

# Chapter 12 A/B Testing and Uplift Modeling

## 12.1 Introduction: From Average Effects to Targeted Marketing

A/B testing is one of the most widely used tools in marketing analytics. Whether testing email subject lines, promotional offers, website layouts, or pricing messages, marketers frequently rely on randomized experiments to measure causal effects.

In this chapter, we begin with **average treatment effects (ATEs)**, which is the traditional goal of A/B testing, and then move beyond averages to **uplift modeling**, which focuses on identifying *who* is most likely to be influenced by a marketing intervention.

Throughout the chapter, we use data from an email marketing experiment contained in the `email.camp.w` dataset.

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## 12.2 The Email Campaign Experiment

The dataset `email.camp.w` comes from a randomized email campaign experiment. Customers were randomly assigned to receive either:

- a **promotional email** (treatment group), or
- **no promotional email** (control group).

The primary outcome of interest is whether the customer responded (e.g., clicked or converted). In addition, the dataset contains several customer characteristics (covariates) such as demographics and prior behavior.

Because treatment assignment was randomized, differences in outcomes between the two groups can be interpreted causally.

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## 12.3 Checking the Randomization Assumption

### 12.3.1 Why Balance Checks Matter

Randomization ensures that treatment and control groups are similar *on average*. However, especially in applied settings, it is good practice to verify that observable covariates are balanced across groups.

Large imbalances may signal problems such as implementation errors or data issues.

### 12.3.2 Randomization Check Using `rand_check()`

The `rand_check()` function from the `MKT4320BGSU` package compares the distribution of selected covariates across treatment groups and automatically applies appropriate statistical tests.

Usage:

- `rand_check(data, treatment, covariates, ft = TRUE, digits = 3)`
- where:
  - `data` is a data frame containing the treatment indicator and covariates.
  - `treatment` is a character string giving the name of the treatment variable. Must identify two or more groups.
  - `covariates` is a character vector of covariate names to include in the randomization check.
  - `ft` is logical; if TRUE (default), return results as a flextable. If FALSE, return a data frame.
  - `digits` is an integer; number of decimal places to display in the output (default = 3).

An example is provided below. When reviewing the output, focus on:

- **Scaled mean differences:** values close to zero indicate good balance.
- **p-values:** large p-values suggest no systematic differences.

Well-balanced covariates support the validity of the experiment.

```
rand_check(data = email.camp.w, treatment = "promotion",  
  covariates = c("recency", "history", "womens", "zip"),  
  ft = TRUE)
```

Variable	Mean		SD	Scaled Mean Difference	p-value
	Treatment	Control			
recency	5.810	5.725	3.504	0.024	0.227
history	245.995	242.539	253.384	0.014	0.495
womens	0.545	0.539	0.498	0.011	0.574
zip:Rural	0.143	0.148	0.353	-0.014	0.395
zip:Suburban	0.459	0.445	0.498	0.027	
zip:Urban	0.398	0.406	0.490	-0.017	

## 12.4 Estimating the Average Treatment Effect (ATE)

### 12.4.1 What Is the ATE?

The **average treatment effect** measures the average impact of the promotion across all customers. In an email campaign, this answers the question: Did sending the promotion increase response rates overall?

### 12.4.2 ATE via Regression

For binary outcomes, a linear regression with a treatment indicator is equivalent to a difference-in-means estimator. When the outcome is binary, this is known as a **linear probability model (LPM)**.

### 12.4.3 Using `easy_ab_ate()`

We estimate the ATE using a regression model that includes the treatment indicator and optionally adjusts for covariates by using the `easy_ab_ate()` function from the `MKT4320BGSU` package.

Usage:

- `easy_ab_ate(model, treatment, ft = TRUE)`
- where:
  - `model` is a fitted linear regression model of class `lm`. This model should include the treatment variable and (optionally) covariates.
  - `treatment` is a character string with the name of the treatment variable (in quotes).
  - `ft` is logical; if `TRUE` (default) return a flextable. If `FALSE`, print full regression results to the console.

