ANCOVA Comparison Simulations: Continuous Outcomes

Kellie Ottoboni

2017-10-09

Continuous data

Step 1: We generated continuous potential outcomes. We used two scenarios. In the first, the treatment effect was constant across strata. We drew a latent random variate v_{ij} from the uniform distribution on $[-4, 4]$. In the second scenario, the treatment effect varied across strata, and we drew the latent random variable according to

$$v_{ij} \sim \begin{cases} \text{Unif}[-4, -1] & : j = 1 \\ \text{Unif}[-1, 1] & : j = 2 \\ \text{Unif}[1, 4] & : j = 3 \end{cases}$$

We generated independent and identically distributed errors ε_{ij} and δ_{ij} and varied the error distribution. The errors were either standard normal (to mimic the usual ANCOVA assumptions), t distributed with two degrees of freedom, standard lognormal, or exponentially distributed, with scale parameter 1 and shifted to have mean zero. The observed $(v_{ij}, \varepsilon_{ij}, \delta_{ij})$ were independent across i and j.

The baseline value for individual i, j was

$$X_{ij} = \frac{-\gamma e^{v_{ij}} + e^{v_{ij}/2}}{2} + \varepsilon_{ij}$$

.

Then we generated potential outcomes as

$$Y_{ij}(Z_{ij}) = \frac{(2Z_{ij} - 1)\gamma e^{v_{ij}} + e^{v_{ij}/2}}{2} + \delta_{ij}.$$

The treatment effect for individual (i, j) is $\gamma e^{v_{ij}}$ and we would like to estimate the average treatment effect in the sample.

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.

Step 3: We repeat step 1 and 2 for different distributions on ε and δ.

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

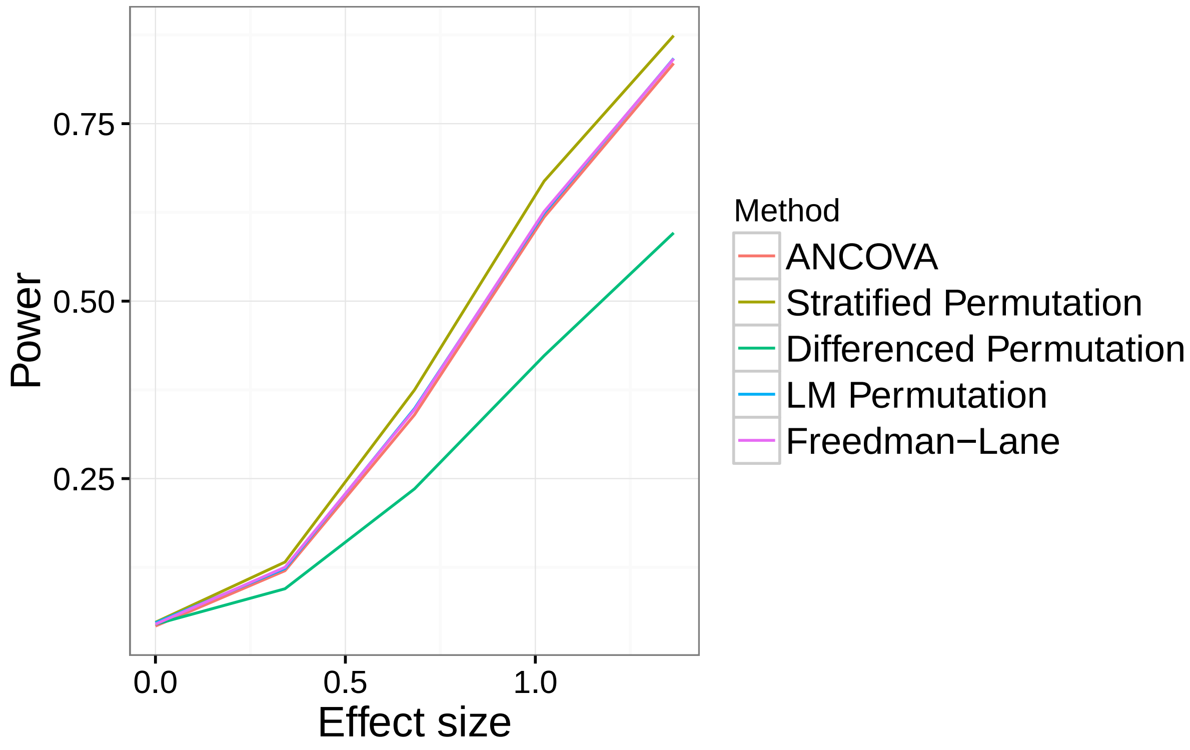
Data-generation, tests, and plotting functions

```
gen_y <- function(gamma, v, error, Z) {
    y1 <- 0.5 * ((2 * Z - 1) * gamma * exp(v) + exp(v/2)) + error
    return(y1)
}

gen_x <- function(gamma, v, error) {
    y0 <- 0.5 * (-1 * gamma * exp(v) + exp(v/2)) + error
    return(y0)
}

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', 't', 'lognormal', 'exponential', or
    # 'x-correlated' 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 if (errors == "x-correlated") {
        epsilon <- rnorm(N)
        Y0 <- gen_x(gamma, v, epsilon)
        delta <- rnorm(N)
        delta[abs(Y0) > 1] <- rnorm(N, sd = 2)
    } 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))
}
```

