

Fig S1A: Distribution of influenza sequence records across year of isolation.

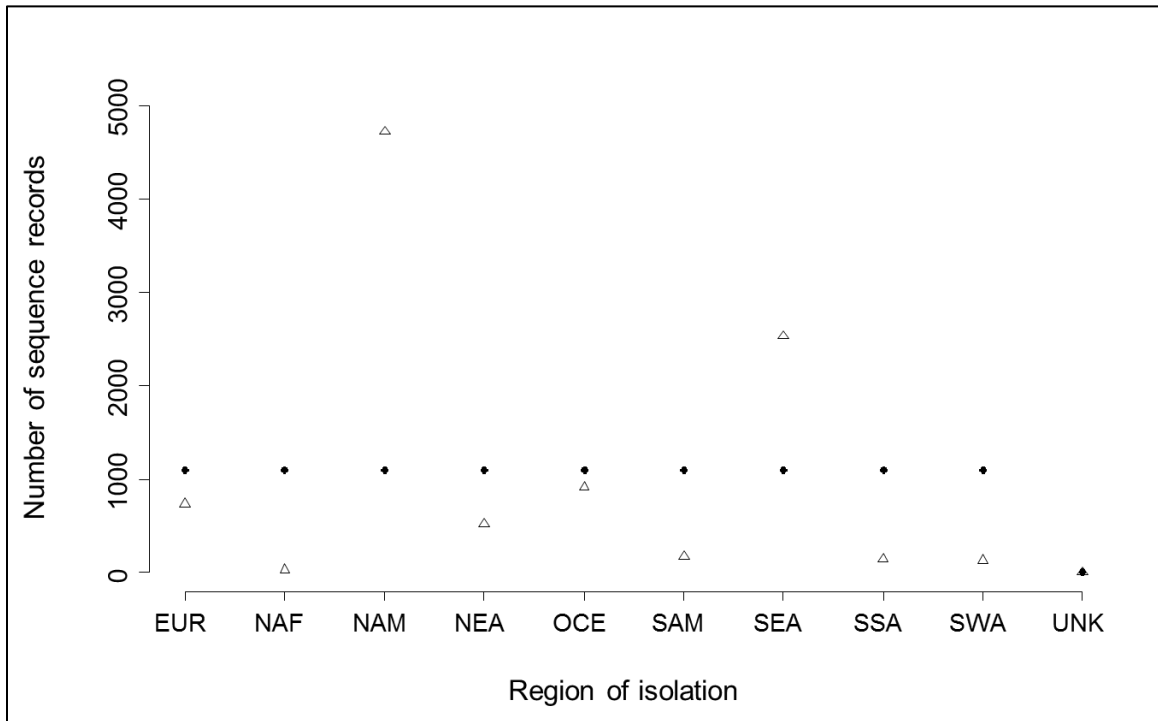


Fig S1B: Distribution of influenza sequence records across region of isolation.

Fig S1: Distribution of influenza sequence records across year and geographic location of

isolation. A) The solid line represents the total occurrences (number of sequence records) before temporal correction (unprocessed). The dotted line indicates the total occurrences after temporal correction. A dashed line is used to connect years 2009 and 2010 because complete data for 2010 was not available at the time of analyses. B) Triangles represent occurrence (number of sequence records) before regional correction (unprocessed). Dots indicate the total occurrences after regional correction. The abbreviations EUR, NAF, NAM, NEA, OCE, SAM, SEA, SSA, SWA, and UNK stand for Europe, North Africa, North America, North-East Asia, Oceania, South America, South-East Asia, Sub-Saharan Africa, South-West Asia, and “Unknown” respectively.

Supplemental Tables S1A, B and C: Population density and Cramer’s V analysis results. In

order to control for the effects of large dataset size on the chi-squared statistic and to further control for population density affects we performed the Cramer’s V test on the chi-squared data before and after population density adjustment. Cramer’s V is used as a post-hoc analysis to determine the strength of an association after the chi-squared test has determined the results to be significant. To further control for the geographic bias in the data, we also adjusted for virus prevalence per capita human population across different regions of the world using data for total population per region from the Population Reference Bureau resource (www.prb.org). We then repeated the chi-squared analysis and performed Cramer’s V test on both datasets. While the absolute values of the chi-squared statistics and p-value changed with population density adjustment, the extreme skewing in VT-host distributions remained significant. We also noticed that although some VTs showed low Cramer’s V measurement (shown in bold; such as VT-13

with V-value **0.055081**), in the majority of cases Cramer's V was still high, providing further support for the nominal association between VT and host, thus validating that the chi-squared test results as reasonable and significant.

