**Vaccine Protection Investigation Use Case:**

**Goal:** Generate Vaccine protection data using OBI/VO format, which can be used for ANOVA analysis, and getting results.

**Three steps of Vaccine Protection Investigation:**

(1) Vaccination, (2) Challenge, and (3) Vaccine Efficacy measurement: CFU reduction assay (instead of survival assessment)

**Description of the dataset:** We have ~20 parameters:

1. CFU differences
2. Vaccine strain
3. Viability (live or dead)
4. BCG
5. Addition of IL12
6. SOD overexpression
7. Gene deletion
8. Host species
9. Host strain
10. Host sex
11. Vaccination route
12. Vaccination dose (after Log transformation)
13. Vaccination age\_G
14. Challenge pathogen strain
15. Challenge route
16. Challenge dose
17. Challenge interval
18. CFU in spleen
19. Significance or not

**Data description:** For each assay, we have data for each parameter. In total, we have about 153 rows of dataset. These data are currently in an Excel format.

**Hypothesis**: some parameters may be more important than others in determining the result of vaccine efficacy.

**Statistical analysis type:** ANOVA

Significance variable: use combination of Significance+CFU difference:

0 – Not significant

1 – Significant

2 – Enhanced protection (e.g., SOD), or enhanced significance. May set up bar of CFU > 2 or some other number.

**Results**: the result of the assay is the vaccine efficacy measurement.

**Conclusion:**

**Questions**:

(1) How to model this use case using OBI/VO. Use OWL for statistical analysis?

(2) Challenge in how to transfer the data into OBI/VO format.

**Significance of this study:** You want to communicate with others who also have similar data types and datasets. Put into OWL standard format, even into ANOVA analysis. Once it is done, and everyone follows, we can then merge with others' data. So our modeling can be considered as a small part of a potential large data set. Our work can be considered as an approval of principal.

**Values for selected parameters:**

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **vax strain** | **live/dead** | **BCG** | **IL-12 (ug)** | **SOD** |  |
| 0 = saline | 0 = alive | 0 = no BCG | amount | 0 = none added |  |
| 1 = RB51 | 1 = irradiated | 1 = BCG added |  | 1 = SOD added |  |
| 2 = S19 | 2 = heat-killed |  |  |  |  |
| 3 = Rev1 | 3 = chemically-killed |  |  |  |  |
| 4 = attenuated B.abortus |  |  |  |  |  |
| 5 = H38 |  |  |  |  |  |
| 6 = S2 |  |  |  |  |  |
| 7 = INTA2 |  |  |  |  |  |
|  |  |  |  |  |  |
| **gene deleted** | **host spp.** | **host str.** | **route** | **strain** | **route** |
| 0 = WT vjbR | 0 = mouse | 0 = BALB/c | 0 = IP | 0 = S2308 | 0 = IP |
| 1 = vjbR deleted | 1 = red deer | 1 = CD1 | 1 = PO | 1 = S544 | 1 = PO |
| 2 = pgm deleted | 2 = buffalo | 2 = outbred | 2 = SC | 2 = 16M | 2 = SC |
| 3 = P39 | 3 = Bos taurus | 3 = C57BL/6 | 3 = IM | 3 = B.mel. bv.3 | 3 = IM |
| 4 = wboA |  |  |  | 4 = B.ovis PA | 4 = IV |
| 5 = wbkA |  |  |  | 5 = S19 | 5 = aerosol |
|  |  |  |  | 6 = H38 | 6 = IC |
|  |  |  |  | 7 = S1330 |  |

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Response: CFU\_diff\_sign  
              Df  Sum Sq Mean Sq  F value    Pr(>F)      
Vax\_strain     1  9.4564  9.4564  83.0867 1.060e-15 \*\*\*  
Live\_dead      1  8.5377  8.5377  75.0152 1.374e-14 \*\*\*  
BCG            1  0.3117  0.3117   2.7386 0.1003097      
IL.12          1  1.1211  1.1211   9.8504 0.0020917 \*\*   
SOD            1  4.6953  4.6953  41.2541 2.186e-09 \*\*\*  
Gene\_deleted   1  0.4697  0.4697   4.1265 0.0442085 \*    
Host\_spp       1  0.0620  0.0620   0.5443 0.4619409      
host\_str       1  1.2265  1.2265  10.7765 0.0013135 \*\*   
sex            1  0.0028  0.0028   0.0244 0.8761106      
Vax\_route      1  0.0119  0.0119   0.1047 0.7468232      
Vax\_Dose\_Log   1  0.5966  0.5966   5.2420 0.0236227 \*    
Vax\_age\_G      1  0.6202  0.6202   5.4491 0.0210768 \*    
Cha\_strain     1  1.1622  1.1622  10.2116 0.0017433 \*\*   
Cha\_route      1  0.1373  0.1373   1.2067 0.2739650      
Cha\_Dose\_log   1  0.0738  0.0738   0.6488 0.4219775      
Cha\_interval   1  1.5008  1.5008  13.1866 0.0004013 \*\*\*  
CFU            1 12.8479 12.8479 112.8854 < 2.2e-16 \*\*\*  
CFU\_dif        1  7.3974  7.3974  64.9956 3.831e-13 \*\*\*  
Residuals    133 15.1372  0.1138                         
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Signif. codes:  0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

**NOTE: Will delete SOD case.**

**Vax strain: 5 (H38) only has two instances; 7 (INTA2) only has one instance.**

**Live or dead: 2 (heat-killed) and 3 (chemically killed) only have one case each. May combine these two together.**

**Summary of a possible use case discussion during OBI Vancouver meeting:**

**Title: Extended** **vaccine protection investigation use case**

**Description:** This use case is an extension of the “vaccine protection investigation” use case introduced in the OBI JBMS paper. This new use case includes 17 parameters, many of them not discussed in the JBMS use case. Specifically, these 17 parameters include: (1) vaccine strain, (2) vaccine viability, (3) Addition of IL-12 as vaccine adjuvant, (4) Addition of SOD antigen, (5) gene deletion, (6) animal (or host) species, (7) animal (or host) strain, (8) animal (or host) sex, (9) vaccination route, (10) vaccination dose, (11) animal age at vaccination, (12) pathogen strain for challenge, (13) challenge route, (14) challenge dose, (15) challenge time (interval after vaccination), (16) colony forming unit (CFU), and (17) reduction of colony forming unit (CFU).

In addition, we have collected ~160 instance data from the literature, which investigated the protection levels of several *Brucella* vaccines at different conditions (with different values of these 18 parameters). The instance data was not included in the OBI JBMS paper.

The **hypothesis** was that some parameters are more important than others in determining the result of the vaccine protection efficacy. An ANOVA analysis was performed and indicated that 12 parameters significantly contribute to the protection (P value < 0.05). The other five parameters do not (P value > 0.05).

**Issues for discussion:** (1) how to model these 17 parameters, which are important for this biomedical investigation and most of them are closely associated with OBI, IAO, and VO; (2) How to model the hypothesis, ANOVA test, and the statistical results using OBI; (3) How to use OBI to help statistical data analysis of instance data? (4) How to extend this study to other ontology-based statistical data analysis if possible?