ANCOVA Comparison Simulations: Discrete Outcomes

Kellie Ottoboni

2017-09-12

Discrete data

Step 1: We generated the covariate sand potential outcomes according to the methods in the continuous outcome section but discretized them by taking the floor. Assume that there are $n_j = 16$ individuals per stratum and treatment assignment is balanced, i.e. 8 people receive each treatment at each stratum. After sampling $(v_{ij}, \varepsilon_{ij}, \delta_{ij})$, we regenerate Z 10,000 times. We repeat this procedure for each distribution of latent variables v and of the errors ε and δ.

Step 2: We regenerate Z and recompute $Y_(Z)$ 10,000 times for each design.

In expectation, the average treatment effect is γ. We compare the empirical power of five tests to detect this treatment effect:

- ANCOVA: we fit a linear model of response Y_1 on baseline Y_0, treatment Z, and a dummy for stratum.
- Stratified permutation: we permute treatment assignment within stratum, then take the difference in means between treated and control outcomes Y_1
- Differenced permutation: we do the same permutation procedure as the stratified permutation test, except we use the difference between outcome and baseline, $Y_1 - Y_0$
- Linear model (LM) permutation: we use the same stratified permutation procedure as above, except use the t-statistic for the coefficient on treatment in the linear regression of Y_1 on Y_0, Z, and stratum dummies
- Freedman-Lane test: see the other Rmd document for a full description of this procedure

