Module 8 Evaluating Immunological Correlates of Protection

Session 9 Validation Using Prentice Criteria and Causal Inference Framework, Design Considerations

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# A Classical Method For Evaluating Surrogate Endpoints - Prentice's criteria

Prentice (1989) established 4 criteria:

- 1. Show treatment effect on disease endpoint
- 2. Show treatment effect on surrogate endpoint (immune marker)
- 3. Show surrogate endpoint correlates with disease endpoint
- Show that probability of disease is independent of treatment status, given the surrogate endpoint
  full treatment effect captured by surrogate endpoint









## Criterion 1: Vaccine Efficacy Sweden Trial I

	Exposed	in DTPa2 group N = 76	Exposed	in DTPa5 group N = 86	Exposed	l in DTPwc group N = 57	Exposed in DT group $N = 74$	Total no.
Clinical definition	Cases (cult pos)	VE% (95% CI)	Cases (cult pos)	VE% (95% CI)	Cases (cult pos)	VE% (95% CI)	Cases (cult pos)	of cases (cult pos)
Cough 1 day or more and positive lab criteria	61 (26)	5.7 (-9.1-19.6)	28 (13)	61.8 (47.4–72.2)	47 (25)	3.1 (-12.9-16.8)	63 (43)	199 (107)
Cough 8 days or more and positive lab criteria	58 (24)	10.4 (-4.4-23.1)	26 (12)	64.5 (50.4-74.6)	46 (25)	5.2 (-10.6-18.8)	63 (43)	193 (104)
Cough 21 days or more and positive lab criteria	35 (17)	43.2 (25.8–56.5)	21 (11)	69.9 (55.6-79.6)	37 (22)	19.9 (1.6-35.3)	60 (43)	153 (93)
Cough 30 days or more and positive lab criteria	29 (15)	44.6 (23.4–60.0)	14 (10)	76.4 (60.9-85.7)	34 (21)	13.5 (−12.5-33.5)	51 (37)	128 (83)
Spasmodic cough 21 days or more	29 (17)	42.4 (19.9–58.5)	14 (10)	75.4 (59.2–85.2)	27 (18)	28.5 (1.6-48.0)	49 (36)	119 (81)

# Criterion 2: Immune responses Sweden Trial I

Assay	Vaccine	No. of samples	1 m dose	onth after 3 (32 days)
IgG anti-PT	DTPa2	164	59.3	53.6-65.7
	DTPa5	170	49.8	45.0-55.1
	DTPwc	119	1.9	1.5-2.4
	DT	139	0.9	0.8-1.1
lgG anti-FHA	DTPa2	164	111.4	100.5123.6
	DTPa5	170	33.3	30.037.1
	DTPwc	119	8.8	7.410.6
	DT	139	0.8	0.70.9
IgG anti-FIM 2/3	DTPa2	164	0.9	0.8-1.0
	DTPa5	170	352.4	304.1-408.3
	DTPwc	119	15.5	9.9-24.1
	DT	139	0.9	0.8-1.0
lgG anti-pertactin	DTPa2	164	0.6	0.6-0.7
	DTPa5	170	116.7	102.8-132.4
	DTPwc	119	12.6	9.7-16.4
	DT	139	0.6	0.6-0.7











How to calculate the ratio of predicted number of cases?

$$VE_{1} = 1 - \frac{p_{v1}}{p_{c}} \implies p_{c} = \frac{1 - VE_{1}}{p_{v1}}$$
$$VE_{2} = 1 - \frac{p_{v2}}{p_{c}} \implies p_{c} = \frac{1 - VE_{2}}{p_{v2}}$$
$$\frac{1 - VE_{1}}{p_{v1}} = \frac{1 - VE_{2}}{p_{v2}} \implies \frac{p_{v1}}{p_{v2}} = \frac{1 - VE_{1}}{1 - VE_{2}}$$













SPS Imm ZOSTAVAX™ induct at 6 weeks postvace	UNOC ed VZV-s	genicity specific imm	y Results
	Geom	etric Mean	Response (N = 691)
	Day 0	Week 6	Fold Rise
gpELISA (units/mL)	278.8	474.7	1.7 (95% CI: 1.6, 1.8)
IFN-γ ELISPOT (SFC/10 <sup>6</sup> PBMC <sup>+</sup> )	34.5	72.0	2.0 (95% CI: 1.8, 2.3)
RCF (responder cells/10 <sup>5</sup> PE	5.7 3MC)	9.7	1.7 (95% CI: 1.6, 1.8)
<sup>†</sup> Spot-forming cells per 10 <sup>6</sup> peripheral b	blood mononuc	lear cells.	22