Table S1A: Population density and Cramer's V analysis results by VT

Variant Type	DF ^a	Result assuming the same prevalence per capita human population across different regions			Result assuming the same prevalence per region		
		Chi-squared value	P-value	Cramer's V	Chi-squared value	P-value	Cramer's V
VT-1	5	1872.08	<1.00E-320	0.435184	2307.531	<1.00E-320	0.483154
VT-2	5	311.84	2.85E-65	0.177614	370.5459	6.59E-78	0.193612
VT-3	5	438.095	1.82E-92	0.210521	601.056	1.8E-128	0.246586
VT-4	5	1913.6	<1.00E-320	0.439984	1243.289	2.06E-272	0.354648
VT-5	5	196.832	1.35E-40	0.141111	344.2334	2.32E-74	0.186611
VT-6	5	620.396	7.9E-132	0.250522	285.4926	1.74E-61	0.169945

					value		
Avian	15	2631.07015	<1.00E-320	0.515914671	2263.898	<1.00E-320	0.478564
Chicken	15	2840.52452	<1.00E-320	0.536056955	3753.136	<1.00E-320	0.616182
Equine	15	9049.3594	<1.00E-320	0.956798711	9389.916	<1.00E-320	0.974636
Human	15	3711.48517	<1.00E-320	0.612753115	3994.254	<1.00E-320	0.635667
Others	15	530.499121	2E-103	0.231661571	587.6761	1.5E-115	0.243826
Swine	15	447.300834	7.63E-86	0.212721564	385.6623	7.09E-73	0.197522

Table S1C: Cramer's V test interpretation

Level of association	Verbal description	Comments
0	No Relationship	Knowing the independent variable does not reduce the number of errors in predicting the dependent variable at all.
.00 to .10	No Association	Variables are independent
.10 to .20	Weak Association	Variables are likely independent

.20 to .30	Moderate Association	Variable may or may not be independent
.30 to .45	Strong Association	Either an extremely good relationship or the two variables are measuring similar concepts
.45 to .99	Redundant	The two variables are probably measuring the same concept.
1	Perfect Relationship	If we know the independent variable, we can perfectly predict the dependent variable.

Adapted from: Cramér, H. (1999). *Mathematical Methods of Statistics*, Princeton University Press

Tables S2A, B and C: Support and confidence for VT-host association rules. The support ($sup(X)$) of a rule is defined as the proportion of records in the dataset which contain all the attributes included in the rule. Hence a bigger support is usually preferred. The confidence of a rule is defined as $conf(X \Rightarrow Y) = sup(X \cup Y) / sup(X)$. Confidence can be interpreted as an estimate of the probability of finding the right-hand-side of the rule in a relationship under the condition that these relationships also contain the left-hand-side. In our case, for each possible rule, we calculated both the support and the confidence. We notice that most of the supports turned out to be very small, likely because the dataset used in this study includes many host groups and VTs and the overall number of records is large. On the other hand, the resulting confidence values were very large in many cases (>0.50 in **bold**), indicating a strong relationship between those host groups and VTs.

Table S2A: Support (same for variant type to host type and vice versa)

Variant type	Host type					
	Avian	Chicken	Equine	Human	Others	Swine
VT-1	0.176429	0.046232	0	0.038139	0.006171	0.018614
VT-2	0.013455	0.002833	0.000101	0.167223	0.000202	0.020536
VT-3	0	0	0	0.138493	0	0.003035
VT-4	0.0609	0.014062	0	0	0.002226	0.000303
VT-5	0	0	0	0.067779	0.000101	0
VT-6	0.031462	0.025594	0	0.001821	0.001214	0.002934
VT-7	0.018412	0.020132	0	0.001619	0.000607	0
VT-8	0.001922	0.000202	0.013657	0	0.000405	0.000303
VT-9	0	0	0	0.023672	0	0
VT-10	0.000506	0.000101	0	0.028326	0	0.000101
VT-11	0.004249	0.005159	0	0	0.006879	0
VT-12	0.004047	0.00263	0	0.000303	0	0.000809
VT-13	0.005867	0.001214	0	0	0	0
VT-14	0.003136	0.002124	0	0	0	0
VT-15	0.001821	0.003541	0	0.001315	0.000405	0.000101
VT-16	0.000303	0.000101	0	0.005969	0	0.000202

