

Lab Week 4: Statistical Matching + Fixed Effects

A replication of study analysis in Ahmadia (2015)

EDS 241 / ESM 244

2026-01-29

Lab Outline

0. Load in the packages and data
 1. Take a look at focal variables
 2. Checking covariate imbalance (pre-matching).
 3. Conduct a matching analysis (Mahalanobis matching)
 4. Evaluate balance after matching
 5. Estimate regression models for each outcome using the matched sample
 6. Practice fixed effects estimation
-

Applied study & data source

This lab uses open-access replication data from:

Ahmadia, G. N., Glew, L., Provost, M., Gill, D., Hidayat, N. I., Mangubhai, S., Purwanto, P., Fox, H. E. (2015). *Integrating impact evaluation in the design and implementation of monitoring marine protected areas*. Philosophical Transactions of the Royal Society B.

Big idea: MPAs are *not randomly placed*. They may be placed in “better” locations which means that treated and control groups are unlikely to make an *apples-to-apples* comparison. AKA, we are up against the nearly universal causal inference problem with non-experimental data, treatment assignment selection bias.

Ahmadia et al. (2015) uses **statistical matching** to construct a more *apples-to-apples* comparison group. In this lab exercise we will approximately replicate the main matching analysis conducted in this study.

i Note

NOTE: When matching, the authors imposed additional restrictions (caliper-style constraints) on some habitat variables. We **do not** fully replicate those constraints here.

Reading reference:

MatchIt Vignette: <https://kosukeimai.github.io/MatchIt/articles/MatchIt.html>

0. Load packages + study data

```
library(tidyverse)      # data wrangling + plotting
library(here)           # portable file paths (project-root relative)
library(janitor)        # clean variable names
library(gtsummary)       # clean summary tables
library(gt)              # optional: render gtsummary nicely
library(MatchIt)         # matching estimation
library(cobalt)          # balance checks + love plots
library(jtools)          # clean regression output summaries
```

Read in the cleaned survey data

```
data_clean <- read_csv(here("week4", "Ahmadia_2015_DataClean.csv"), show_col_types = FALSE)
```

1. Create variable description table for key variables in the matching analysis

[

Variable Matching	Descriptions Covariates)	(Treatment, - Ahmadia (2015)]	Outcomes,
Variable Matching	Descriptions Covariates)	(Treatment, - Ahmadia	Outcomes (2015)
Label	Description		
treated_mpa (Treatment)	Site is inside a Marine Protected Area (1 = inside MPA , 0 = ou		
biomass_fisheries (Outcome)	Biomass of key fisheries families (Serranidae, Lutjanidae, Haemul		
biomass_ecological (Outcome)	Biomass of herbivorous fish families (Acanthuridae, Scaridae, Sig		
dist_deep_water (Covariate)	Covariate: Distance to deep water (50 m depth contour), in mete		
ssta_freq (Covariate)	Frequency of sea-surface temperature anomalies (SSTA)		
reef_exposure (Covariate)	Reef wave exposure (Exposed, Semi-exposed, Sheltered).		
reef_slope (Covariate)	Reef slope (Flat, Slope, Wall)		
reef_type (Covariate)	Reef type (Patch, Fringing, Barrier, Atoll).		
dist_mangroves (Covariate)	Distance to nearest mangrove habitat, in meters (m).		
dist_fishing_settlement (Covariate)	Distance to nearest fishing settlement, in meters (m).		
dist_market (Covariate)	Distance to primary market, in meters (m).		
pollution_risk (Covariate)	Watershed pollution risk. (1 = Low; 2 = Medium; 3 = High).		
monsoon_direction (Covariate)	Monsoon wind exposure direction. (Northwest (NW), Southeast		

2. Check imbalance before matching (covariate balance table)

Goal: Compare covariate distributions between `treated_mpa` and control sites *before* matching.

```
data_clean %>%
  select(
    treated_mpa, dist_to_deep_water, ssta_freq, reef_exposure,
    reef_slope, reef_type,
    dist_mangroves, dist_fish_settl, dist_market,
    pollution_risk, monsoon_direction) %>%
 tbl_summary(
  by = treated_mpa,
  statistic = list(
    all_continuous() ~ "{mean} ({sd})",
    all_categorical() ~ "{n} ({p}%)"
  )
) %>%
  modify_header(label ~ "***Covariate***") %>%
  modify_spanning_header(c("stat_1", "stat_2") ~ "***Group***")
```

Your turn (write answers in the lab)

Q1. Based on the balance table, name two covariates that look most different between MPA and non-MPA sites.