Note that to use this function, you must first create a linear regression model using the `lm()` function. The model should have a response variable as the dependent variable, the treatment variable as an independent variable, and any additional covariates as additional independent variables. The results should be saved to an object. For example:

- `object <- lm(response ~ treatment + cov_1 + cov_2 + ... + cov_k, data = data)`

```
m_ab_visit <- lm(visit ~ promotion + recency + history + womens + zip,
                 data = email.camp.w)
easy_ab_ate(model = m_ab_visit, treatment = "promotion", ft = TRUE)
```

Characteristic	Without Covariates		With Covariates	
	Beta	p-value	Beta	p-value
(Intercept)	0.106	<0.001	0.151	<0.001
promotion	0.049	<0.001	0.050	<0.001
recency			-0.006	<0.001
history			0.000	<0.001
womens			0.046	<0.001
zip				
Rural			—	
Surburban			-0.053	<0.001
Urban			-0.065	<0.001
p-value	<0.001		<0.001	

	Without Covariates		With Covariates	
Characteristic	Beta	p-value	Beta	p-value
R <sup>2</sup>	0.005		0.024	

```
m_ab_spend <- lm(spend ~ promotion + recency + history + womens + zip,
                 data = email.camp.w)
easy_ab_ate(model = m_ab_spend, treatment = "promotion", ft = TRUE)
```

	Without Covariates		With Covariates	
Characteristic	Beta	p-value	Beta	p-value
(Intercept)	0.651	<0.001	1.265	0.011
promotion	0.436	0.108	0.450	0.097
recency			-0.081	0.042
history			0.000	0.703
womens			0.049	0.858
zip				
Rural			—	
Surburban			-0.596	0.144
Urban			0.098	0.814
p-value	0.11		0.032	
R <sup>2</sup>	0.000		0.001	

The table compares two models:

- **Without covariates:** a pure A/B comparison.
- **With covariates:** a regression-adjusted estimate.

The treatment coefficient represents the average change in response probability caused by the promotion in isolation (in the without covariates column) or when controlling for other variables (in the with covariates column).

## 12.4.4 Why Average Effects Are Not Enough

While the ATE is useful, it hides important heterogeneity:

- Some customers may respond very positively.
- Others may be unaffected or even respond negatively.

From a managerial perspective, sending promotions to everyone may be inefficient or costly. This motivates **uplift modeling**, which focuses on targeting customers who are most likely to be influenced.

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## 12.5 Introduction to Uplift Modeling

### 12.5.1 What Is Uplift?

**Uplift** measures the *incremental* effect of treatment on an individual. That is, how much more likely is this customer to respond *because* they received the promotion?

This differs from standard prediction, which focuses on response likelihood regardless of treatment.

### 12.5.2 Two-Model (Indirect) Approach

The two-model approach estimates:

- one model estimated on treated customers, and
- one model estimated on control customers.

The difference between their predicted outcomes for a given customer is the estimated uplift.

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## 12.6 Estimating Uplift with `easy_uplift()`

### 12.6.1 Model Specification

The outcome variable can be either continuous, like amount spent (outcome) after a promotion (treatment), or it can be binary, like if they visited or not (outcome) after a promotion (treatment). To perform a uplift modeling using regression, we will use the `easy_uplift()` function from the

`MKT4320BGSU` package. This function performs uplift modeling based on either logistic regression (for binary outcomes) or linear regression (for continuous outcomes). The function uses the two-model, indirect modeling approach.

Usage:

- `easy_uplift(model, treatment, newdata = NULL, bins = 10, aspect_ratio = NULL)`
- where:
  - `model` is a fitted regression model of class `glm` (binary logit) or `lm`.
  - `treatment` is a character string giving the name of the treatment variable. The variable must have exactly two levels and be coded as (0/1), logical, or ("Yes", "No").
  - `newdata` is an optional data frame on which to compute uplift (e.g., holdout or test data). If `NULL`, uplift is computed on the model data.
  - `bins` is an integer; number of groups used for the uplift tables and plots. Must be between 5 and 20. Default is 10.
  - `aspect_ratio` is an optional numeric aspect ratio applied to all plots. Default is `NULL`.

In order to use the function, we must first create our base model:

- The base model is usually a model with no interactions included, along with the treatment variable. But if known interactions are to be used, the base model can include the interactions also.
- The base model must contain the treatment variable.