Table S2B. Confidence values from host type to variant type

Variant type	Host type					
	Avian	Chicken	Equine	Human	Others	Swine
VT-1	0.547051	0.373061	0	0.08035	0.338889	0.396552
VT-2	0.041719	0.022857	0.007353	0.352302	0.011111	0.4375
VT-3	0	0	0	0.291773	0	0.064655
VT-4	0.188833	0.113469	0	0	0.122222	0.006466
VT-5	0	0	0	0.142796	0.005556	0
VT-6	0.097553	0.206531	0	0.003836	0.066667	0.0625
VT-7	0.057089	0.162449	0	0.00341	0.033333	0
VT-8	0.00596	0.001633	0.992647	0	0.022222	0.006466
VT-9	0	0	0	0.049872	0	0
VT-10	0.001568	0.000816	0	0.059676	0	0.002155
VT-11	0.013174	0.041633	0	0	0.377778	0
VT-12	0.012547	0.021224	0	0.000639	0	0.017241
VT-13	0.018193	0.009796	0	0	0	0
VT-14	0.009724	0.017143	0	0	0	0
VT-15	0.005646	0.028571	0	0.002771	0.022222	0.002155
VT-16	0.000941	0.000816	0	0.012575	0	0.00431

Table S2C. Confidence values from variant type to host type

Variant type	Host type					
	Avian	Chicken	Equine	Human	Others	Swine
VT-1	0.617783	0.161885	0	0.133546	0.021608	0.065179
VT-2	0.065842	0.013861	0.000495	0.818317	0.00099	0.100495
VT-3	0	0	0	0.978556	0	0.021444
VT-4	0.785901	0.181462	0	0	0.028721	0.003916
VT-5	0	0	0	0.99851	0.00149	0
VT-6	0.499197	0.4061	0	0.028892	0.019262	0.046549
VT-7	0.451613	0.493797	0	0.039702	0.014888	0
VT-8	0.116564	0.01227	0.828221	0	0.02454	0.018405
VT-9	0	0	0	1	0	0
VT-10	0.017422	0.003484	0	0.97561	0	0.003484
VT-11	0.26087	0.31677	0	0	0.42236	0
VT-12	0.519481	0.337662	0	0.038961	0	0.103896
VT-13	0.828571	0.171429	0	0	0	0
VT-14	0.596154	0.403846	0	0	0	0
VT-15	0.253521	0.492958	0	0.183099	0.056338	0.014085
VT-16	0.046154	0.015385	0	0.907692	0	0.030769

Tables 3A and 3B: ANOVA model test and results. An ANOVA model is used to identify factors that truly affect a particular response. Our model looked at the main effects of: host type, VT, HA subtype, NA subtype and the two-way interactions of host type by VT, host type by HA, host type by NA, VT by HA and VT by NA using the number of records as the response variable. From the ANOVA output, we see that the overall model is significant with a p-value F statistics <0.0001 indicating that the model is valid. Since the interaction of host type and NA is significant (p-value 0.0037), we know that at least one pair of response variables for different combinations of host type and NA is different from each other. Hence there is no need to look at their main effects because the possible significance of their main effects could be driven by their interactions. We also see that the p-value for the interaction of VT and host is less than 0.0001, thus verifying our conclusion that VT is highly associated with host type. Neither the interaction of VT and HA nor VT and NA is significant implying that there is insufficient evidence to conclude association between VT and either NA or HA subtype. Therefore, the association between host type and VT remains verified.

Table S3A: ANOVA model test

Source	DF ^a	Sum of Squares	Mean Square	F Value ^b	Pr>F ^c
Model	214.00	4236219.29	19795.42	2.37	<0.0001
Error	165.00	1375505.14	8336.40		
Corrected Total	379.00	5611724.43			

^aDegrees of freedom

^bRatio produced by dividing the Mean Square for the Model by the Mean Square for Error.