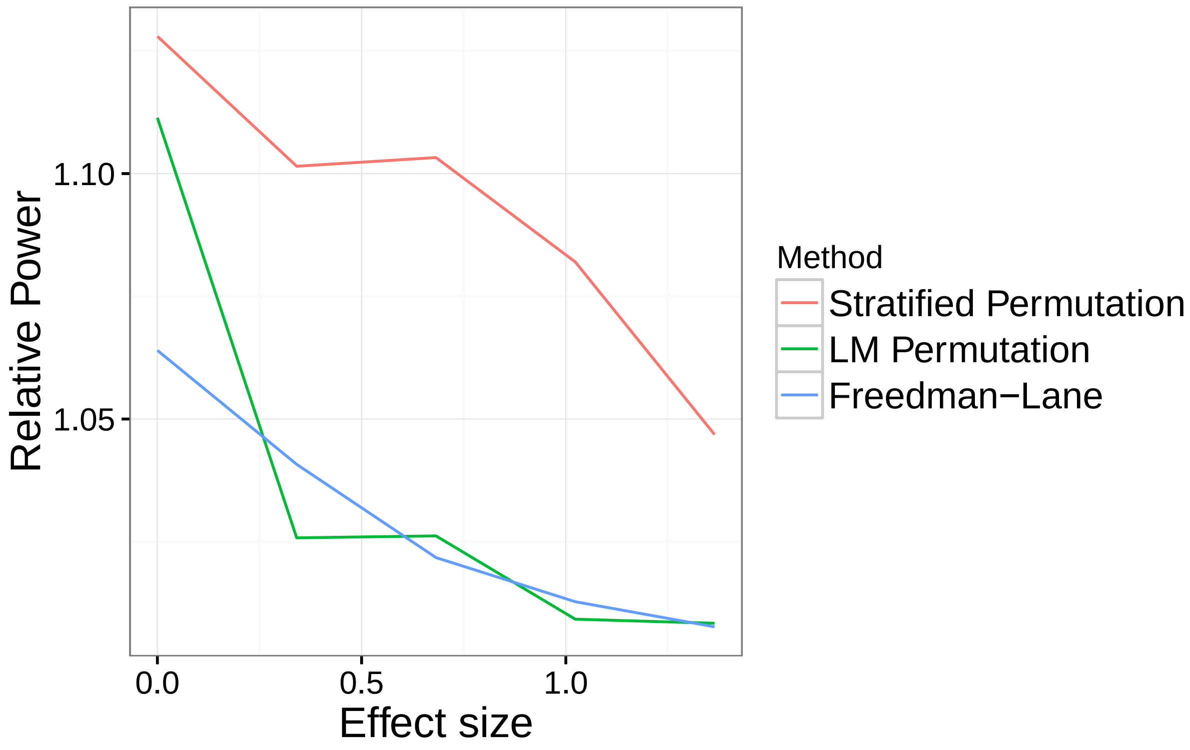
```
compute_power <- function(pvalues) {
    sapply((0:99)/100, function(p) mean(pvalues <= p, na.rm = TRUE))
}

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))
}


plot_power_ratio_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")
    gamma_power_alpha <- apply(gamma_power_alpha, 2, function(x) x/gamma_power_alpha[,
        "ANCOVA"])
    melt(gamma_power_alpha, value.name = "Power") %>% mutate(Method = Var2) %>%
        mutate(Effect = rep(gamma_vec, 5)) %>% filter(Method !=
        "Differenced Permutation") %>% filter(Method != "ANCOVA") %>%
        ggplot(aes(x = Effect, y = Power)) + geom_line(aes(color = Method)) +
        xlab("Effect size") + ylab("Relative Power") + 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))
}
```