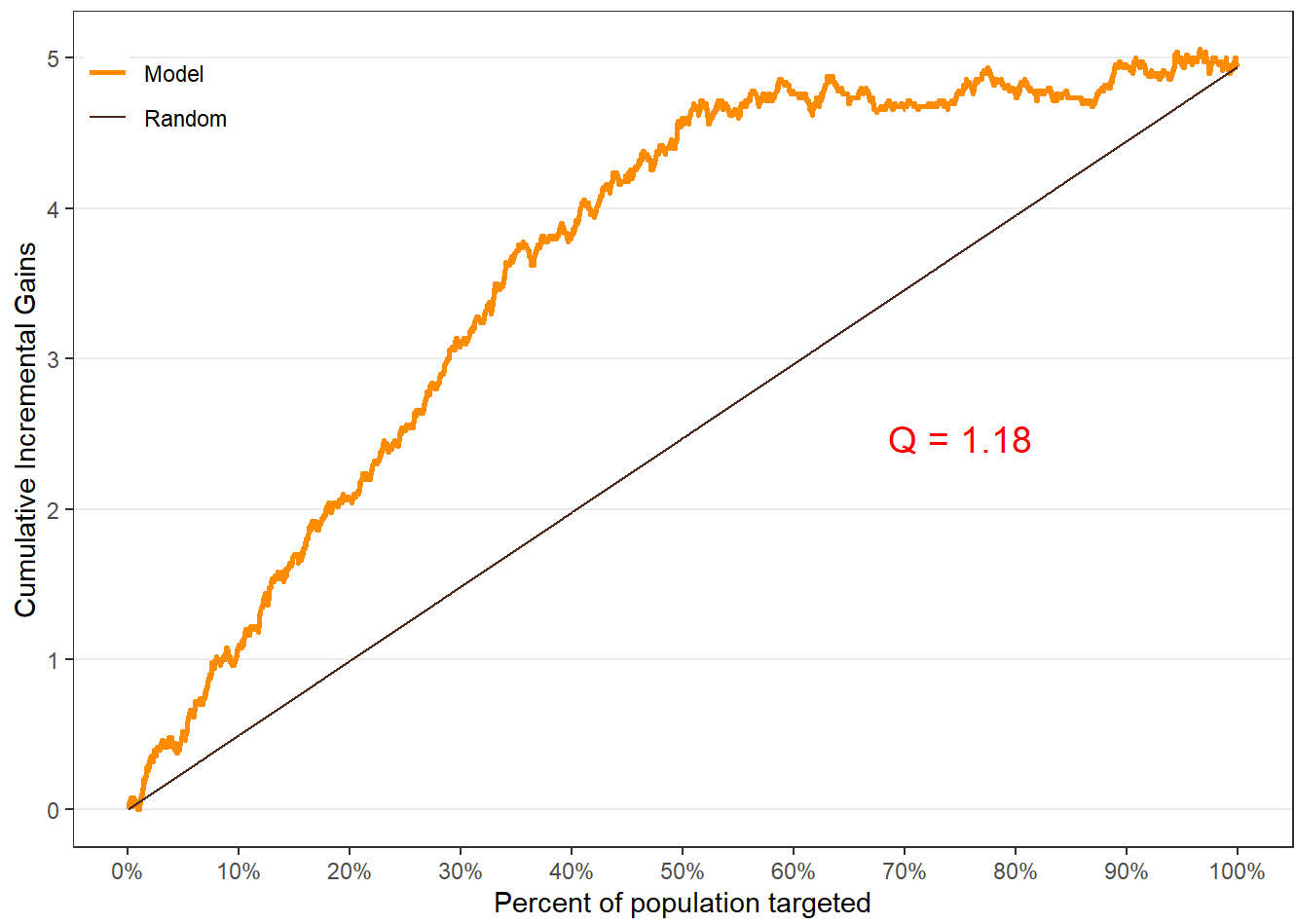
Base model examples:

```
email_visit <- glm(visit ~ promotion + recency + history + zip + womens,  
                  data=email.camp.w, family="binomial")  
email_spend <- lm(spend ~ promotion + recency + history + zip + womens,  
                 data=email.camp.w)
```