^cSignificance probability associated with the F statistic

Table S3B: ANOVA effect results

Source	DF	Type III SS	Mean Square	F Value	Pr>F
VT	16.00	434378.56	27148.66	3.26	<0.0001
Host type	5.00	177167.36	35433.47	4.25	0.0012
HA subtype	15.00	100148.53	6676.57	0.80	0.6755
NA subtype	9.00	133120.71	14791.19	1.77	0.0766
VT*host	32.00	880039.26	27501.23	3.30	<0.0001
Host*HA	26.00	243146.63	9351.79	1.12	0.3222
Host*NA	20.00	366398.40	18319.92	2.20	0.0037
VT*HA	43.00	422496.01	9825.49	1.18	0.2312
VT*NA	29.00	36821.40	1269.70	0.15	1.0000

Additional supplemental material:

R code used for data de-biasing and for the correction of geo-temporal bias:

```
##### R code for Distribution of influenza sequence records across year/location of
isolation#####
#####
# Read in the year data after data cleaning (9998)
#####
```

```

dataold=read.table("C:/Users/lmy/Desktop/year.txt",header=T)
dataold=table(dataold)

npyear=as.vector(dataold)

#get rid of the data before the year of 1961
npyear=npyear[27:75]

year=dimnames(dataold)$dataold
year=as.numeric(year[27:75])

avg=9885/49

plot(year,npyear,type="l",ylim=c(0,2000),lwd=2,xlab="Year of isolation",ylab="Number of
sequence records",cex.lab=1.5,cex.axis=1.5)
lines(x=c(2009,2010), y =c(1754,15), type = "l", lty=2,lwd=2)
points(year[1:49],rep(avg,49),pch=16)
legend(1965,1000,pch=c(NA,16),cex=1.5,lty=c(1,0),lwd=c(2,NA),c("Sequence records for
unprocessed data","Sequence records for processed data"))

#####
# Read the region data (after deleting the records before year of 1961) (9885)
#####
dataold=read.table("C:/Users/lmy/Desktop/region.txt",header=T)
dataold=table(dataold)
dataold

np=as.vector(dataold)
re=dimnames(dataold)$dataold

avg=(9885-3)/9
new=c(rep(avg,9),3)

plot(dataold,type="p",ylim=c(0,5000),pch=2,xlab="Region of isolation",ylab="Number of
sequence records",cex.lab=1.5,axes=F)
points(new,pch=16)
legend(4,4500,pch=c(2,16),c("Sequence records for unprocessed data","Sequence records for
processed data"),cex=1.5)

axis(1,xlim=c(1:10),at=c(1:10),labels=c("EUR","NAF","NAM","NEA","OCE","SAM","SEA","
SSA","SWA","UNK"),cex.axis=1.3)
axis(2,ylim=c(0:5000),at=c(0,1000,2000,3000,4000,5000),labels=c("0","1000","2000","3000","4
000","5000"),cex.axis=1.4)

##### R code for assigning weight for each
records#####

```

```

# Read in the raw data from Jyothi
yearold=read.table("C:/Users/lmy/Desktop/yearold.txt",header=T)
yearold=table(yearold)

##number of sample per year
npyear=as.vector(dataold)
#get rid of year 2010 for which complete data is not available
npyear=npyear[1:75]

year=dimnames(dataold)$dataold
year=as.numeric(year[1:75])
year1=as.character(year)

plot(year,npyear,type="l",col="red",lwd=2,main="Sample Size by Year")

#Now set up the standard for year cutoff
total=9998
prop=npyear/total
cumsum=cumsum(npyear)
prop2=cumsum/total
rbind(year1,prop2)

#Get rid of the data before 1961, because the cumulative propotion is less than 0.01
#aaa=sum(npyear[1:27])
#bbb=c(aaa,npyear[28:75])
#ccc=c(1961,year[28:75])
#plot(ccc,bbb,type="l",col="red",lwd=2,main="Sample Size by Year using Jyothi's data")

x=year[27:75]
y=npyear[27:75]

plot(x,y,type="l",col="red",lwd=2,main="Sample Size by Year from 1961 to 2009")

# if we make the assumption that same occurrences for each year
# we have different ways to do this, but this one makes sure the total count will be the same

avg=total/length(x)
wyear=rep(avg,length(x))/y

weights=cbind(x,y,wyear)
weights

write.table(weights, file = "C:/Documents and
Settings/lmy/Desktop/yearweight.csv",sep="," ,row.names = TRUE)

#Finish the year correction!