Gaussian error terms, constant additive treatment effect

```
load("continuous_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")
```



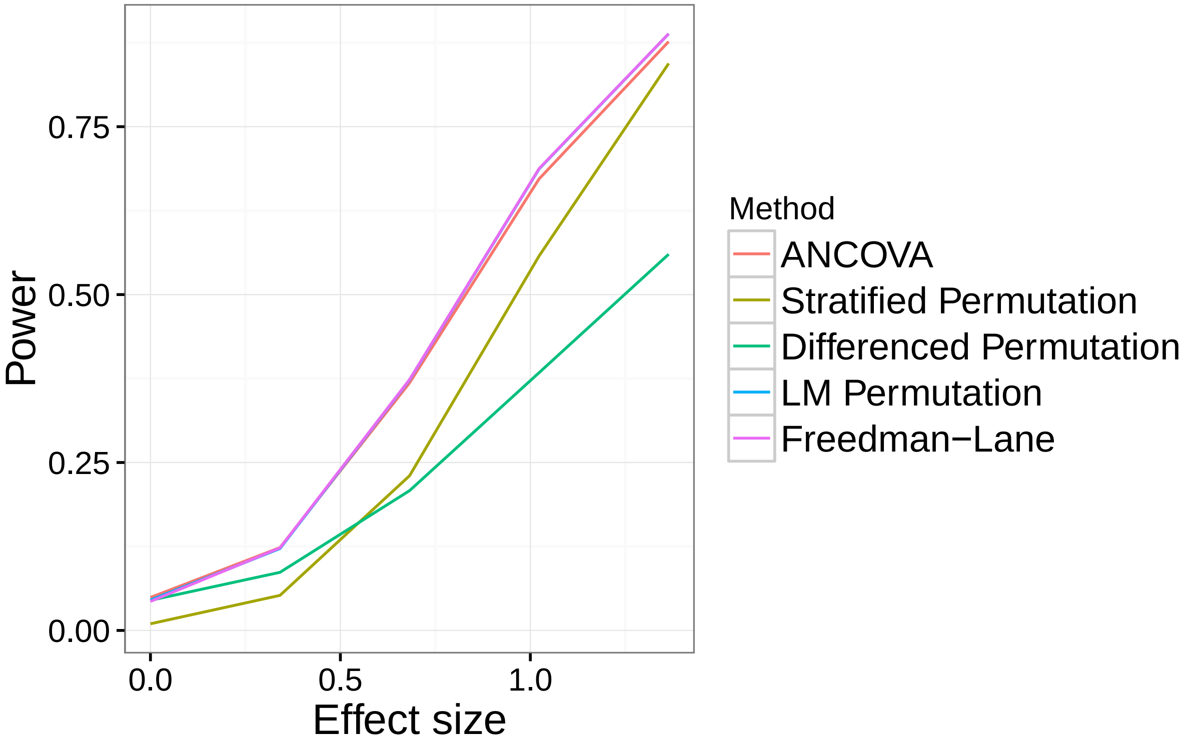
```
plot_power_ratio_gamma(gamma_power, tr_effect, 0.05, "Power at level 5%, Constant Treatment Effect")
```