### SPS: VZV Antibody (gpELISA) Titers by HZ Case Status

			ZOSTAVAX™ (N=691)		Placebo (N=704)
	Case Status	n	Response (95% CI)	n	Response (95% CI)
Week 6	Developed HZ	9	271.9 (161.9, 456.7)	23	181.6 (133.5, 246.9)
GMT	Did not develop HZ	658	478.4 (444.6, 514.7)	661	296.2 (273.3, 321.1)
Week 6	Developed HZ	9	1.1 (0.9, 1.4)	23	0.9 (0.8, 1.1)
GMFR from Day 0	Did not develop HZ	646	1.7 (1.6, 1.8)	650	1.0 (1.0, 1.0)
GMFR = G	eometric mean foldr	ise			
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## SPS: VZV IFN-γ ELISPOT Counts by HZ Case Status

			ZOSTAVAX™ (N=691)		Placebo (N=704)
	Case Status	n	Response (95% CI)	n	Response (95% CI)
Week 6	Developed HZ	7	39.4 (7.9, 196.6)	21	17.4 (8.8, 34.4)
GMC	Did not develop HZ	599	72.5 (63.9, 82.3)	621	32.2 (28.5, 36.4)
Week 6	Developed HZ	7	2.7 (0.6, 12.9)	21	1.1 (0.5, 2.2)
GMFR from Day 0	Did not develop HZ	575	2.0 (1.8, 2.3)	590	0.9 (0.8, 1.1)

	SPS: HZ	: VZ Ca	ZV RCF by se Status	/	
			ZOSTAVAX™ (N=691)		Placebo (N=704)
	Case Status	n	Response (95% CI)	n	Response (95% CI)
Week 6	Developed HZ	9	7.0 (4.2, 11.6)	22	3.8 (2.4, 5.9)
GMC	Did not develop HZ	659	9.7 (9.1, 10.5)	665	5.4 (5.0, 5.9)
Week 6	Developed HZ	9	3.1 (0.5, 19.2)	21	1.3 (0.8, 2.1)
GMFR from Day 0	Did not develop HZ	633	1.7 (1.6, 1.8)	641	0.9 (0.8, 1.0)
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# Other Measures of Correlation

■ Adjusted likelihood reduction factor (LRF<sub>adj</sub>)

- Alonso et al 2004

 The LRF quantifies how much information is gained by adding surrogate (S) into a model with only treatment effect (Z) based on the likelihood ratio test (LRT)

$$LRF_{adj} = \frac{1 - \exp\{-LRT(S + Z \mid Z)/n\}}{1 - \exp\{-LRT(S + Z \mid I)/n\}}$$

- LRF<sub>adj</sub> is bounded between (0, 1)

■ LRF<sub>adi</sub> = 0 if surrogate and true endpoint are independent

■ LRF<sub>adj</sub> = 1 if surrogate and true endpoint is perfectly correlated

- General concept that can be applied in different settings

Antibody titers by gpELISA	Proportion of Treatment Effect Explained (PTE)	LRF <sub>adj</sub>
6-wk titers	0.293	0.550
Foldrise from baseline	0.286	0.363
Titer + foldrise	0.459	0.593
I[foldrise>1.52]	0.580	0.681
Titer + I[foldrise>1.52]	0.783	0.810





022 Imm	unog	enicity	/ Results
I ZOSTAVAX™ indu gpELISA (units/mL	ced VZV-: ) at 6 wee	specific ant ks postvac	ibody responses cination
	Geom	netric Mean	Response (gpELISA)
	Day 0	Week 6	Fold Rise
Vaccine (N=1136)	283.6	660.0	2.3 (95% Cl: 2.2, 2.4)
Placebo (N=1133)	292.8	293.1	1.0 (95% CI: 1.0, 1.0)
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022	2: VZV Antib by HZ	o C	dy (gpELI Case Statu	SA) s	) Titers
			ZOSTAVAX™ (N=1164)		Placebo (N=1223)
	Case Status n		Response (95% CI)	n	Response (95% CI)
Week 6	Developed HZ 2	4	454.1 (300.2, 687.0)	89	178.3 (140.0, 227.1)
GMT	Did not develop HZ 108	6	659.3 (624.1, 696.6)	1079	294.2 (275.7, 313.9)
Week 6	Developed HZ 2	4	1.6 (1.2, 1.9)	89	1.0 (0.9, 1.0)
GMFR from Day 0	Did not develop HZ 108	5	2.3 (2.2, 2.4)	1078	1.0 (1.0, 1.0)
GMFR = G	eometric mean foldrise				
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#### Correlate of Protection Analysis From Two Phase III Trials (Antibody Responses by gpELISA)

