Tracking global outbreak of Hepatitis Delta Virus By Christopher John Peterson, Himanshi Sharma and Dayanidhi Tandra

Project Purpose

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Our efforts with the project were targeted on identifying the diseases that supplemented the growth of HDV and help in tracking the outbreak in HDV. 2) Bootstrapping
* Randomly sample data to estimate case distribution
* Resulted in 583 significant diseases amongst HDV patients 3) Logistic Model Chances of getting infected by HDV

With	Female	Male	
No disease	9.8	1%	11.76%
only HBV	99.9	9%	99.99%
Only Heart			
Diseases	18.6	9%	15.80%
Only Diabetes	17.3	5%	14.62%

HDV cases in USA (2008-2010) grouped by State

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*Costal area are highly affected

Exploratory Data Analysis

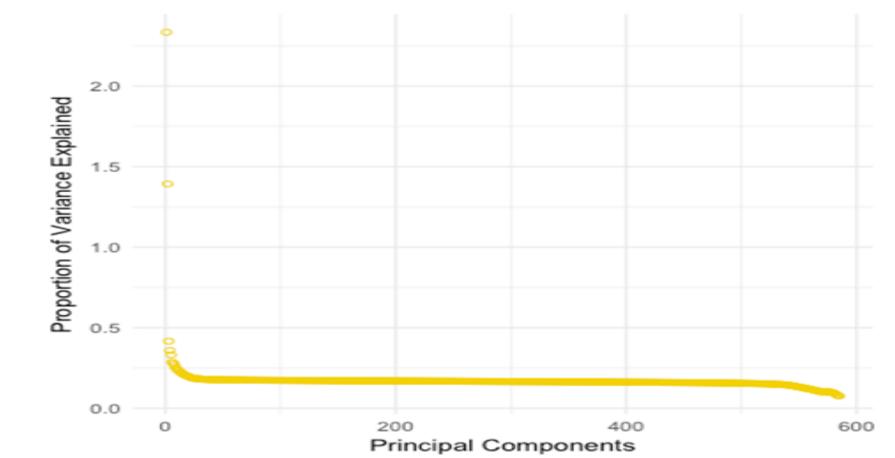
1) Frequent Items by Misra-Gries

S.No	Diagnosis Code Pairs	Frequency Counter	0.0	200 400 Principal Components	600
1	2724_4019	74			
2	7030_70715	6	2) SMOTE for Class Balancing		
3	5715_71590	4			
4	7030_78720	9	P	No (HDV – cases)	Yes (HDV+ cases)
5	7032_25000	104			
6	7030_41400	36	Original	1359926	2788
7	2809_7030	181	After resampling	5576	5576
8	311_7032	41	with SMOTE		
9	3051_7032	35			
10	2720_4019	37	1 and		
11	7032_78720	10			All AND ENDER
				the second	

Predictive Modelling

Input Demographic Info of patients along with dummy for 580 significant diseases

1) PCA



Output The odds of having HDV given demographics and diseases

Conclusion

Bootstrapping yielded too many potential diseases. Logistic regression model helped find the odds of having HDV and can help with reducing the list of disease that supplement the growth of HDV as we continue to work with Prof. Weller.

> Datasets are provided by Weller Lab, Salt Lake City.

Acknowledgements



For more visualization please scan this.