adopt a systematic approach for annotating more hashtags based on urls within the tweets. We pair non-annotated hashtags with web urls, based on co-occurrence within posts. We extract relevant text content from each url destination (most commonly news articles from foxnews.com, cnn.com, bbc.co.uk) and build a corpus of texts related to each hashtag. We then classify the url texts in one of our 5 topics using the MALLET [20] text classification framework trained for our topics of interest. As a result, we get a frequency distribution of topic classification for frequent (associated with at least 5 texts) hashtags. The topic annotation of the hashtag is the topic of highest frequency. The number of hashtags and their usage statistics in our final topic-annotated set are presented in Table II (columns Users and Uses/HT). The Celebrities hashtags do not occur frequently enough in the CRAWL dataset and hence we exclude them from our analysis.

V. GENOTYPE MODEL VALIDATION IN TWITTER

To qualify the genotype model as a meaningful representation of social network users, we demonstrate that the genotype

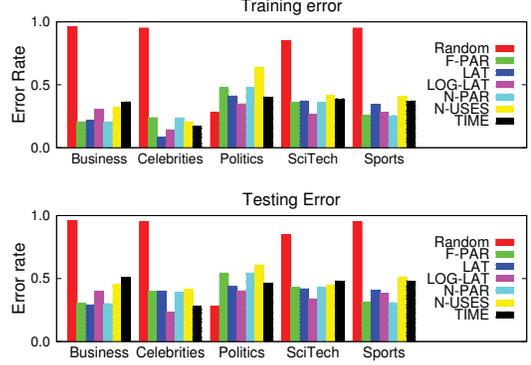


Fig. 1: Training and testing accuracy of hashtag classification in a leave-one-out Linear Discriminant classification.

model is capable of capturing stable individual user behavior for a given topic. We seek to evaluate the stability of configuration of multiple users' genotype values within a topic, and use a classification task and the obtained (training/testing) accuracy as a measure of consistency for our genotype model. Within this context, we compare different genotype dimensions and evaluate the level to which each of them captures characteristic invariant properties of a social media user.

A. Topic consistency for individual users

Our hypothesis is that individual users exhibit consistent behavior of adopting and using hashtags (stable genotype) within a known topic. If we are able to capture such invariant user characteristics in our genotype metrics then we can turn to employing the genotypes for applications. We compute genotype values according to our collection of hashtags with known topics by training a per-user Linear Discriminant (LD) topic classifier to learn the separation among topics. Consider, for example, the LOG-LAT genotype metric: for a user u , we have a set of observed LOG-LAT values (based on multiple hashtags) that are associated with the corresponding topics. If the user u is consistent in her reaction to all topics, then the LOG-LAT values per topic will allow the construction of a classifier with low training and testing error. It is also noted that each hashtag does end up having a topic distribution, but for the scope of this study, a sufficient hashtag classification should at least agree in the topic of greatest probability/likelihood, which is what is presented here.

The consistency of user responses is evaluated using a leave-one-hashtag-out validation: given the full set of (u, h) response values, we withhold all pairs including a validation hashtag h and employ the rest of the pairs involving hashtags

	Bus.	Celeb.	Poli.	Sci./Tech.	Sport	E[x]
Random Error	0.96	0.95	0.28	0.85	0.95	0.45
F-PAR	0.50	0.88	0.61	0.15	0.09	0.41
LAT	0.09	0.46	0.18	0.19	0.25	0.21
LOG-LAT	0.05	0.13	0.19	0.12	0.03	0.13
N-PAR	0.09	0.50	0.88	0.09	0.03	0.40
N-USES	0.45	0.42	0.90	0.22	0.56	0.54
TIME	1.0	1.0	0.01	0.92	0.88	0.61

TABLE III: Error rates of the NB consensus topic classification. $E[x]$ is the expected error across topics.

of known topic to estimate the individual user’s topic genotype. We repeat this for all genotype metrics. The training and testing error rate for this experiment are presented in Fig. 1, and their similar error rates demonstrate how consistent users are at classifying hashtags into topics. In both cases, our genotype metrics enable significantly lower error rates as compared to a Random model (i.e. random prediction based on number of hashtags within a topic), demonstrating that, in general, genotype metrics capture consistent topic-wise behavior. One exception is the Politics topic as it has comparatively many more hashtags than other topics, skewing the random topic distribution resulting in slightly lower error. Across genotype metrics, we observe that normalized latency of adoption (LOG-LAT) is more consistent per user than alternatives.