Study Protocol	Population	Vaccine Effect on incidence of HZ	Vaccine effect on antibody response	Correlation between antibody and risk of HZ
004 sub-study (n=1328)	60+ years	51% (p <.0001)	1.7 fold (p <.0001)	38% risk reduction per one-log-unit increase (p <.0001)
022 case- cohort (N=22439, n=2269)	50-59 years	70% (p <.0001)	2.3 fold (p <.0001)	31% risk reduction per one-log-unit increase (p <.0001)

VZV antibody response measures (natural log scale):

(1) gpELISA titer at 6 weeks

(2) gpELISA fold rise at 6 weeks (6-week titer/baseline titer)

### Proportion of Treatment Effect Explained (PTE) in 004 and 022

Antibody responses by gpELISA	004	022
6-wk titers	0.293	0.251
Foldrise from baseline	0.286	0.220
Titer + foldrise	0.459	0.426
Foldrise > Cutoff?	0.580	0.405
Titer + I[foldrise>cutoff]	0.783	0.645
Cutoff = 1.52 for protocol 0	04 and 1.44 for p	rotocol 022







		Obse Outc in tr	erved ome ials	Surrogate Outcome		
Treatment	Subject index	S	Т	<i>S</i> (0)	<i>S</i> (1)	
	1	obs	obs	$S_i^{obs}$		
Z=0	2	obs	obs	$S_i^{obs}$		
(Control)		obs	obs	$S_i^{obs}$		
	m	obs	obs	$S_i^{obs}$		
	m+1	obs	obs		$S_i^{obs}$	
Z=1	m+2	obs	obs		$S_i^{obs}$	
(Treatment)		obs	obs		$S_i^{obs}$	
	n	obs	obs		$S_i^{obs}$	

#### **Principal Stratification**

Principal strata are defined by the pair of values of the potential outcomes S(0) and S(1), assuming both S(0) and S(1) are known. If S is a binary variable with levels Low and High, then based on the potential outcomes of S(0) and S(1), subjects can be classified into different strata:

If received placebo	If received vaccine	Note
$S_i(0) = Low$	$S_i(1) = High$	Vaccine has positive effect on S
$S_i(0) = Low$	$S_i(1) = Low$	Vaccine has no effect
$S_i(0) = High$	$S_i(1) = High$	Vaccine has no effect
$S_i(0) = High$	$S_i(1) = Low$	Vaccine has negative

The fourth stratum shows that the patient has high immunogenicity if received placebo and low immunogenicity if received vaccine, which should be empty theoretically.

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#### Definition of Principal Surrogate

Average causal necessity

 $\Pr[T(1) = 1 \mid S(0) = S(1) = s] = \Pr[T(0) = 1 \mid S(0) = S(1) = s]$ 

*Interpretation:* Treatment cannot change the probability of HZ without changing S. (S(0) = S(1) = s suggests treatment does not affect S.)

Average causal sufficiency

 $\Pr[T(1) = 1 \mid S(0) = s_0, S(1) = s_1] \neq \Pr[T(0) = 1 \mid S(0) = s_0, S(1) = s_1]$ for all  $\mid s_0 - s_1 \mid > c \ge 0$ 

*Interpretation:*  $S(0) = s_0$ ,  $S(1) = s_1(s_0 \neq s_1)$  suggests that treatment has an impact on S. The inequality suggests that the treatment affects the clinical outcome T through the surrogate S. A change in S induces a change in probability of clinical outcome (T).

#### Imputing 'Missing Values' of S(0) and S(1) (Miao, Li, Gilbert and Chan, 2013)

• Deterministic regression imputation (single imputation)

The imputed values are exactly the predicted value based on the regression model and the predictive uncertainty is ignored. Only one set of the "complete" data is obtained after the imputation.

• Random regression imputation (multiple imputations)

The imputed value for a particular patient is draw from a normal distribution with the predicted value of the patient as the mean and the prediction error as the standard deviation. Multiple imputations are carried out to account for the uncertainty in prediction.

		HZ status	Potential Sur gpELIS	rogate: 6-wk A titer
Treatment Group	Patient	Т	<i>S</i> (0)	<i>S</i> (1)
	1	$T_i^{obs}$	$S_i^{obs}$	$S_i^{imp}$
	2	$T_i^{obs}$	$S_i^{obs}$	$S_i^{imp}$
Z=0 (Placebo)		$T_i^{obs}$	$S_i^{obs}$	$S_i^{imp}$
	m	$T_i^{obs}$	$S_i^{obs}$	$S_i^{imp}$
	m+1	$T_i^{obs}$	$S_i^{imp}$	$S_i^{obs}$
	m+2	$T_i^{obs}$	$S_i^{imp}$	$S_i^{obs}$
Z=1 (Vaccine)		$T_i^{obs}$	$S_i^{imp}$	$S_i^{obs}$
	n	$T_i^{obs}$	$S_i^{imp}$	$S_{i}^{obs}$