Response: Between the MPA and non-MPA site we see huge differences in distance to mangrove sites. Also big differences in low pollution risk between them.

Q2. Pick one of those imbalanced covariates and explain why it might confound the estimate of the effect of MPAs on fish biomass.

Response: The imbalance in low pollution risks between the MPA and non-MPA might confound the fish biomass since MPAs might have a greater biomass simply because pollution is less severe in it when compared to non-MPA sites.

Covariate	Group	
	Control (non-MPA) N = 53 ¹	MPA site N = 108 ¹
dist_to_deep_water	656 (905)	627 (913)
ssta_freq	25 (8)	25 (5)
reef_exposure		
Exposed	35 (66%)	92 (85%)
Semi-exposed	18 (34%)	16 (15%)
reef_slope		
Flat	7 (13%)	10 (9.3%)
Slope	45 (85%)	90 (83%)
Wall	1 (1.9%)	8 (7.4%)
reef_type		
Barrier	8 (15%)	10 (9.3%)
Fringing	45 (85%)	93 (86%)
Patch	0 (0%)	5 (4.6%)
dist_mangroves	9,679 (14,229)	4,618 (5,165)
dist_fish_settl	25,646 (28,199)	32,505 (31,537)
dist_market	124,152 (49,763)	139,918 (66,406)
pollution_risk		
High	0 (0%)	1 (0.9%)
Low	33 (62%)	84 (78%)
Medium	20 (38%)	23 (21%)
monsoon_direction		
NW	19 (36%)	62 (57%)
SE	34 (64%)	46 (43%)

¹ Mean (SD); n (%)

Matching plan (what are we trying to estimate?)

In `{MatchIt}`, most distance-based matching procedures (like nearest-neighbor matching) target is to estimate:

ATT: Average Treatment effect on the Treated

Why? When using matching methods we typically **keep treated units** and then select control units that most closely match them.

Population and inference become different populations. We analyze MPAs of this kind rather than broader ones.

Q4. What does ATT mean in the context of this MPA evaluation setting?

Response: Measures impact of a treatment specifically on those who received it by comparing their outcomes to matched control groups.

3. Mahalanobis Matching

Matching criteria used in Ahmadia (2015)

- `method = "nearest-neighbor"`: Nearest neighbor matching
- `distance = "mahalanobis"`: Mahalanobis distance
- `ratio = 2`: Two controls matched to each treated unit (2:1 ratio; control/treated)
- `replace = TRUE`: Controls can be reused (matched to multiple treated units)

NOTE: This is the *main* matching method implemented in Ahmadia (2015) with the exception of the caliper-style constraints.

```
# 1) Set a seed for reproducible matching
set.seed(2412026)

# 2) Fit a nearest-neighbor Mahalanobis matching model

match_model <- matchit(
  treated_mpa ~ dist_to_deep_water + ssta_freq + reef_exposure +
    reef_slope + reef_type + dist_mangroves + dist_fish_settl +
    dist_market + pollution_risk + monsoon_direction,
  data = data_clean,
```

```

method = "nearest",           # Nearest neighbor matching
distance = "mahalanobis",    # Mahalanobis distance
ratio = 2,                   # 2:1 control/treated ratio)
replace = TRUE )             # With replacement

```

```

# Extract matched dataset
matched_data <- match.data(match_model)

```

```

# Inspect matching summary
summary(match_model)

```

Call:

```

matchit(formula = treated_mpa ~ dist_to_deep_water + ssta_freq +
  reef_exposure + reef_slope + reef_type + dist_mangroves +
  dist_fish_settl + dist_market + pollution_risk + monsoon_direction,
  data = data_clean, method = "nearest", distance = "mahalanobis",
  replace = TRUE, ratio = 2)

```

Summary of Balance for All Data:

	Means Treated	Means Control	Std. Mean Diff.
dist_to_deep_water	627.0960	655.7936	-0.0314
ssta_freq	25.4444	24.5094	0.1830
reef_exposureExposed	0.8519	0.6604	0.5390
reef_exposureSemi-exposed	0.1481	0.3396	-0.5390
reef_slopeFlat	0.0926	0.1321	-0.1362
reef_slopeSlope	0.8333	0.8491	-0.0422
reef_slopeWall	0.0741	0.0189	0.2108
reef_typeBarrier	0.0926	0.1509	-0.2013
reef_typeFringing	0.8611	0.8491	0.0349
reef_typePatch	0.0463	0.0000	0.2203
dist_mangroves	4618.4108	9679.3287	-0.9799
dist_fish_settl	32505.0449	25646.2642	0.2175
dist_market	139918.0030	124152.3646	0.2374
pollution_riskHigh	0.0093	0.0000	0.0967
pollution_riskLow	0.7778	0.6226	0.3732
pollution_riskMedium	0.2130	0.3774	-0.4016
monsoon_directionNW	0.5741	0.3585	0.4360
monsoon_directionSE	0.4259	0.6415	-0.4360
	Var. Ratio	eCDF Mean	eCDF Max
dist_to_deep_water	1.0168	0.0271	0.0924

ssta_freq	0.4116	0.0749	0.1651
reef_exposureExposed	.	0.1915	0.1915
reef_exposureSemi-exposed	.	0.1915	0.1915
reef_slopeFlat	.	0.0395	0.0395
reef_slopeSlope	.	0.0157	0.0157
reef_slopeWall	.	0.0552	0.0552
reef_typeBarrier	.	0.0584	0.0584
reef_typeFringing	.	0.0121	0.0121
reef_typePatch	.	0.0463	0.0463
dist_mangroves	0.1317	0.0755	0.1707
dist_fish_settl	1.2507	0.0780	0.1988
dist_market	1.7808	0.1061	0.3515
pollution_riskHigh	.	0.0093	0.0093
pollution_riskLow	.	0.1551	0.1551
pollution_riskMedium	.	0.1644	0.1644
monsoon_directionNW	.	0.2156	0.2156
monsoon_directionSE	.	0.2156	0.2156

Summary of Balance for Matched Data:

	Means	Treated Means	Control Means	Std. Dev.	Mean Diff.
dist_to_deep_water	627.0960	344.4758		0.3097	
ssta_freq	25.4444	25.5370		-0.0181	
reef_exposureExposed	0.8519	0.8380		0.0391	
reef_exposureSemi-exposed	0.1481	0.1620		-0.0391	
reef_slopeFlat	0.0926	0.0556		0.1278	
reef_slopeSlope	0.8333	0.9120		-0.2112	
reef_slopeWall	0.0741	0.0324		0.1591	
reef_typeBarrier	0.0926	0.0880		0.0160	
reef_typeFringing	0.8611	0.9120		-0.1473	
reef_typePatch	0.0463	0.0000		0.2203	
dist_mangroves	4618.4108	3903.1137		0.1385	
dist_fish_settl	32505.0449	23907.6888		0.2726	
dist_market	139918.0030	138886.2537		0.0155	
pollution_riskHigh	0.0093	0.0000		0.0967	
pollution_riskLow	0.7778	0.7963		-0.0445	
pollution_riskMedium	0.2130	0.2037		0.0226	
monsoon_directionNW	0.5741	0.5093		0.1311	
monsoon_directionSE	0.4259	0.4907		-0.1311	
	Var.	Ratio	eCDF Mean	eCDF Max	Std. Dev.
					Pair Dist.
dist_to_deep_water	3.0661	0.1022	0.2176		0.6162
ssta_freq	1.4678	0.0244	0.0926		0.7032
reef_exposureExposed	.	0.0139	0.0139		0.1434
reef_exposureSemi-exposed	.	0.0139	0.0139		0.1434

reef_slopeFlat	.	0.0370	0.0370	0.1278
reef_slopeSlope	.	0.0787	0.0787	0.2112
reef_slopeWall	.	0.0417	0.0417	0.1591
reef_typeBarrier	.	0.0046	0.0046	0.0160
reef_typeFringing	.	0.0509	0.0509	0.1473
reef_typePatch	.	0.0463	0.0463	0.2203
dist_mangroves	1.6708	0.0714	0.1759	0.7967
dist_fish_settl	1.0892	0.1147	0.3056	0.6229
dist_market	2.0937	0.1334	0.3889	0.5956
pollution_riskHigh	.	0.0093	0.0093	0.0967
pollution_riskLow	.	0.0185	0.0185	0.0445
pollution_riskMedium	.	0.0093	0.0093	0.0226
monsoon_directionNW	.	0.0648	0.0648	0.2247
monsoon_directionSE	.	0.0648	0.0648	0.2247

Sample Sizes:

	Control	Treated
All	53.	108
Matched (ESS)	17.69	108
Matched	37.	108
Unmatched	16.	0
Discarded	0.	0

Your turn

Q5. Report how many treated units were matched and how many control sites were included in the matched data.