B. Topic consistency within the network

While individual users may exhibit some inconsistencies in how they behave w.r.t. hashtags within a topic, an ensemble of users’ genotypes remain more consistent overall. To demonstrate this effect, we extend our classification-based evaluation to the the network level. We implement a network-wide ensemble-based Naive Bayes (NB) classifier that combines output of individual user classifiers to achieve network-wide consensus on the topic classification of each validation hashtag. Details on the network level classifier are available in the Supplement [18].

Table III summarizes the testing error rate of our NB scheme for classifying hashtags into topics in a leave-one-hashtag-out validation. The consensus error rate decreases compared to local classifiers (Fig. 1), demonstrating that the genotypes, as a complex, are more stable and consistent than individual users. The lowest error rate of 0.13 is achieved when using the LOG-LAT metric.

The latency genotype metrics that are most invariant (LAT and LOG-LAT) implicitly normalize their time scales of response with respect to the user’s own frequency of activity, which is a feature not captured by the absolute TIME metric, or any of the other metrics. Furthermore, both of these metrics incorporate the network structure, measuring the message offset since the earliest exposure to the hashtag via a followee. LOG-LAT has a slight advantage over LAT because it suppresses the background noise of each hashtag measurement. However, LOG-LAT has the disadvantage that it is dependent on a network-wide latency measurement for the same hashtag, which might be harder to obtain in practice. In this sense, LAT is a more practical genotype dimension when summarizing individual user behavior in real time.

While the system of all user genotypes exhibits significant consistency (high classification accuracy), it is interesting to

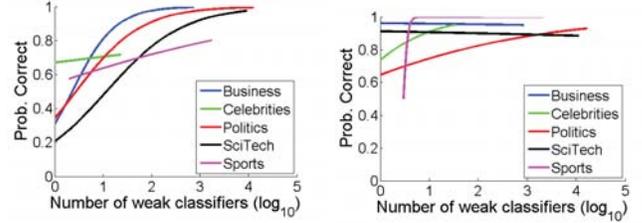


Fig. 2: Accuracy of the network classification as a function of the number of local classifiers (SNAP). Logistic function is fit to each topics accuracy.

understand how many user genotypes are needed to obtain a good classification (i.e. detect a network-wide topic-specific spread). We observe an increasing classification accuracy with the number of users included in the NB scheme. Figures 2a and 2b show the dependence of accuracy on number of local LD classifiers included per topic. All curves increase sharply, indicating that variability within individuals is easily overcome by considering a small subset of users within the network. The accuracy of LOG-LAT increases “faster” to its optimal level for increasing number of local classifiers, since the LOG-LAT metric features a network wide normalization and thus contains global information.

VI. TOPIC-SPECIFIC INFLUENCE BACKBONES

As we demonstrate in the previous section, user behavior remains consistent within a topic. A natural question inspired by this observation is whether topics propagate within similar regions of the shared medium that is the follower network structure. By observing the behavior of agents (adoption, reposting, etc.) one can reveal the underlying backbones along which topic-specific information is disseminated. In this section, we study the propagation of hashtags within Twitter to identify *topical influence backbones* — sub-networks that correspond to the dynamic user behavior. We superimpose the latter over the static follower structure and perform a thorough comparative analysis to understand their differences. The topical backbones in combination with the individual user genotypes will then enable various applications as we show in the subsequent section.

An *influence edge* $e_i(u, v)$ connects a followee u who has adopted at least one hashtag h within a topic T_i before the corresponding follower v . Hence, the influence network $N_i(U, E_i)$ for topic T_i is a subnetwork of the follower network $N(U, E)$ (including the same set of nodes U and a subset of the follower edges $E_i \in E$). We weight the edges of the influence network by the number of hashtags adopted by the followee after the corresponding follower within the same topic.

First, we seek to understand the differences between the influence backbones and the static follower network. Figure 3 presents the overlap among influence backbones and their corresponding follower network. For this comparison, we augment an influence network with all follower edges among the same nodes to obtain the corresponding follower network. In the figure, each network is represented by a node whose size is proportional to the network size (in edges). Connection width