```

```

plot(x,y,type="l",col="red",lwd=2,main="Sample Size by Year using Jyothi's data")
points(x,rep(avg,length(x)),pch=16)

#####
##for region do the same thing
regionold=read.table("C:/Users/LMY/Desktop/regionold.txt",header=T)
regionold=table(regionold)

npreion=as.vector(regionold)
region=dimnames(regionold)$regionold

avg2=(total-3)/9
wregionsub=rep(avg2,9)/npreion[1:9]
wregion=c(wregionsub,1)

weights2=cbind(region,npreion,wregion)
weights2

write.table(weights2, file = "C:/Documents and
Settings/lmy/Desktop/result2.csv",sep="," ,row.names = TRUE)

#Finish the year correction!
plot(npreion,col="red",lwd=2,main="Sample Size by region",xlab="Regions",ylab="number
per region")
points(c(rep(avg2,9),6),pch=16)
legend(x=8,y=4000,c("old","new"),col=c("red","black"),pch=c(1,16))

#####
#####
#####adjust: same prevalence per 1000 population#####

regionold=read.table("C:/Users/LMY/Desktop/regionadjust.txt",header=T)
regionold=table(regionold)

npreion=as.vector(regionold)
region=dimnames(regionold)$regionold

total=9885
relative=scan()
sumrelative=sum(relative)

records=(total-3)*(relative/sumrelative)

wregionsub=records/npreion[1:9]
wregion=c(wregionsub,1)

```

```

weights2=cbind(region,npregion,wregion)
weights2

write.table(weights2, file = "C:/Users/lmy/Desktop/regionadjustresult.csv",sep=",",row.names =
TRUE)

#Finish the year correction!
plot(npregion,col="red",lwd=2,main="Sample Size by region",xlab="Regions",ylab="number
per region")
points(c(records,3),pch=16)
legend(x=8,y=4000,c("old","new"),col=c("red","black"),pch=c(1,16))

```

SAS code:

```

data flu;
input host$ vt$ H$ N$ count;
datalines;
Avian VT-01 1 . 1
Avian VT-01 10 1 1
Avian VT-01 10 2 2
Avian VT-01 10 3 3
Avian VT-01 10 4 3
Avian VT-01 10 5 4
Avian VT-01 10 6 2
Avian VT-01 10 7 83
Avian VT-01 10 8 5
Avian VT-01 10 9 2
Avian VT-01 11 . 1
Avian VT-01 11 1 8
Avian VT-01 11 2 11
Avian VT-01 11 3 5
Avian VT-01 11 4 2
Avian VT-01 11 6 4
Avian VT-01 11 7 1
Avian VT-01 11 8 2
Avian VT-01 11 9 45
Avian VT-01 12 2 1
Avian VT-01 12 3 4
Avian VT-01 12 4 4
Avian VT-01 12 5 7
Avian VT-01 13 6 1
Avian VT-01 13 9 1
Avian VT-01 14 6 1
Avian VT-01 15 2 1
Avian VT-01 15 6 1

```

Avian VT-01 15	8	1
Avian VT-01 15	9	3
Avian VT-01 16	3	2
Avian VT-01 1	1	61
Avian VT-01 1	2	6
Avian VT-01 1	3	1
Avian VT-01 1	5	1
Avian VT-01 1	6	2
Avian VT-01 1	8	1
Avian VT-01 1	9	1
Avian VT-01 2	1	13
Avian VT-01 2	2	10
Avian VT-01 2	3	43
Avian VT-01 2	4	1
Avian VT-01 2	5	9
Avian VT-01 2	6	1
Avian VT-01 2	7	3
Avian VT-01 2	8	1
Avian VT-01 2	9	21
Avian VT-01 3	.	1
Avian VT-01 3	1	5
Avian VT-01 3	2	28
Avian VT-01 3	3	7
Avian VT-01 3	5	6
Avian VT-01 3	6	35
Avian VT-01 3	7	3
Avian VT-01 3	8	54
Avian VT-01 3	9	1
Avian VT-01 4	.	1
Avian VT-01 4	1	1
Avian VT-01 4	2	15
Avian VT-01 4	3	9
Avian VT-01 4	4	4
Avian VT-01 4	5	1
Avian VT-01 4	6	100
Avian VT-01 4	7	2
Avian VT-01 4	8	18
Avian VT-01 4	9	4
Avian VT-01 5	.	6
Avian VT-01 5	1	531
Avian VT-01 5	2	53
Avian VT-01 5	3	27
Avian VT-01 5	4	1
Avian VT-01 5	6	1
Avian VT-01 5	7	8
Avian VT-01 5	8	2