	Evaluati	on of Princip	al Surrogate
н	Categorize p responses (	ootential outcomes S) into 4 groups	s of immune
	S(0) or S(1)	Postvaccination Titer	Postvaccination Fold rise from baseline
	1	Low	Low
	2	High	Low
	3	Low	High
	4	High	High
1	Define princ according to Evaluate ave causal suffic	ipal strata as 11, 2 pairs of S(0) and erage causal nece iency using imput	22,, 13, I S(1) essity and average ation method

Freq and Proba Vacc	bility of HZ with ine has no effec	in the ct on th	Princi ne sur	pal Si rogate	trata ( Ə	where
			Strat	um		
Frequency		11	22	33	44	Tota
	HZ	0	13	0	3	16
Placebo Group	No HZ	0	204	1	103	308
	Pr(HZ=1) (%)		5.99	0.00	2.83	4.94
	HZ	1	14	0	0	15
Vaccine Group	No HZ	4	327	3	0	334
	Pr(HZ=1) (%)	20.00	4.11	0.00		4.30
(	Overall VE = 13	% (p =	0.340	5)		

	an et	fect o	n surro	gate		/ 400	
			S	Stratum			
Frequency		12	13	14	24	34	Total
Dlaacha	HZ	0	1	35	35	1	72
Placebo	No HZ	0	5	156	582	17	760
Group	Pr(HZ=1)		16.67	18.32	5.67	5.56	8.65
	HZ	0	2	0	7	0	9
vaccine	No HZ	3	21	158	568	0	750
Group	Pr(HZ=1)	0.00	8.70	0.00	1.22		1.19
Overall V	F = 86.3% (	95%		5% 94	0%)	n<0.0	01

#### **Multiple Imputations**

The imputation was repeated multiple times based on regression models to obtain 1000 "complete" datasets. For each imputed dataset, estimate the treatment effect within the principal strata based on Cox regression model with age and gender as the covariates:

- the total number of observations in each stratum
- the p-value of the treatment effect from the Cox regression model
- the estimated treatment effect (hazard ratio) from the Cox regression model

















## **Flexible Subsampling Methods**

- Nested case-control method
- Case-cohort method
- "Hybrid" method
- Common features
  - Subsample = all cases + some non-cases
  - Feasible when the covariate history is potentially accessible for each cohort member
  - Sampling done for full cohort and stored in the site for future shipping and analysis

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- Cox proportional hazards model is the base











### Parameter Estimates from The Case-Cohort Method

- Regression parameter estimate is consistent (Prentice 1986)
- Standard" variance estimator based on partial likelihood
  - The inverse of the information matrix underestimates the variance
- Asymptotic variance estimator (Self & Prentice 1988)
  - Simplified by decomposing into two parts (Therneau & Li 1999; Langholz & Jiao 2007)
  - Can be implemented by using Cox regression software returning dfbeta residuals, e.g., SAS PHREG or Splus coxph

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 $V = I^{-1} + (1 - n_{sc} / n_c) D'_{sc} D_{sc}$ 

- Jackknife robust variance estimator (Barlow 1994)
  - Empirical version of the asymptotic variance
  - Can be used in more complex sampling schemes







Comparison of Subsampling Methods: Simulation I N = 20300, average case number = 113, subcohort proportion = 10%							
Average N in analysis	Beta_hat	Sample Variance	Standard Variance	Asymptotic Variance	Jackknife Robust Variance		
Full Cohort 20300*	0.5000	0.0075	0.0074 <b>0.0149</b> **				
Case Cohort 2132	0.5011	0.0083	0.0074 <b>0.0158</b>	0.00820 <b>0.01653</b>	0.00816 <b>0.01649</b>		
Case Control 678	0.5071	0.0104	0.0101 <b>0.0205</b>				
Hybrid 2640	0.5035	0.0098	0.0097 <b>0.0195</b>				



Сс N = 203	Meth	rison o ods: S e cases = 11	f Subs Simulat 3, subcohor	samplin tion II t proportion =	ng = 2.8%
	Beta_hat	Sample Variance	Standard Variance	Asymptotic Variance	Jackknife Robust Variance
Full Cohort 20300	0.4993	0.0074	0.0074 <b>0.0148</b>		
Case Cohort 678	0.5041	0.0108	0.0075 <b>0.0184</b>	0.01046 <b>0.02130</b>	0.01049 <b>0.02133</b>
Case Control 678	0.5048	0.0101	0.0100 <b>0.0202</b>		
Hybrid 1227	0.5053	0.0100	0.0099 <b>0.0200</b>		