Data-generation, tests, and plotting functions

```r
gen_y <- function(gamma, v, error, Z) {
    y <- floor(0.5 * ((2 * Z - 1) * gamma * exp(v) + exp(v/2)) +
        error)
    return(y)
}

gen_x <- function(gamma, v, error) {
    x <- floor(0.5 * (-1 * gamma * exp(v) + exp(v/2)) + error)
    return(x)
}

generate_simulated_data <- function(gamma, effect, errors, n = c(16,
    16, 16)) {
    # Input: gamma = multiplier for the magnitude of the
    # treatment effect effect = 'same effect' or 'heterogeneous'
    # errors = 'normal' or 'heavy' n = number of individuals at
    # each stratum Returns: a dataframe containing columns named
    # Y1 (response), Y0 (baseline), Z (treatment), gamma_vec
    # (treatment effect per individual), stratumID (stratum),
    # stratum_effect (beta coefficient per individual), and
    # epsilon (errors)

    stratumID <- rep(1:3, times = n)
    N <- sum(n)

    # What is the treatment effect?
    if (effect == "same effect") {
        v <- runif(N, min = -4, max = 4)
    } else if (effect == "heterogeneous") {
        v <- rep(0, N)
        v[stratumID == 1] <- runif(n[1], min = -4, max = -1)
        v[stratumID == 2] <- runif(n[2], min = -1, max = 1)
        v[stratumID == 3] <- runif(n[3], min = 1, max = 4)
    } else {
        stop("invalid parameter effect")
    }

    # Generate errors
    if (errors == "normal") {
        epsilon <- rnorm(N)
        delta <- rnorm(N)
    } else if (errors == "t") {
        epsilon <- rt(N, df = 2)
        delta <- rt(N, df = 2)
    } else if (errors == "lognormal") {
        epsilon <- rlnorm(N)
        delta <- rlnorm(N)
    } else if (errors == "exponential") {
        epsilon <- rexp(N) - 1
        delta <- rexp(N) - 1
    } else {
        stop("invalid errors parameter")
    }

    # Generate covariates
    Z <- rep(0:1, length.out = N)
    Y0 <- gen_x(gamma, v, epsilon)
    Y1 <- gen_y(gamma, v, delta, Z)
    return(data.frame(Y1, Y0, Z, v, stratumID, epsilon, delta))
}

generate_simulated_pvalues <- function(dataset, reps = 1000) {
    # Inputs: dataset = a dataframe containing columns named Y1
    # (response), Y0 (baseline), Z (treatment), and stratumID
    # (stratum) Returns: a vector of p-values first element is
    # the p-value from the ANCOVA second element is the p-value
    # from the stratified two-sample permutation test third
    # element is the p-value from the linear model test,
    # permuting treatment fourth element is the p-value from the
    # Freedman-Lane linear model test, permuting residuals

    # ANCOVA
    modelfit <- lm(Y1 ~ Y0 + Z + factor(stratumID), data = dataset)
    resanova <- summary(aov(modelfit))
    anova_pvalue <- resanova[[1]]["Z", "Pr(>F)"]

    # Stratified permutation test of Y1
    observed_diff_means <- mean(dataset$Y1[dataset$Z == 1]) -
        mean(dataset$Y1[dataset$Z == 0])
    diff_means_distr <- stratified_two_sample(group = dataset$Z,
        response = dataset$Y1, stratum = dataset$stratumID, reps = reps)
    perm_pvalue <- t2p(observed_diff_means, diff_means_distr,
        alternative = "two-sided")

    # Diffed permutation test of Y1-Y0
    dataset$diff <- dataset$Y1 - dataset$Y0
    observed_diff_means2 <- mean(dataset$diff[dataset$Z == 1]) -
        mean(dataset$diff[dataset$Z == 0])
    diff_means_distr2 <- stratified_two_sample(group = dataset$Z,
        response = dataset$diff, stratum = dataset$stratumID,
        reps = reps)
    perm_pvalue2 <- t2p(observed_diff_means2, diff_means_distr2,
        alternative = "two-sided")

    # Permutation of treatment in linear model
    observed_t1 <- summary(modelfit)[["coefficients"]]["Z", "t value"]

    # Freedman-Lane linear model residual permutation
    lm2_no_tr <- lm(Y1 ~ Y0 + factor(stratumID), data = dataset)
    dataset$lm2_resid <- residuals(lm2_no_tr)
    lm2_yhat <- fitted(lm2_no_tr)

    lm1and2_t_distr <- replicate(reps, {
        dataset[, c("Z_perm", "lm2_resid_perm")] <- permute_within_groups(dataset[,
            c("Z", "lm2_resid")], dataset$stratumID)
        lm1_perm <- lm(Y1 ~ Y0 + Z_perm + factor(stratumID),
            data = dataset)

        dataset$response_fl <- lm2_yhat + dataset$lm2_resid_perm
        lm2_perm <- lm(response_fl ~ Y0 + Z + factor(stratumID),
            data = dataset)

        c(summary(lm1_perm)[["coefficients"]]["Z_perm", "t value"],
            summary(lm2_perm)[["coefficients"]]["Z", "t value"])
    })
    lm_pvalue <- t2p(observed_t1, lm1and2_t_distr[1, ], alternative = "two-sided")
    fl_pvalue <- t2p(observed_t1, lm1and2_t_distr[2, ], alternative = "two-sided")

    return(c(ANCOVA = anova_pvalue, `Stratified Permutation` = perm_pvalue,
        `Differenced Permutation` = perm_pvalue2, `LM Permutation` = lm_pvalue,
        `Freedman-Lane` = fl_pvalue))
}
```