Avian VT-01 5	9	4
Avian VT-01 6	.	6
Avian VT-01 6	.	1
Avian VT-01 6	1	37
Avian VT-01 6	14	1
Avian VT-01 6	2	30
Avian VT-01 6	3	3
Avian VT-01 6	4	6
Avian VT-01 6	5	18
Avian VT-01 6	6	8
Avian VT-01 6	8	38
Avian VT-01 6	9	2
Avian VT-01 7	.	2
Avian VT-01 7	1	9
Avian VT-01 7	2	6
Avian VT-01 7	3	122
Avian VT-01 7	4	5
Avian VT-01 7	5	1
Avian VT-01 7	6	2
Avian VT-01 7	7	28
Avian VT-01 7	8	2
Avian VT-01 7	9	5
Avian VT-01 8	.	1
Avian VT-01 8	2	1
Avian VT-01 8	4	24
Avian VT-01 9	1	2
Avian VT-01 9	2	46
Avian VT-01 9	4	2
Avian VT-01 9	5	5
Avian VT-01 9	6	3
Avian VT-01 9	8	1
Avian VT-01 9	9	6
Avian VT-01 .	1	1
Avian VT-01 .	6	1
Avian VT-02 12	5	2
Avian VT-02 12	9	2
Avian VT-02 1	1	5
Avian VT-02 1	2	1
Avian VT-02 2	1	1
Avian VT-02 3	2	26
Avian VT-02 3	5	1
Avian VT-02 3	6	3
Avian VT-02 3	8	8
Avian VT-02 4	2	1
Avian VT-02 4	6	3
Avian VT-02 4	8	4

Avian VT-02 5	1	8
Avian VT-02 5	2	6
Avian VT-02 5	3	3
Avian VT-02 6	1	4
Avian VT-02 6	2	33
Avian VT-02 6	5	2
Avian VT-02 6	7	1
Avian VT-02 6	8	4
Avian VT-02 7	7	1
Avian VT-02 9	1	2
Avian VT-02 9	2	8
Avian VT-02 9	4	1
Avian VT-02 9	5	1
Avian VT-02 .	2	1
Avian VT-04 10	3	2
Avian Vt-04 10	4	1
Avian VT-04 10	7	8
Avian VT-04 11	2	3
Avian VT-04 11	3	2
Avian VT-04 11	6	1
Avian VT-04 11	8	4
Avian VT-04 11	9	22
Avian VT-04 12	5	12
Avian VT-04 13	6	1
Avian VT-04 1	1	29
Avian VT-04 1	2	1
Avian VT-04 1	3	4
Avian VT-04 1	5	1
Avian VT-04 1	6	1
Avian VT-04 1	8	2
Avian VT-04 1	9	1
Avian VT-04 2	1	5
Avian VT-04 2	2	2
Avian VT-04 2	3	3
Avian VT-04 2	7	1
Avian VT-04 2	9	2
Avian VT-04 3	.	3
Avian VT-04 3	1	6
Avian VT-04 3	2	10
Avian VT-04 3	3	1
Avian VT-04 3	4	3
Avian VT-04 3	5	1
Avian VT-04 3	6	28
Avian VT-04 3	8	101
Avian VT-04 3	9	1
Avian VT-04 4	.	1