Once the base model is created, we are already to use the `easy_uplift()` function:

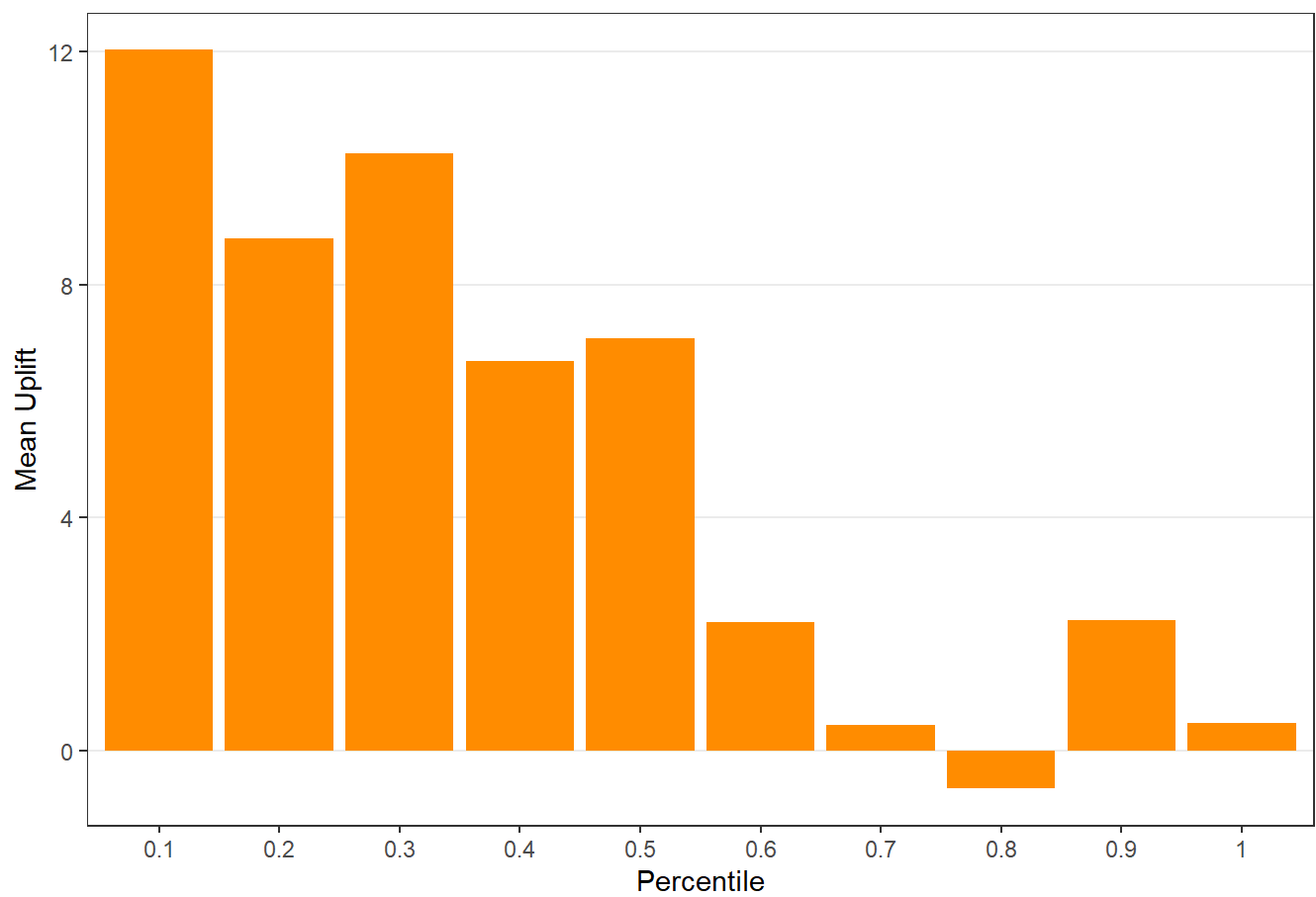
```
visit_uplift <- easy_uplift(model = email_visit, treatment = "promotion")  
visit_uplift$plots
```

```
$qini
```