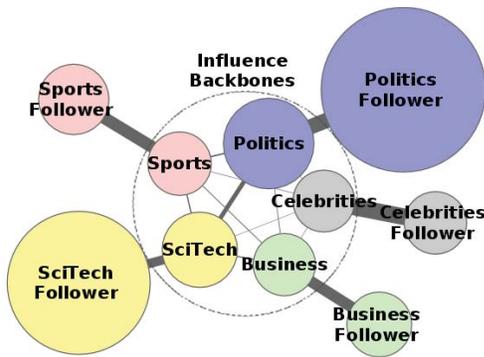


Fig. 3: Overlap among topic influence and corresponding follower subnetworks (in SNAP). Each network is represented as a node, with every topic represented by an influence (encircled in the middle) and a follower network. Node sizes are proportional to the size of the network (ranging from 120k for Celebrities to 42m for Politics Follower). Edge width is proportional to the Jaccard similarity of the networks (ranging from 10^{-3} inter-topic edges to 10^{-1} between corresponding influence-follower networks).

is proportional to the *Jaccard Similarity (JS)* (measured as the relative overlap $|E_i \cap E_j|/|E_i \cup E_j|$) of the edge sets of the networks. The Jaccard similarity for influence and follower networks varies between 0.16 for Sports to 0.3 for Celebrities. The influence networks across topics do not have high overlap (JS values not exceeding 0.01), with the exception of Sci/Tech and Politics with $JS = 0.07$. This may be explained partially by the fact that these are the largest influence networks (5 and 11 million edges respectively). Another reason could be that there are some “expert” nodes who are influential and active in both topics. The degree distribution within the topic backbones also changes (w.r.t. the static structure) with highest impact on low degree nodes and significantly lower fraction of reciprocal links between users (see Supplement [18]).

Beyond network sizes and overlap, we also quantify the structural differences of the influence backbone in terms of connected components. A *strongly connected component (SCC)* is a set of nodes with directed paths among every pair, while in a *weakly connected component (WCC)* connectivity via edges regardless of their direction is sufficient. Figure 4 compares the sizes of the largest SCC and WCC in the topic-specific networks as a fraction of the whole network size. When ignoring the direction (i.e. considering WCC), both the influence and follower structures have a single large component amounting to about 99% of the network. The communities that are active within a topic are connected, showing a network effect in the spread of hashtags, as opposed to multiple disjoint groups which would suggest a more network-agnostic adoption. When, however, one takes direction into consideration (SCC bars in Fig. 4), the size of the SCC reduces drastically in the influence backbones. Less directed cycles remain in the influence backbone, resulting in a structure that is close to a directed acyclic graph with designated root sources (first adopters), middlemen (transmitters) and leaf consumers. The reduction in the size of the SCC is most drastic in the Celebrities topic, indicative of a more explicit traditional media structure: sources (celebrity outlets or profiles) with a large audience of followers and lacking feedback or cyclic influence.

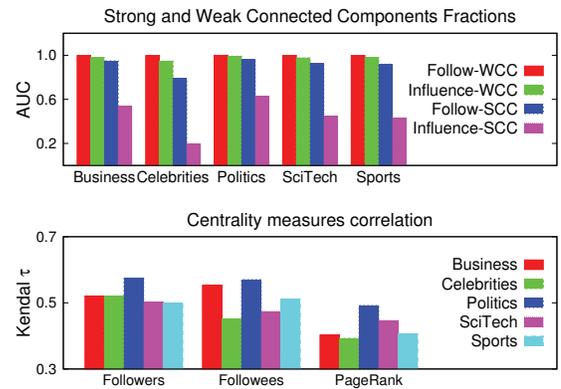


Fig. 4: Largest weakly and strongly connected component (WCC and SCC) sizes as a fraction of the network size (top); and Kendall τ rank correlation of node importance measures for the influence and follower networks (bottom) (SNAP).

How does a user’s importance change when comparing influence to following? In Figure 4 (bottom) we show the correlation of node ranking based on number of followers, followees and PageRank [21] in the influence and follower networks. The correlation of each pair of rankings is computed according to the *Kendall τ* rank correlation measure. The correlation is below 0.5 for all measures and topics. Global network importance (PageRank) is the most distorted when retaining only influence edges (0.4 versus 0.5 on average), while locally nodes with many followers (or followees) tend to retain proportional degrees in the influence network.

Our comparative analysis of the influence and follower structure demonstrates that the influence backbone is quantitatively different from the overall follower network. The explanation for this lies in the fact that the influence backbone is based on the dynamic behavior of users (information dissemination on specific topics), while the follower structure represents the static topic-agnostic media channels among users. Not all followees tend to exert the same amount of influence over their audiences in the actual information dissemination process, giving rise to distinct topic-specific influence backbones. We obtain similar behavior in the smaller Twitter data set CRAWL (omitted due to space limitation).