Avian VT-04 4	1	2
Avian VT-04 4	2	5
Avian VT-04 4	3	1
Avian VT-04 4	5	3
Avian VT-04 4	6	47
Avian VT-04 4	8	21
Avian VT-04 4	9	1
Avian VT-04 5	1	33
Avian VT-04 5	2	46
Avian VT-04 5	3	15
Avian VT-04 5	5	1
Avian VT-04 5	6	1
Avian VT-04 5	8	1
Avian VT-04 5	9	5
Avian VT-04 6	.	5
Avian VT-04 6	1	15
Avian VT-04 6	2	18
Avian VT-04 6	3	2
Avian VT-04 6	4	4
Avian VT-04 6	5	3
Avian VT-04 6	8	16
Avian VT-04 7	.	3
Avian VT-04 7	1	34
Avian VT-04 7	2	13
Avian VT-04 7	3	19
Avian VT-04 7	7	4
Avian VT-04 7	8	1
Avian VT-04 8	4	3
Avian VT-04 9	1	2
Avian VT-04 9	2	13
Avian VT-06 5	1	8
Avian VT-06 6	1	81
Avian VT-06 6	2	12
Avian VT-06 9	2	210
Avian VT-07 5	1	181
Avian VT-07 9	2	1
Avian VT-08 13	.	1
Avian VT-08 16	3	1
Avian VT-08 5	1	1
Avian VT-08 5	2	1
Avian VT-08 6	2	1
Avian VT-10 11	9	1
Avian VT-10 12	1	1
Avian VT-10 1	1	2
Avian VT-10 2	8	1
Avian VT-10 3	1	1

Avian VT-10 3	2	1	
Avian VT-10 3	8	1	
Avian VT-10 4	6	3	
Avian VT-10 5	1	1	
Avian VT-10 6	8	1	
Avian VT-10 7	1	1	
Avian VT-10 9	1	4	
Avian VT-10 9	2	1	
Avian VT-11 7	2	42	
Avian VT-12 10	7	2	
Avian VT-12 11	.	1	
Avian VT-12 12	5	5	
Avian VT-12 14	5	3	
Avian VT-12 1	1	1	
Avian VT-12 3	6	1	
Avian VT-12 4	9	1	
Avian VT-12 5	1	7	
Avian VT-12 5	2	6	
Avian VT-12 5	3	1	
Avian VT-12 6	.	1	
Avian VT-12 6	8	7	
Avian VT-12 7	1	1	
Avian VT-12 7	4	1	
Avian VT-12 9	2	2	
Avian VT-13 1	1	1	
Avian VT-13 4	6	1	
Avian VT-13 5	1	13	
Avian VT-13 5	3	1	
Avian VT-13 5	9	1	
Avian VT-13 9	2	1	
Avian VT-14 5	1	58	
Avian VT-15 10	8	1	
Avian VT-15 1	1	1	
Avian VT-15 5	2	1	
Avian VT-16 3	2	1	
Avian VT-16 3	8	3	
Avian VT-16 4	8	1	
Avian VT-16 7	1	23	
Avian VT-16 7	2	3	
Chicken VT-01	11	1	1
Chicken VT-01	11	2	1
Chicken VT-01	11	3	1
Chicken VT-01	1	1	1
Chicken VT-01	2	2	1
Chicken VT-01	3	2	3
Chicken VT-01	3	6	1

Chicken VT-01	4	6	3
Chicken VT-01	4	8	1
Chicken VT-01	5	1	361
Chicken VT-01	5	2	11
Chicken VT-01	5	9	3
Chicken VT-01	6	1	25
Chicken VT-01	6	2	2
Chicken VT-01	6	4	1
Chicken VT-01	7	2	1
Chicken VT-01	7	3	14
Chicken VT-01	7	4	4
Chicken VT-01	7	7	4
Chicken VT-01	9	2	18
Chicken VT-02	3	2	5
Chicken VT-02	5	1	6
Chicken VT-02	6	1	2
Chicken VT-02	6	3	1
Chicken VT-02	7	2	1
Chicken VT-02	9	2	13
Chicken VT-04	2	2	1
Chicken VT-04	3	6	7
Chicken VT-04	3	8	1
Chicken VT-04	4	2	1
Chicken VT-04	5	.	5
Chicken VT-04	5	1	1
Chicken VT-04	5	2	63
Chicken VT-04	5	3	1
Chicken VT-04	6	2	9
Chicken VT-04	6	8	1
Chicken VT-04	7	1	7
Chicken VT-04	7	2	26
Chicken VT-04	7	3	13
Chicken VT-04	7	7	1
Chicken VT-04	9	2	2
Chicken VT-06	5	1	15
Chicken VT-06	6	1	1
Chicken VT-06	6	2	1
Chicken VT-06	9	2	236
Chicken VT-07	5	1	194
Chicken VT-07	9	2	5
Chicken VT-08	9	2	1
Chicken VT-10	7	3	2
Chicken VT-11	7	2	51
Chicken VT-12	5	1	5
Chicken VT-12	5	2	16
Chicken VT-12	6	1	1