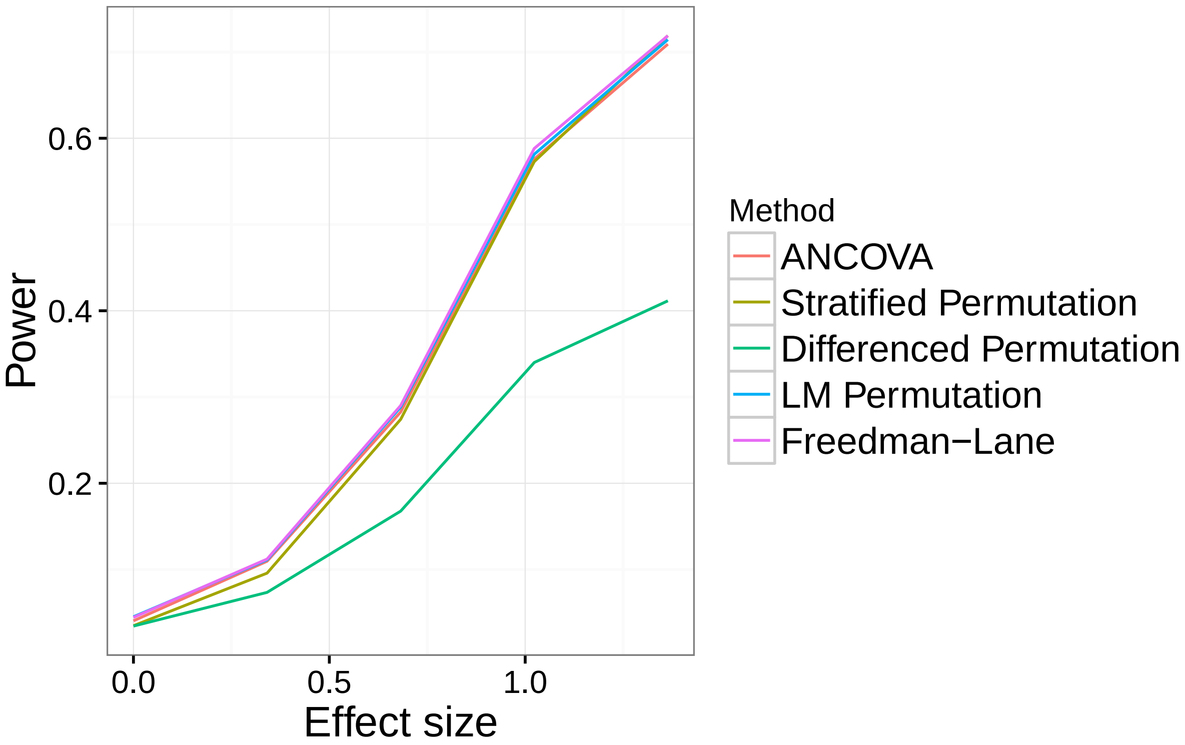
```
compute_power <- function(pvalues) {
    sapply((0:99)/100, function(p) mean(pvalues <= p, na.rm = TRUE))
}
```

```
plot_power_curves <- function(power_mat, title) {
    melt(power_mat) %>% mutate(pvalue = Var1/100) %>% mutate(Method = Var2) %>%
        ggplot(aes_string(x = "pvalue", y = "value", color = "Method")) +
        geom_line() + geom_abline(intercept = 0, slope = 1, linetype = "dashed") +
        xlab("P-value") + ylab("Power") + ggtitle(title) + theme_bw() +
        theme(axis.text.x = element_text(size = 12), axis.text.y = element_text(size = 12),
            axis.title = element_text(size = 16), title = element_text(size = 16),
            legend.title = element_text(size = 12), legend.text = element_text(size = 14),
            strip.text.x = element_text(size = 12))
}

plot_power_gamma <- function(powermat_list, gamma_vec, alpha,
    title) {
    gamma_power_alpha <- t(sapply(powermat_list, function(x) x[floor(alpha *
        nrow(x)), ]))
    colnames(gamma_power_alpha) <- c("ANCOVA", "Stratified Permutation",
        "Differenced Permutation", "LM Permutation", "Freedman-Lane")
    melt(gamma_power_alpha, value.name = "Power") %>% mutate(Method = Var2) %>%
        mutate(Effect = rep(gamma_vec, 5)) %>% ggplot(aes(x = Effect,
        y = Power)) + geom_line(aes(color = Method)) + xlab("Effect size") +
        theme_bw() + theme(axis.text.x = element_text(size = 12),
        axis.text.y = element_text(size = 12), axis.title = element_text(size = 16),
        title = element_text(size = 16), legend.title = element_text(size = 12),
        legend.text = element_text(size = 14), strip.text.x = element_text(size = 12))
}
```