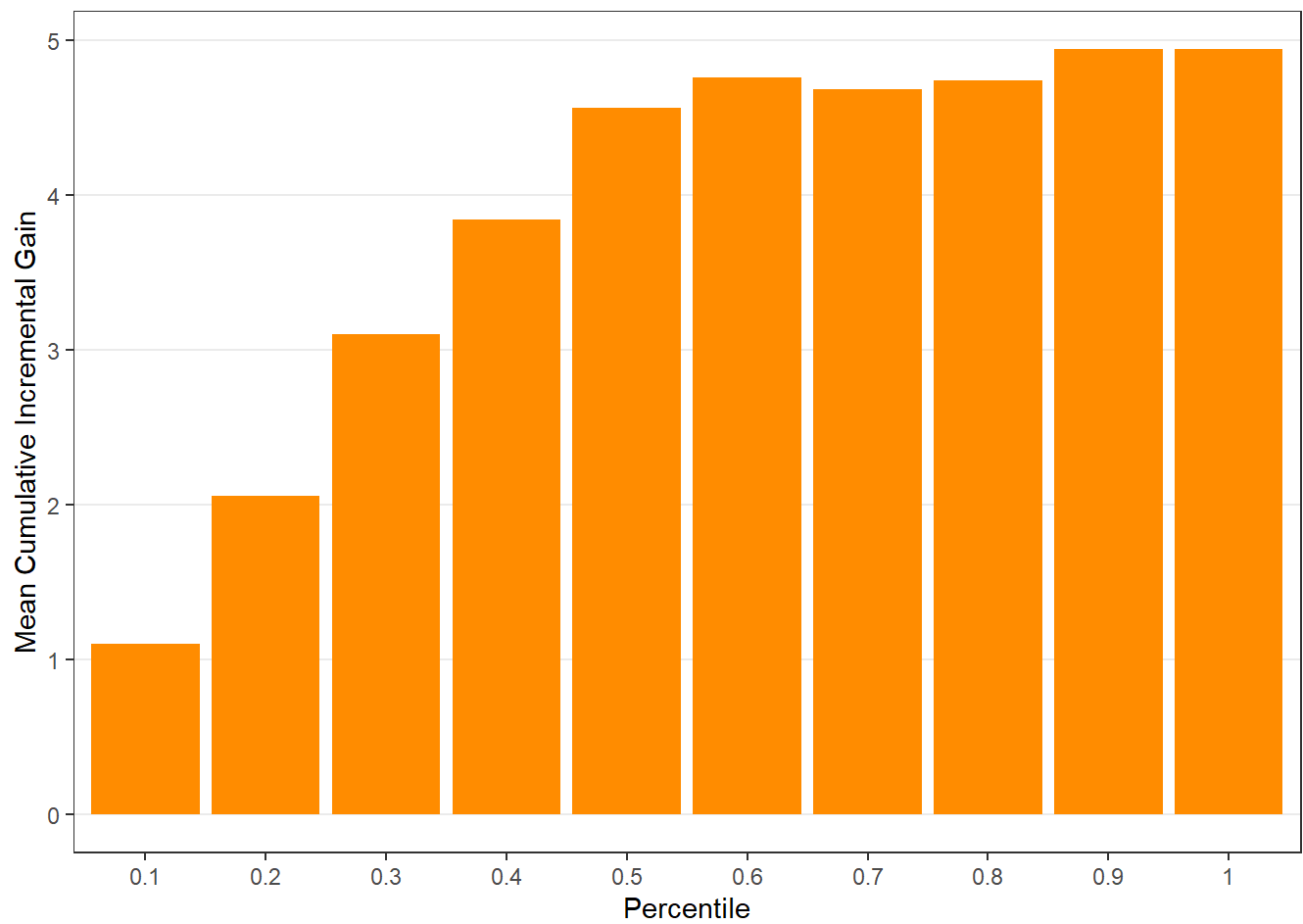
\$uplift





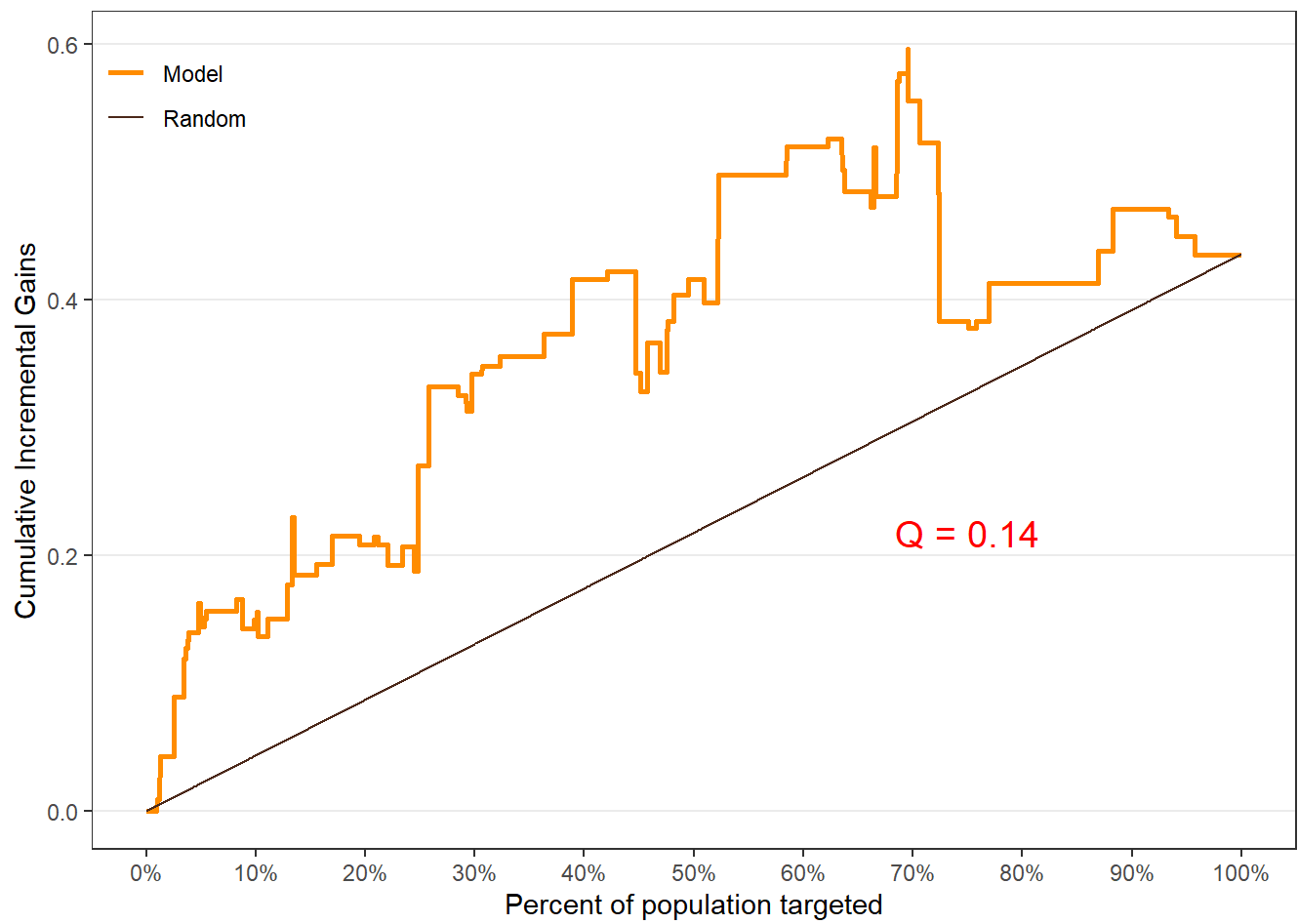