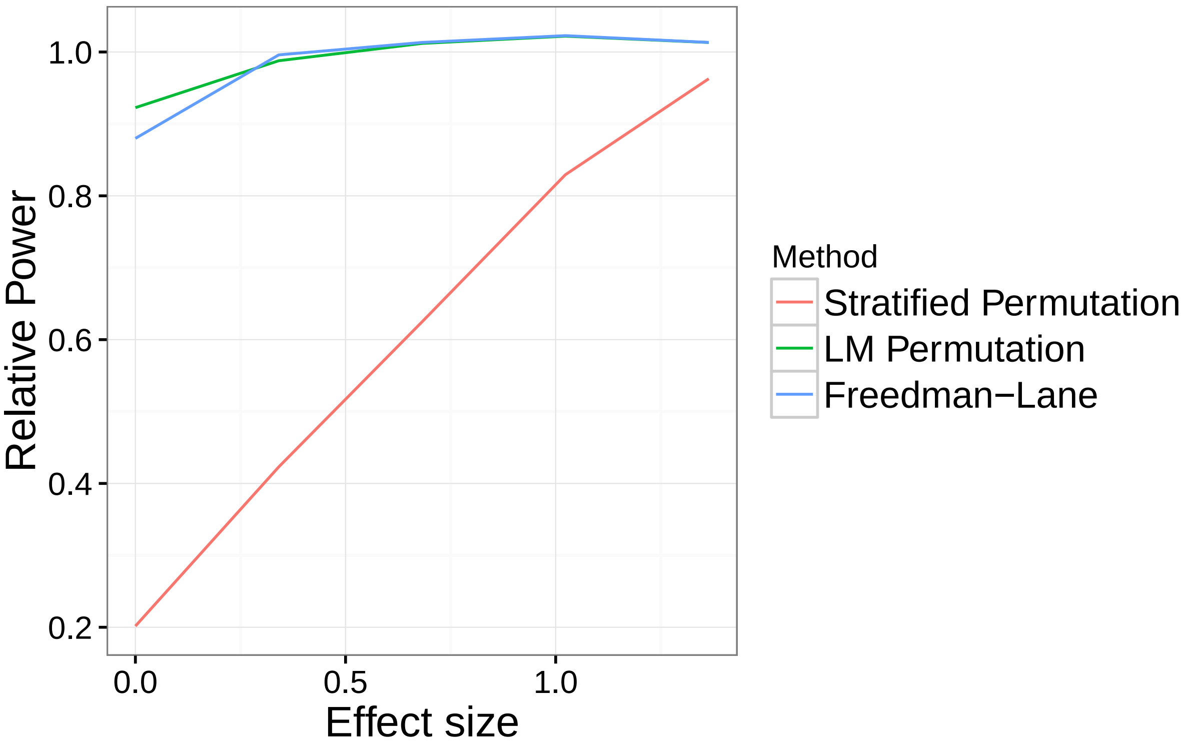
First, we let the v_{ij} have the same distribution across strata and generated normally distributed errors. We varied γ from 0 to 0.2 in steps of 0.05. In the random populations that were generated, this corresponded to population average treatment effects of 0, 0.34, 0.68, 1.02, and 1.36, respectively. 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%. Power for all tests increased with the effect size, though the differenced permutation test lagged behind the rest. This is unsurprising, as the correlation between baseline X and outcome Y was low: it was highest at 0.33 when $\gamma = 0$ and decreased to approximately 0 when $\gamma = 0.2$. The parametric and permutation linear model tests perform comparably and are plotted on top of each other, while the stratified permutation test has slightly more power.

Gaussian error terms, heterogeneous treatment effect

```
load("continuous_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
```



```
plot_power_ratio_gamma(gamma_power_het, tr_effect_het, 0.05,
    "Power at level 5%, Heterogeneous Treatment Effect")
```



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. Four of the five tests had the correct level of 5%, while the stratified permutation test rejected only 1% of the time. Both the stratified and differenced permutation tests had lower power than the linear model tests as the effect size increased. The correlation between baseline X and outcome Y was low but nontrivial (between 0.04 and 0.44), so this result makes some sense: it is beneficial for power to control for the baseline in the linear model, but the correlation is too low to make the differencing method useful.

Comparison of error distributions

We varied the distributions of the errors ε and δ and examined the power of the five tests. Recall that these are not errors in the linear model framework, but more like disturbances on the potential outcomes and baseline measures for each individual. These disturbances affect the distributions of X and Y, which may impact the power of the parametric ANCOVA, and affect the variances of X and Y, which may make one method of controlling for the baseline more effective than another. We fixed $\gamma = 0.2$ and let the errors have a standard normal distribution, a normal distribution with variance depending on the magnitude of X (either standard deviation of 1 if $|X| \leq 1$ or standard deviation of 2 otherwise), a t distribution with 2 degrees of freedom, a standard log normal distribution, or an exponential distribution with parameter 1, shifted to have mean zero.