VII. APPLICATIONS OF GENOTYPES AND BACKBONES

In this section, we employ the user genotypes and the topic-specific backbones for two important applications: (i) prediction of hashtag adopters and influencers and (ii) latency minimization of topical information spread. In both applications knowledge of individual genotypes and influence backbones enables superior performance compared to the static network structure on its own.

Topic-specific influence prediction. We employ the influence structure and the user genotypes to predict likely influencers/adopters for a hashtag. We aim to answer the following question: *Which followees are likely to influence a given user to adopt a hashtag of a certain topic and analogously which followers are likely to adopt a hashtag?* This question is

of paramount importance from both research and practical perspectives. On one hand, uncovering the provider-seeker influence will further our understanding of the global network information dynamics. On the other hand, the question has practical implications for social media users offering guidelines on following high-utility sources or keeping the follower audience engaged.

In this experiment, we consider (h, u) pairs, for users who have at least 10 followees and have used the hashtag at least once. The goal is to predict the subset of all followees who have used the hashtag prior to the user in question and similarly all adopting followers who are likely to use the hashtag later. We construct three predictors utilizing the follower structure that rank influencers/adopters by *Followees*, *Followers* and *Reciprocal* links. We also construct three activity-based predictors utilizing genotypes and influence edges and ranking influencers/adopters by their activity *Act*, topic-specific activity *Topic Act* and activity combined with centrality in the corresponding backbone *RW+Act*. All predictors do not have information about the spread of the specific hashtag. More details on the predictors are available in the Supplement [18].

A prediction instance is defined by a user u and an adopted hashtag h . Only a subset $I(u, h)$ of all structural followees/followers of the user are true influencers/adopters (positives for the prediction task). Our goal is to predict the subset of true influence neighbors using their features and local influence structure (excluding information about the same hashtag h). A good predictor ranks the true neighbors first. In order to overcome the effect of sparsity in the data, we consider prediction of instances for which at least one candidate followee is not isolated in the influence network after removing the links associated with the target hashtag. We measure true positive and false positive rates for increasing value of k (the maximal rank of predicted influencers/adopters) and compute the average area under the curve (AUC) as a measure of the predictor quality. We report this measure within each topic in Figure 5 for the SNAP (top) and CRAWL (bottom) datasets and for influence followees (left) and adopter (right) prediction. Overall, in both datasets, the genotype-based predictors outperform the structure-only counterparts. The existence of a reciprocal follow link is the best structure-only predictor implying the importance of bi-directional links which often may correspond to a friendship relationship [5]. The genotype-based predictors relying on topic specific activity, overall activity and the influence structure allow over 20% improvement with respect to the reciprocity predictor and above two-fold improvement compared to number of followees/followers predictors. Although node information alone (*Act* and *Topic Act*) provides a good accuracy, this effect is even stronger when combining them with the knowledge of the topic influence network in the composite *RW+Act* predictor. The *RW+Act* increases the rank of followees who have influenced the same user or other users within the same topic for different hashtags.

The predictor performance is similar in the CRAWL dataset (Fig. 5), showing the generalization of our models to different types of data. The smaller improvement in CRAWL (compared to SNAP) can be explained partially by sparser usage of our analysis hashtags or due to possibly evolving genotypes of users over longer time frames, a hypothesis we are planning

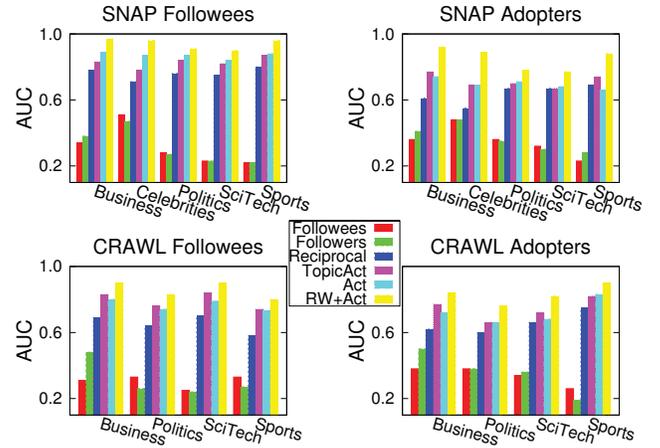


Fig. 5: Influential followee and adopter prediction accuracy. We consider several predictors of a user’s influencers by a hashtag in a known topic. Genotype-based predictors (*Act*, *Topic Act* and *RW+Act*) perform better than follower structure-only counterparts (*Followee*, *Followee* and *Reciprocal*).

to evaluate as future work.