Constant additive treatment effect

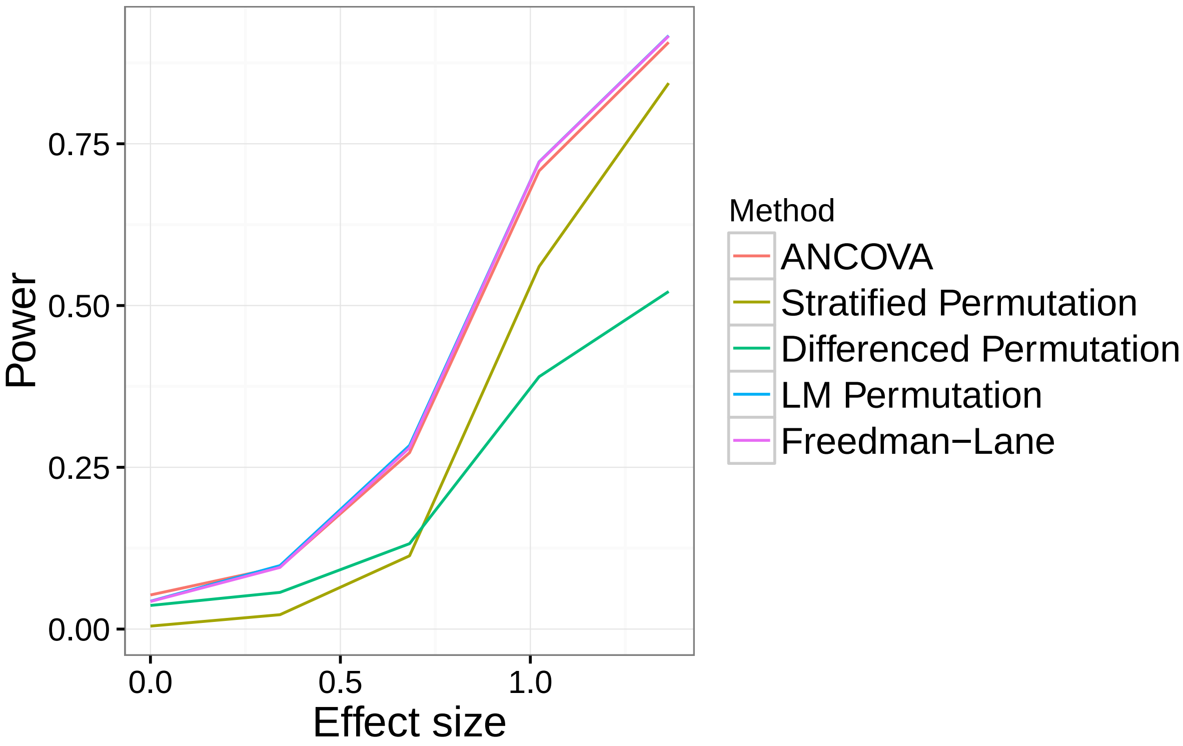
```
load("discrete_outcomes/vary_gamma_results.Rda")
gamma_vec <- seq(0, 0.2, by = 0.05)
gamma_power <- lapply(gamma_res, function(x) apply(x, 2, compute_power))
plot_power_gamma(gamma_power, tr_effect, 0.05, "Power at level 5%, Constant Treatment Effect")
```



First, we let the v_{ij} have the same distribution across strata and generated normally distributed errors. We varied γ from 0 to 0.2 in steps of 0.05. In the random populations that were generated, this corresponded to population average treatment effects of 0, 0.34, 0.68, 1.02, and 1.36, respectively. Figure 1 shows the empirical power (rate of rejection in the 10,000 simulations) at level 5% for these increasing effect sizes. When the effect size was zero, all five tests had the correct level of 5%, though the stratified and differenced permutation tests rejected 3.5% of the time. The differenced permutation test had substantially lower power than the rest, again because the correlation between baseline X and outcome Y was low. In this case, the unadjusted stratified test had comparable power to the linear model based tests.

Heterogeneous treatment effect

```
load("discrete_outcomes/vary_gamma_het_results.Rda")
gamma_vec <- seq(0, 0.2, by = 0.05)
gamma_power_het <- lapply(gamma_res_het, function(x) apply(x,
    2, compute_power))
plot_power_gamma(gamma_power_het, tr_effect_het, 0.05, "Power at level 5%, Heterogeneous Treatment Effe
```



Next, we varied the distribution of v_{ij} across strata and generated normally distributed errors. Once again, we varied γ from 0 to 0.2 in steps of 0.05. The corresponding population average treatment effects were of 0, 0.34, 0.68, 1.02, and 1.36, respectively. Figure 2 shows the empirical power at level 5% for these increasing effect sizes. The pattern here is nearly identical to Figure 2 in the continuous outcome simulations, so we leave out further comments.