Kendall's tau = 0.689; p = 0.005

`$c.gain`

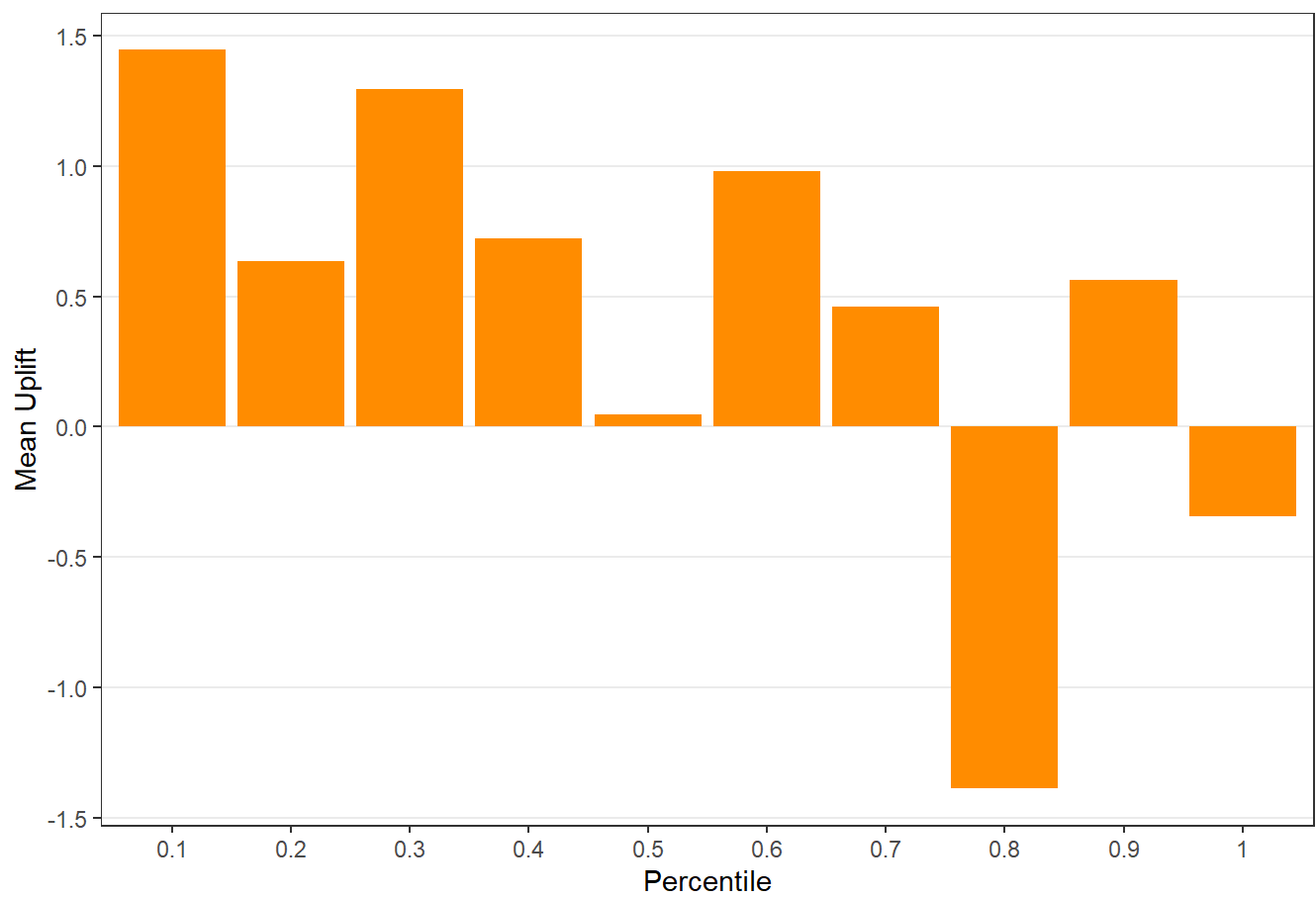


```
spend_uplift <- easy_uplift(model = email_spend, treatment = "promotion")  
spend_uplift$plots
```

```
$qini
```

