



BIG DATA ANALYTICS FOR CYBER SECURITY

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Malware Pandemic







Malware is hard to detect!







Key Challenge

- Statistics from Symantec WINE Dataset
 - # of Detections <<< # of Infections</p>







Problem Statement







Our Approaches

Feature based prediction method
 Proposed a set of novel features

• Epidemic model inspired by SIR model

 Ensemble method that merges the previous two methods with other stateof-the-art techniques.

FEATURE BASED PREDICTION MODEL

1st Method









Feature Based Method

Each record= (Host, Malware, File name, Infection time, Detection time)





Detection/Patch Incompetence

- Each record= (Host h, Malware m, File name f, Infection time i, Detection time t)
- Detection time Infection time (Detection Incompetence¹)
 - How good/bad is a user h at detecting malware m?
 - How easy/hard is it to detect malware m?
- Patch time Infection time (Patch Incompetence¹)
 - How good/bad is a user at patching a vulnerability/malware?
 - How easy/hard is it to patch a vulnerability/malware?
- Average these values for each host → host-level detection/patch incompetence
- Some other similar features, e.g., Detection time Malware signature release time

1: These two are the most simplest features.





- Each record= (Host h, Malware m, File name f, Infection time i, Detection time t)
- Detection Ability (ADA) of host h is the weighted sum of Detection Hardness (ADH) of malware detected by h.

$$ADA(h) = \sum_{(f,m,t) \in dH(h)} w_{12}(h, f, m, t) \cdot ADH(m)$$

A subset of WINE records, where Host = h

• Detection Hardness of malware *m* is the weighted sum of Detection Ability of hosts that detected *m*.

$$ADH(m) = \sum_{(f,h,t) \in dM(m)} w_{21}(m,f,h,t) \cdot ADA(h)$$





BiFixpoint Algorithm

Algorithm 1: BiFixpoint **Input** : $\mathcal{H}, \mathcal{M}, T$ (*T is a training set *) **Output**: ADA, ADH 1 forall $h \in \mathcal{H}$, $ADA(h) \leftarrow \frac{1}{|\mathcal{H}|}$ (* initialize *) 2 forall $m \in \mathcal{M}, ADH(m) \leftarrow \frac{1}{|\mathcal{M}|}$ Uniform initialization change \leftarrow true; while change do $ADA'(\tilde{h}) \leftarrow \sum_{(f,m,t) \in dH(h)} w_{12}(h,f,m,t) * ADH(m)$ 5 $ADH(m) \leftarrow \sum_{(f,h,t) \in dM(m)} w_{21}(m, f, h, t) * ADA(h)$ 6 if $ADA' \sim ADA$ and $ADH' \equiv ADH$ then **Recursive calculation** 7 change \leftarrow false 8 else 9 $ADA \leftarrow ADA'$ and $ADH \leftarrow ADH'$ 10 We prove that convergence is end 11 \mathbf{end} 12always guaranteed! return ADA, ADH $\mathbf{13}$





Collaborative Features

- Given two *similar*¹ hosts h_1 and h_2
 - Suppose h_1 was infected by m.
 - h_2 is likely to be infected soon with prob ~ $sim(h_1, h_2)$.
- *cf*(*h*,*m*) is the estimated prob. of host *h* being infected by *m* (considering similarity).
- cf(C,m) is the sum of cf(h,m), where h is a host in country C.



1: We defined various similarity measures based on calculated features.





Time Lag Features

- Today's infection ratio depends on not only today's features but also past features.
- Very high dimensional feature space

	day	Feature #1	Feature #1 (-1 day)	Feature #1 (-7 day)	 Infected Host Ratio	
80% Training	d					
	d+1				Ground Truth	
	÷					
20% Test	d+n				Ground Truth vs.	
	:				Predictions	





Recap of Features

- Features from raw values
 - Detection time Infection time (Detection Incompetence)
 - Patch time Infection time (Patch Incompetence)
 - Some features calculated from raw data
- Features from BiFixpoint Algorithm
 - Detection ability, Patch ability for hosts
 - Detection hardness, Patch hardness for malware
- Collaborative Features
 - Infection numbers based on host similarity
- Country Human Development Index, ...
- Time lag features
- Country level aggregation \rightarrow Regression Problem



