

Principal Surrogate Evaluation with **pseval**

Basics

pseval is designed to analyze data from a **randomized clinical trial** in order to assess the **surrogate** value of a post-randomization measurement. Start by describing the study **design**, including augmentations.

```
p1 <- psdesign(data = data,
  Z = Z, Y = Y.obs, S = S.obs,
  BIP = BIP, CPV = CPV)
```

design

The counterfactual **surrogate** S.1 is missing for many subjects, thus we need to define a model to **integrate** over the missing values.

```
p1 <- p1 +
  integrate_parametric(S.1 ~ BIP)
```

integration

The **risk model** describes the relationship between the **outcome** Y, the **surrogate** S.1, and the **treatment** Z. Use the risk model that is most appropriate for your outcome type, binary, count, or time-to-event.

```
p1 <- p1 +
  risk_binary(Y ~ S.1 * Z,
  D=500, risk.logit)
```

risk model

Estimation and **bootstrap** inference are done in separate steps. The main method is estimated maximum likelihood, but pseudo-score is available for a subset of models.

```
p1 <- p1 + ps_estimate() +
  ps_bootstrap()
```

estimation

Specifics combine model components together with the '+' sign

Study Design specification and

psdesign controls the dataset that is being used, and how to map variables to their roles in the analysis. The "keys" to the left of "=" map to variables in data

```
a <- psdesign(data = data, Z = Z,
  Y = Y.obs, S = S.obs, BIP = W)

b <- psdesign(data = data, Z = Z,
  Y = Surv(time.obs, event.obs),
  tau = .25, S = S.obs,
  BIP = W, CPV = CPV, BSM = V1,
  weights = p, covariate = X)
```

data frame treatment clinical outcome surrogate augmentation survival outcome other mappings

Risk Model distribution of the outcome

risk_* functions define the assumed relationship between Y, S.1, and Z. The default formula is $Y \sim S.1 * Z$

binary outcome

```
a + risk_binary(risk = risk.logit)
a + risk_binary(risk = risk.probit)
```

time to event outcome

```
a + risk_exponential()
a + risk_weibull()
```

count outcome

```
a + risk_poisson(); a + risk_continuous()
```

continuous outcome

Options

flexible spline

```
a + risk_binary(Y ~ bs(S.1, df = 2) * Z)
a + risk_exponential(D = 200)
a + risk_poisson(Y ~ S.1 * Z + offset(t))
```

Integration over the missing

integrate_* functions control how the missing counterfactual variables are handled

Parametric: Assumes normal distribution conditional on a BIP + other variables
`a + integrate_parametric(S.1 ~ BIP)`

Semiparametric: Assumes location and scale vary as functions of BIP + other variables, no assumption about distribution of S
`a + integrate_semiparametric(
 formula.location = S.1 ~ BIP,
 formula.scale = S.1 ~ 1)`

Nonparametric: Totally empirical, requires categorical S and W
`a + integrate_nonparametric(S.1 ~ BIP)`

Estimation post-estimation and plotting

```
est <- a + ps_estimate(method = "BFGS")
a + ps_estimate(method = "pseudo-score")
boot <- est + ps_bootstrap(n.boots = 50,
  start = binary.est$estimates$par)
```

see ?optim for options

Post estimation

```
summary(boot)
calc_risk(boot, contrast = "TE")
calc_STG(boot) # total gain statistic
```

summary of parameters

```
plot(boot, contrast = "TE")
plot(boot, contrast = "logRR")
plot(boot, contrast = "RD",
  CI.type = "pointwise")
```

plots of different CEP

```
calc_risk(boot,
  contrast = function(R0, R1) 1 - R1/R0)
```

custom