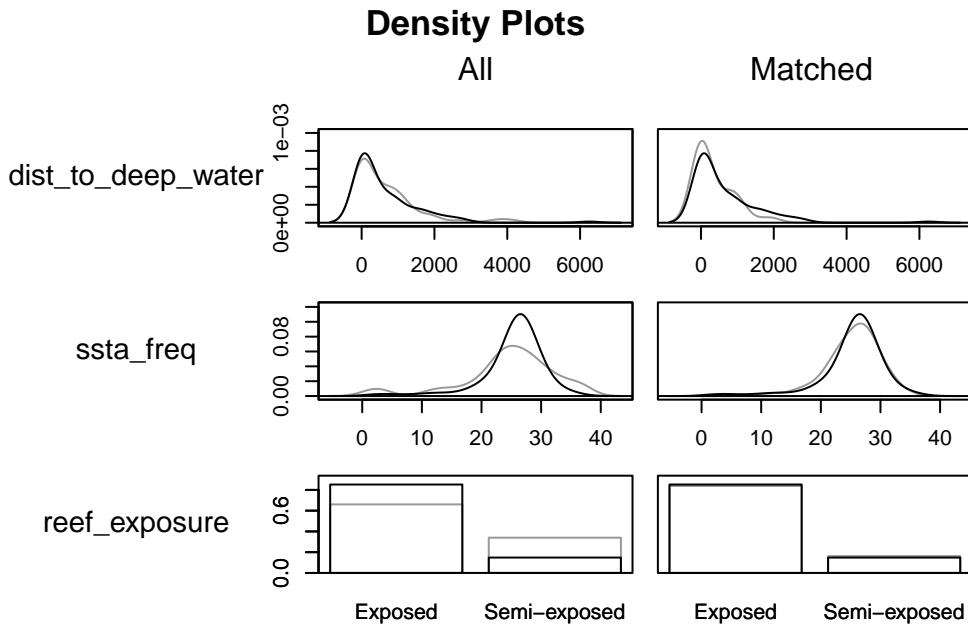
Response: 108 treated units were matched and 37 control sites were included in the matched data.

Q6. Find the covariate with the largest standardized mean difference (SMD) *after matching*. Which covariate is it?

Response: The co-variate with the largest standardized mean difference after matching is distance to deep water.

Visualize balance on the covariates using `plot()` with `type = "density"`

```
plot(match_model, type = "density", interactive = FALSE,
     which.xs = ~dist_to_deep_water + ssta_freq + reef_exposure)
```



4. Evaluate balance after matching (love plot + balance table)

```
# Create nicer variable labels for plots/tables
nice_names <- data.frame(
  old = c(
    "dist_to_deep_water", "ssta_freq", "reef_exposure", "reef_slope",
    "reef_type", "dist_mangroves", "dist_fish_settl", "dist_market",
    "pollution_risk", "monsoon_direction"),
  new = c(
    "Distance to deep water", "SSTA frequency", "Reef exposure", "Reef slope",
    "Reef type", "Distance to mangroves (m)", "Distance to fishing settlement (m)",
    "Distance to market (m)", "Watershed pollution risk", "Monsoon direction (SE/NW)"))
```

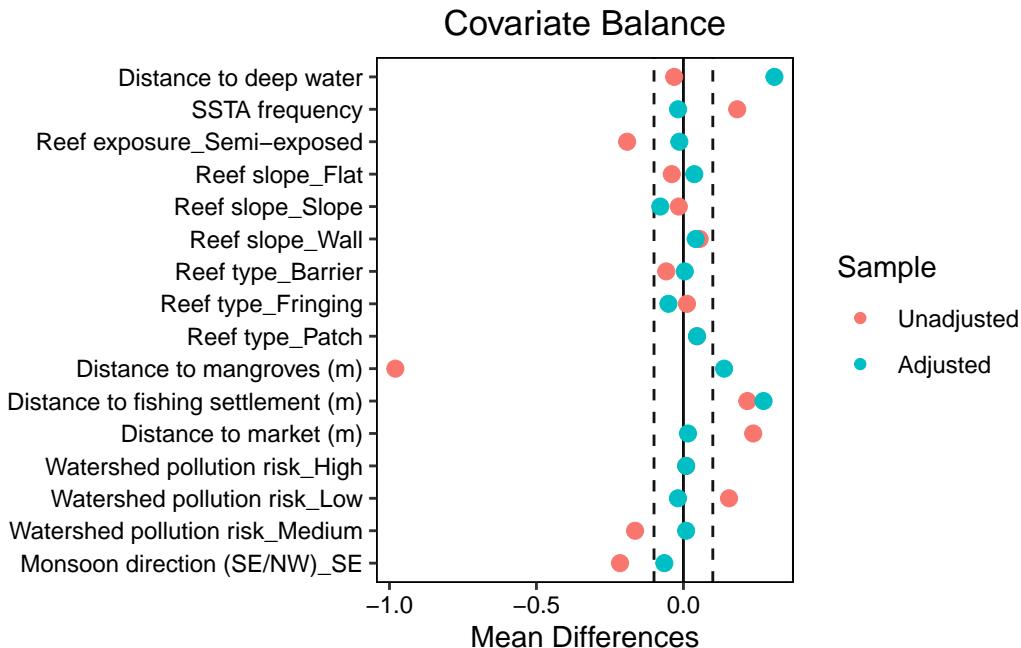
Create a Love plot to visualize standardized mean differences (before & after matching)

```
love.plot(
  match_model,
  stats = "mean.diffs",
```

```

thresholds = c(m = 0.1),
var.names = nice_names
)