2nd Method

EPIDEMIC PREDICTION MODEL





Epidemic Model

- SIR Model models the the dynamics of infectious disease.
- Sometimes used for social rumor diffusion.
- Does not fit the spread of malware.
 - **Recovered** doesn't precisely capture the dynamics of malware spread.
 - Transition rate is not designed for malware.
 - Network data may not always be available.



b = the rate at which susceptible people become infectious
r = the rate at which infectious people recover/develop immunity





DIPS Epidemic Model

- "Recovered" \rightarrow "Detected" and "Patched"
- Carefully designed transition rates
- S(t), I(t), D(t) and P(t) are the number of susceptible, infected, detected and patched hosts at time t
- S(t), I(t), D(t) and P(t) are recursively defined.







How to predict with DIPS

- Find the optimal set of parameters with Least Square Method to minimize the sum of (true-prediction)²
- Train with the target country-malware pair.
 - Initialization \rightarrow local optimal \rightarrow not stable learning
- Learning algorithm (two phases)
 - First, train the parameters with all countries and malware
 - Second, train again only for the target country-malware







DIPS - Susceptible



- $S \rightarrow I$ in between *t* and *t*+1: $\beta(t) \cdot S(t) \cdot I(t)^1$
- $D \rightarrow S: (1 \delta(t)) \cdot D(t)$
- $S \rightarrow P: \theta(t) \cdot S(t)$
- $S(t+1) = S(t) \beta(t) \cdot S(t) \cdot I(t) \theta(t) \cdot S(t) + (1 \delta(t)) \cdot D(t)$

1: This is from SIR model.



DIPS - Detected



- $I \rightarrow D: \gamma_0 \cdot DET(t)$, where DET(t) is the true detection numbers at time t
- $D \rightarrow S: (1 \delta(t)) \cdot D(t)$
- $D \rightarrow P: \delta(t) \cdot D(t)$
- $D(t) = \gamma_0 \cdot DET(t)$





DIPS-exp Epidemic Model

- Modeling of "Birth" of the SIR model
- $\sigma(t)$ is added.







3rd Method

ENSEMBLE PREDICTION MODEL





Combine Prediction Models

- Combine Feature Method and DIPS.
- Use DIPS prediction results as additional features.







Not Enough Training Data

- To predict number of hosts infected by malware *m*, train jointly with similar malware
- Discover similar malware with Dynamic Time Warping to calculate time-series similarity
- Lots of noise
 Symantec WINE dataset
 Patched
 Patched
 Malware downloaded
 Infected released
 Detected
 Host state





Robust Regression

- Need a robust regression
- Gaussian Process Regression
 - Very strong Bayesian regression method
 - Less parametric (Parameters are calculated from data with maximum likelihood.)



Linear combination of weighted features + regularization term





ESM Model

	Feature #1	Feature #2	DIPS output	 Infected Host Ratio
80% Training (m)				
80% Training (m1)				
: :				
20% Test (m)				







Experiment Environment

- Top 50 Most Infectious Malware, Top 40
 Country in GDP per capita → 2000 Predictions
- 1.45M unique hosts, 2.99M records
- FBP
- DIPS, DIPS-exp
- FUNNEL: state-of-the-art epidemic model
- ESMO (FBP + DIPS + DIPS-exp +Similar Malware)
- ESM1 (ESM0 + FUNNEL)





Measurements

- MAE*=|true infections predicted infections|
- $MSE = (true infection ratio predicted infection ratio)^2$
- RMSE = sqrt(MSE)
- NRMSE
- Pearson Correlation Coefficient





FUNNEL (prior art)

- State of the art epidemic model for human disease
- C.C. between truths and predictions are very bad. Prediction for country-malware pair







Feature Based Prediction



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DIPS







ESMO







Error Values

Model	MAE*	RMSE	NRMSE
FBP	73.74	0.00170	0.179
Funnel	127.83	0.00269	0.226
DIPS	32.36	0.00083	0.165
DIPS-Exp	36.56	0.00096	0.223
ESM_0	39.41	0.00115	0.150
ESM_1	41.84	0.00118	0.151
FBP^+_{Funnel}	79.01	0.00189	0.179

















References

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