Network latency minimization. Another important problem that can be addressed given knowledge of topic-specific user behavior is that of improving the speed of information dissemination. Fast information dissemination is critical for social-media-aided disaster relief, large social movement coordination (such as the Arab Spring of 2010), as well as time-critical health information distribution in developing regions. In such scenarios, genotypes and the influence structure among users are critical for improving the overall “latency” of the social media network. In this subsection, we demonstrate the utility of our individual user models for latency minimization.

Consider a directed path in a topic-specific influence backbone N , defined by a sequence of nodes $P = (u_1, u_2, \dots, u_k)$. The *path latency* $l(P)$ is defined as the sum of topic-specific latencies (*Time* measure of the genotype) $l(P) = \sum_{j=1, \dots, k-1} \text{Time}(u_j, u_{j+1})$ of all nodes except the destination. The *source-destination latency* (or just latency) $l(u_1, u_k) = \min_{P: u_1 \rightarrow u_k} l(P)$ is defined as the minimum path latency considering all directed paths between the target nodes. The concept of latency is similar to that of shortest path length, except that “length” is measured according to the responsiveness of traversed nodes (i.e., minimal time until u_k ’s adoption of a hashtag introduced by u_1). The *average network latency* is defined as the mean of all node pair latencies. Given a directed network $N(V, E)$ and latency for every node, we define the problem of k *Latency Minimization* (k -*LatMin*) as finding the k best target nodes, whose latency reduction leads to the largest average network latency decrease. We assume that specific nodes could be targeted to reduce their individual latency. In real application scenarios, node latency can be reduced by timely and relevant content recommendation to target nodes and/or financial incentives. For our analysis we optimistically assume that every node’s latency could be reduced to 0, however, node-wise constraints can be incorporated according to known limitations of users.

One can show (via a reduction from the *Set cover* problem)

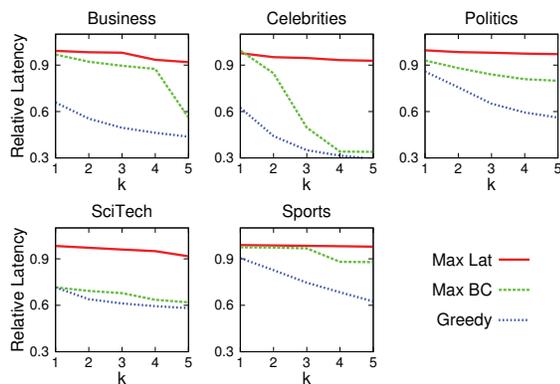


Fig. 6: Comparison of three heuristics for Latency Minimization in the SNAP dataset. The traces show the relative (w.r.t. the original) average network latency as a function of the number of targeted nodes k .

that k -LatMin is NP-hard. We consider three heuristics: *Max Lat* targets nodes in descending order of their latency values; *Max BC* targets nodes in decreasing order of their structural node betweenness-centrality measure; and *Greedy* targets nodes based on their maximal decrease of average latency combining both structural (centrality) and genotype (latency) information.

Figure 6 shows the performance of the three heuristics in minimizing the average latency in subgraphs (of size 500 nodes) of the largest strongly connected components within the influence backbones of our SNAP dataset. Considering the node genotypes (Max Lat) or the influence backbone (Max BC) on their own is less effective than jointly employing both (Greedy) across all topics. The Greedy heuristic enables about 2-fold reduction of the overall network latency by targeting as few as 1% (5 out of 500 nodes) of the user population. It is interesting to note that in Sports and Celebrities, since there are central nodes of large degrees, the betweenness-centrality criterion performs almost as good as Greedy.

VIII. CONCLUSION

We introduced the social media genotype—a genetically-inspired framework for modeling user participation in social media. Features captured by the user genotypes define the *actual topic-specific* user behavior in the network, while the traditionally analyzed follower network defines only *what is possible* in the information dissemination process. Within our genotype model, each network user becomes an individual with a unique and invariant behavioral signature within the topic-specific content dissemination. In addition, we demonstrated that users are embedded in topic-specific influence backbones that differ structurally from the follower network.

We instantiated our topic-based genotype and backbone framework within a large real-world network of Twitter and employed it for the tasks of (i) discovering topic-specific influencers and adopters, and (ii) minimizing the network-wide information dissemination latency. The genotype framework, when combined with the topic-specific influence backbones, enabled good influence predictive power, achieving improvement by more than 20% over using the follower structure alone. In the latency minimization application, we demonstrated that the knowledge of topic backbones and genotypes

can enable 2-fold reduction of the overall network latency by reducing the latency of appropriately selected 1% of the user population.

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