Chicken	VT-12 6	2	1
Chicken	VT-12 7	3	2
Chicken	VT-12 9	2	1
Chicken	VT-13 5	1	35
Chicken	VT-14 5	1	12
Chicken	VT-15 6	1	1
Chicken	VT-16 5	2	3
Chicken	VT-16 7	1	10
Chicken	VT-16 7	2	8
Equine	VT-02 3	8	1
Equine	VT-10 3	8	126
Equine	VT-10 7	7	9
Human	VT-01 1	1	83
Human	VT-01 1	2	1
Human	VT-01 2	2	49
Human	VT-01 3	2	134
Human	VT-01 5	1	107
Human	VT-01 7	3	1
Human	VT-01 7	7	2
Human	VT-02 1	1	1652
Human	VT-02 3	2	1
Human	VT-03 1	2	39
Human	VT-03 3	2	1330
Human	VT-05 1	1	670
Human	VT-06 5	1	13
Human	VT-06 9	2	5
Human	VT-07 5	1	16
Human	VT-08 3	2	280
Human	VT-09 3	2	234
Human	VT-12 5	1	3
Human	VT-13 5	1	13
Human	VT-15 1	1	59
Others	VT-01 10	8	2
Others	VT-01 11	9	1
Others	VT-01 13	2	1
Others	VT-01 1	1	2
Others	VT-01 2	3	5
Others	VT-01 3	2	2
Others	VT-01 3	3	1
Others	VT-01 3	6	5
Others	VT-01 3	8	4
Others	VT-01 4	5	1
Others	VT-01 4	6	1
Others	VT-01 5	1	25
Others	VT-01 5	2	2
Others	VT-01 5	3	1

Others	VT-01	7	3	5
Others	VT-01	7	7	1
Others	VT-01	7	9	1
Others	VT-01	9	9	1
Others	VT-02	3	8	1
Others	VT-02	5	2	1
Others	VT-04	11	6	1
Others	VT-04	11	8	2
Others	VT-04	4	6	2
Others	VT-04	5	2	4
Others	VT-04	5	3	8
Others	VT-04	5	4	1
Others	VT-04	6	4	1
Others	VT-04	7	2	3
Others	VT-05	1	1	1
Others	VT-06	5	.	1
Others	VT-06	5	1	3
Others	VT-06	9	2	8
Others	VT-07	5	1	6
Others	VT-10	3	2	1
Others	VT-10	3	8	3
Others	VT-11	7	2	68
Others	VT-13	5	1	4
Swine	VT-01	1	1	128
Swine	VT-01	1	2	15
Swine	VT-01	3	2	34
Swine	VT-01	3	3	2
Swine	VT-01	5	1	5
Swine	VT-02	1	1	79
Swine	VT-02	1	2	57
Swine	VT-02	2	3	3
Swine	VT-02	3	1	4
Swine	VT-02	3	2	57
Swine	VT-02	4	6	1
Swine	VT-02	9	2	2
Swine	VT-03	1	2	1
Swine	VT-03	3	2	29
Swine	VT-04	1	1	1
Swine	VT-04	5	2	2
Swine	VT-06	1	1	2
Swine	VT-06	3	2	1
Swine	VT-06	5	1	1
Swine	VT-06	9	2	25
Swine	VT-08	3	2	1
Swine	VT-10	3	2	1
Swine	VT-10	3	8	2

```
Swine VT-12 1    1    3
Swine VT-12 1    2    1
Swine VT-12 3    2    4
Swine VT-13 3    2    1
Swine VT-15 1    1    2
;
```

```
proc GLM
data=flu;
class vt host H N;
model count = vt host H N vt*host H*host N*host H*vt N*vt ;
run;
```