```



5. Estimate differences in outcomes using the matched sample

- When matching *with replacement*, some control sites were matched multiple times and receive larger weights.
- So we estimate outcome differences using the **weights** provided by `match.data()`.

Regression (Outcome 1): Herbivorous fisheries families biomass

```

reg_ecological <- lm(biomass_ecological ~ treated_mpa,
                      data = matched_data,
                      weights = weights)

summ(reg_ecological, model.fit = FALSE)

```

Observations	145			
Dependent variable	biomass_ecological			
Type	OLS linear regression			
<hr/>				
Est.	S.E.	t val.	p	
(Intercept)	290.77	106.02	2.74	0.01
treated_mpaMPA site	79.50	122.84	0.65	0.52

Standard errors: OLS

Regression (Outcome 2): Key fisheries families biomass

```
reg_fisheries <- lm(biomass_fisheries ~ treated_mpa,
                     data = matched_data,
                     weights = weights)

summ(reg_fisheries, model.fit = FALSE)
```

Observations	145			
Dependent variable	biomass_fisheries			
Type	OLS linear regression			
<hr/>				
Est.	S.E.	t val.	p	
(Intercept)	64.23	52.47	1.22	0.22
treated_mpaMPA site	107.78	60.79	1.77	0.08

Standard errors: OLS

View biomass differences by treatment group as simple weighted mean comparisons:

```
matched_data %>%
  group_by(treated_mpa) %>%
  summarize(
    n_obs = n(),
    avg_biomass_ecological = weighted.mean(biomass_ecological, w = weights),
    avg_biomass_fisheries = weighted.mean(biomass_fisheries, w = weights),
    .groups = "drop") %>%
  gt() %>%
  tab_header(title = "Weighted mean outcomes in matched sample")
```

[

Weighted mean outcomes in matched sample]			
Weighted mean outcomes in matched sample			
treated_mpa	n_obs	avg_biomass_ecological	avg_biomass_fisheries
Control (non-MPA)	37	290.7664	64.2348
MPA site	108	370.2682	172.0131

Your turn

Q7. Interpret one coefficient from the regressions above (choose ecological *or* fisheries). Write the interpretation of coefficient in plain language.

Response: On average MPA sites have a fish biomass of 172 more than non-MPA sites.

Q8. What is the biggest remaining threat to causal interpretation of regression coefficients after matching?

Response: We have confounding variables that are unaccounted for.

6. Fixed Effects Estimation - An Applied Example

Replication of fixed effects estimator from applied study:

Dudney, J., Willing, C. E., Das, A. J., Latimer, A. M., Nesmith, J. C., & Battles, J. J. (2021). *Nonlinear shifts in infectious rust disease due to climate change*. Nature communications, 12(1), 5102.

In this section we will look at a simple fixed effects (FE) example using panel-style data, where the same units (plots) are observed over multiple years (1995, 2016).

The key issue: observations from the same plot are likely to share stable characteristics (soil type, microclimate, slope, management history) that we don't measure well—and those unobserved factors can bias a naïve regression.