Table 1 shows the empirical power (rejection rate among 10,000 simulations) for each of these error distributions and tests, where the v_{ij} came from a single distribution across strata. In all cases, the correlation between baseline and outcome was lower than 0.05 in magnitude. Thus, the stratified permutation test, which omits the baseline measurement, had the highest power for all error distributions. All three linear model based tests had roughly the same rejection rate. The differenced permutation test had substantially less power than the other methods, due to the low correlation between baseline and outcome. Power was highest for homoskedastic normally distributed errors and was lowest when errors were heteroskedastic.

Table 2 shows the same results, but where the distribution of v_{ij} varied across strata. In this case, the three linear model based tests had the highest power for each error distribution. While the correlation between baseline and outcome was still nearly zero, controlling for it in the linear model tended to increase precision. The stratified permutation test lost power for this reason. The differenced permutation test continued to have low power. Interestingly, the power of each of the tests was somewhat higher than when the treatment effects were homogeneous across strata. This is somewhat surprising as the linear model does not fully describe the relationship between baseline and outcome: interaction terms between baseline and stratum ID are needed in the model to capture this variation across strata.

```
gaussian_homogeneous <- gamma_power[[which(abs(gamma_vec - 0.2) <
    1e-06)]]
```

```
load("continuous_outcomes/gaussian_heterogeneous.Rda")
```

```
load("continuous_outcomes/t_homogeneous.Rda")
```

```
load("continuous_outcomes/t_heterogeneous.Rda")
```

```
load("continuous_outcomes/lognormal_homogeneous.Rda")
```

```
load("continuous_outcomes/lognormal_heterogeneous.Rda")
```

```
load("continuous_outcomes/exponential_homogeneous.Rda")
```

```
load("continuous_outcomes/exponential_heterogeneous.Rda")
```

```
load("continuous_outcomes/corr_errors_homogeneous.Rda")
```

```
load("continuous_outcomes/corr_errors_heterogeneous.Rda")
```

```
powers <- list(gaussian_homogeneous, corr_errors_homogeneous,
    t_homogeneous, lognormal_homogeneous, exponential_homogeneous,
    gaussian_heterogeneous, corr_errors_heterogeneous, t_heterogeneous,
    lognormal_heterogeneous, exponential_heterogeneous)
summary05 <- t(sapply(powers, function(x) x[5, ]))
summary05 <- data.frame(rep(c("Normal", "Normal, heter.", "t(2)",
    "Log Normal", "Exponential"), 2), summary05)
colnames(summary05) <- c("Errors", "ANCOVA", "Stratified Permutation",
    "Differenced Permutation", "LM Permutation", "Freedman-Lane")
```

```
summarytab_constant <- xtable(summary05[1:5, ], digits = 3, caption = "Empirical power at level $0.05$ 
    label = "tab:power_grid1")
print(summarytab_constant, include.rownames = FALSE)
```

Errors	ANCOVA	Stratified Permutation	Differenced Permutation	LM Permutation	Freedman-Lane
Normal	0.835	0.874	0.596	0.842	0.841
Normal, heter.	0.503	0.541	0.421	0.509	0.511
t(2)	0.440	0.481	0.226	0.448	0.450
Log Normal	0.687	0.709	0.277	0.696	0.698
Exponential	0.780	0.820	0.712	0.793	0.791

Table 1: Empirical power at level 0.05 for simulated data with constant additive treatment effects

```
summarytab_het <- xtable(summary05[6:10, ], digits = 3, caption = "Empirical power at level $0.05$ for 
    label = "tab:power_grid2")
print(summarytab_het, include.rownames = FALSE)
```

Errors	ANCOVA	Stratified Permutation	Differenced Permutation	LM Permutation	Freedman-Lane
Normal	0.877	0.844	0.554	0.887	0.891
Normal, heter.	0.633	0.631	0.520	0.644	0.643
t(2)	0.543	0.512	0.215	0.550	0.551
Log Normal	0.711	0.608	0.252	0.730	0.731
Exponential	0.814	0.786	0.651	0.820	0.816

Table 2: Empirical power at level 0.05 for simulated data with heterogeneous treatment effects