Read in the data & change fixed effect to factor variables

By Coding `plot` and `year` as factors lets us include them as indicator (dummy) variables in an FE regression.

```
data_fe <- read_csv(here("week4", "Dudney2021_study_data.csv"), show_col_types = FALSE) %>%
  mutate(year=factor(year), plot=factor(plot))
```

Estimate a “no fixed effects” baseline model

```
mod1_nofe <- lm(perinc ~ vpd + I(vpd^2) + dbh + density,
                  data = data_fe)

summ(mod1_nofe, model.fit = FALSE, digits = 3)
```

	Observations	294		
	Dependent variable	perinc		
	Type	OLS linear regression		
	Est.	S.E.	t val.	p
(Intercept)	-0.615	0.122	-5.027	0.000
vpd	0.126	0.022	5.712	0.000
I(vpd^2)	-0.005	0.001	-5.119	0.000
dbh	-0.001	0.001	-2.499	0.013
density	-0.000	0.000	-3.287	0.001

Standard errors: OLS

Estimate the fixed effects model: Add in the fixed effects for `plot` & `year`

- `plot` fixed effects absorb all time-invariant differences across plots (e.g., baseline soil quality)
- `year` fixed effects absorb common shocks shared by all plots in a given year (e.g., a region-wide drought year)

```
fe_lm <- lm(perinc ~ vpd + I(vpd^2) + dbh + density + plot + year,
              data = data_fe)

summ(fe_lm, model.fit = FALSE, digits = 3)
```

Observations	294
Dependent variable	perinc
Type	OLS linear regression

Your turn

Q9. Compare the coefficient on vpd in the no-FE model vs the FE model. Did the estimate get larger, smaller, or change sign? What does that suggest about confounding from unobserved plot differences?

Response: It increased by a factor or two. Therefore our plot was potentially adding bias to our vapor deficit variables.

Q10. Why include year fixed effects? Give one concrete example of a “year shock” that could bias estimates if not controlled (choose a different example than provided above).

Response: _____ Year should be included because certain years it would significantly change vapor deficit, for example when el nino occurs.

Q11. Why include plot fixed effects? Give one concrete example of a “time-invariant plot difference” that could bias estimates if not controlled (choose a different example than provided above).

Response: _____ Density might be necessary to include.

	Est.	S.E.	t val.	p
(Intercept)	-1.199	0.770	-1.556	0.122
vpd	0.227	0.093	2.449	0.016
I(vpd^2)	-0.010	0.002	-4.209	0.000
dbh	-0.001	0.001	-0.973	0.332
density	-0.001	0.000	-2.275	0.024
plot2	0.092	0.177	0.516	0.606
plot3	0.140	0.180	0.778	0.438
plot4	0.118	0.186	0.634	0.527
plot5	0.181	0.185	0.978	0.330
plot6	0.136	0.126	1.079	0.283
plot7	0.007	0.101	0.066	0.948
plot8	0.198	0.262	0.757	0.450
plot9	0.070	0.149	0.472	0.638
plot10	0.156	0.117	1.336	0.184
plot11	0.147	0.169	0.871	0.385
plot13	0.160	0.167	0.957	0.340
plot14	0.344	0.122	2.816	0.006
plot15	0.107	0.198	0.542	0.589
plot16	0.207	0.222	0.933	0.352
plot17	0.161	0.121	1.329	0.186
plot18	0.125	0.187	0.668	0.505
plot19	0.107	0.194	0.554	0.580
plot20	0.138	0.204	0.677	0.500
plot21	0.144	0.179	0.805	0.422
plot22	0.197	0.158	1.249	0.214
plot23	0.090	0.141	0.638	0.525
plot24	0.112	0.158	0.704	0.483
plot25	0.142	0.230	0.618	0.537
plot26	0.186	0.223	0.831	0.408
plot28	0.170	0.190	0.894	0.373
plot29	0.078	0.155	0.504	0.615
plot30	0.266	0.230	1.157	0.249
plot31	0.131	0.160	0.815	0.416
plot32	0.103	0.157	0.656	0.513
plot34	0.118	0.194	0.610	0.543
plot35	0.265	0.261	1.017	0.311
plot36	0.025	0.121	0.207	0.836
plot37	0.131	0.165	0.799	0.426
plot38	0.747	0.088	8.439	0.000
plot39	-0.012	0.091	-0.134	0.894
plot40	0.082	0.090	0.915	0.362
plot41	0.231	0.121	1.907	0.059
plot42	0.423	0.263	1.607	0.110
plot43	0.366	0.142	2.584	0.011
plot44	0.296	0.202	1.462	0.146
plot45	0.038	0.116	0.333	0.740
plot46	0.248	0.143	1.733	0.085
plot47	0.543	0.143	3.795	0.000