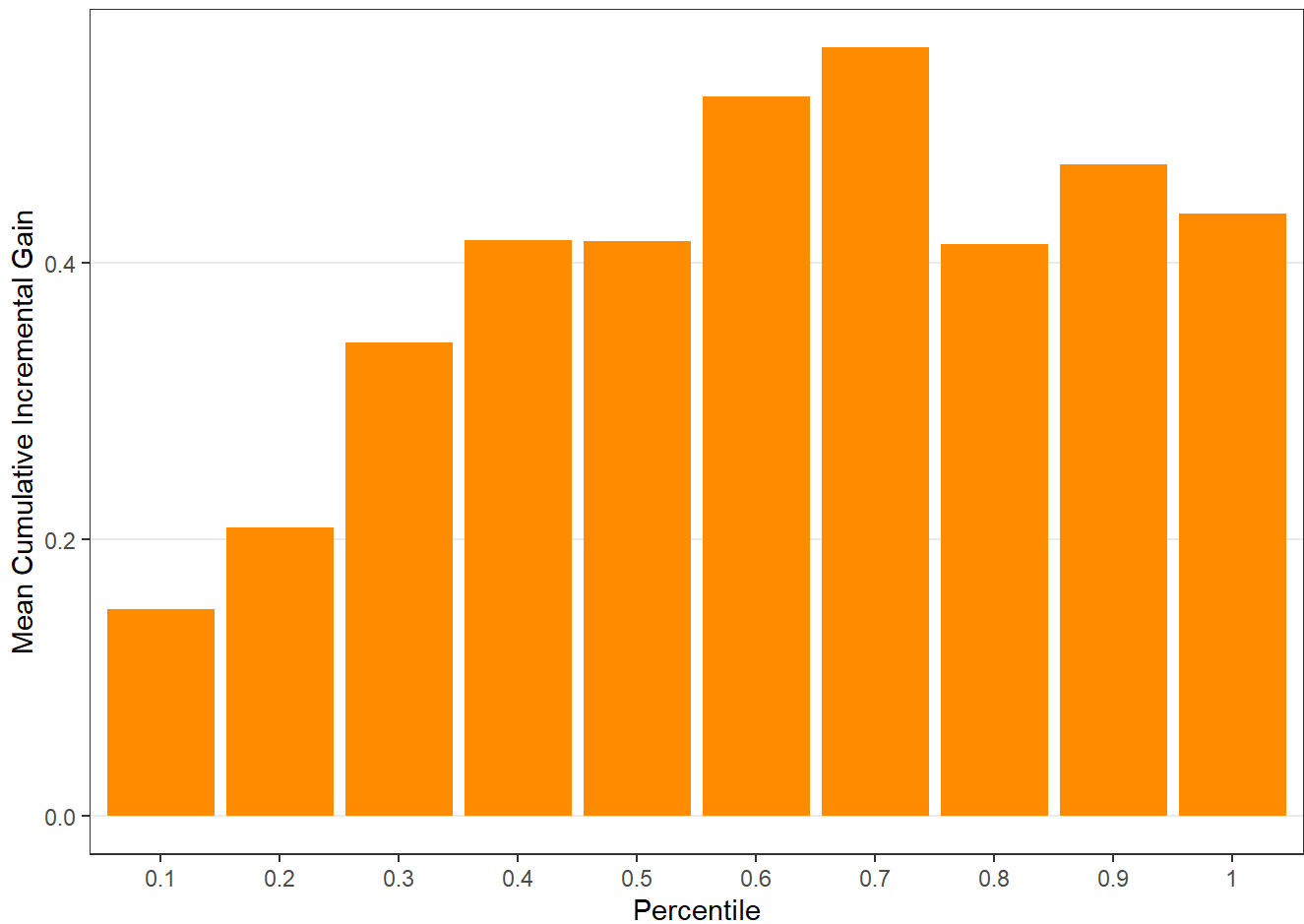


\$uplift



Kendall's tau = 0.556; p = 0.029

`$c.gain`



## 12.6.2 Interpreting Core Outputs

The uplift object includes:

- predicted individual-level lift appended to original data ( `$all` ),
- uplift table by percentile group ( `$group` ),
- diagnostic plots, including:
  - uplift by group ( `$plots$uplift` ),
  - cumulative gain ( `$plots$c.gain` ),
  - Qini curve ( `$plots$qini` ).

Customers in the top-ranked groups should exhibit the largest incremental gains from treatment.

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## 12.7 Diagnosing Uplift with Lift Plots

### 12.7.1 Why Lift Diagnostics Matter

Lift diagnostics help explain *why* uplift varies across customers and which covariates drive heterogeneity.

### 12.7.2 Using `easy_liftplots()`

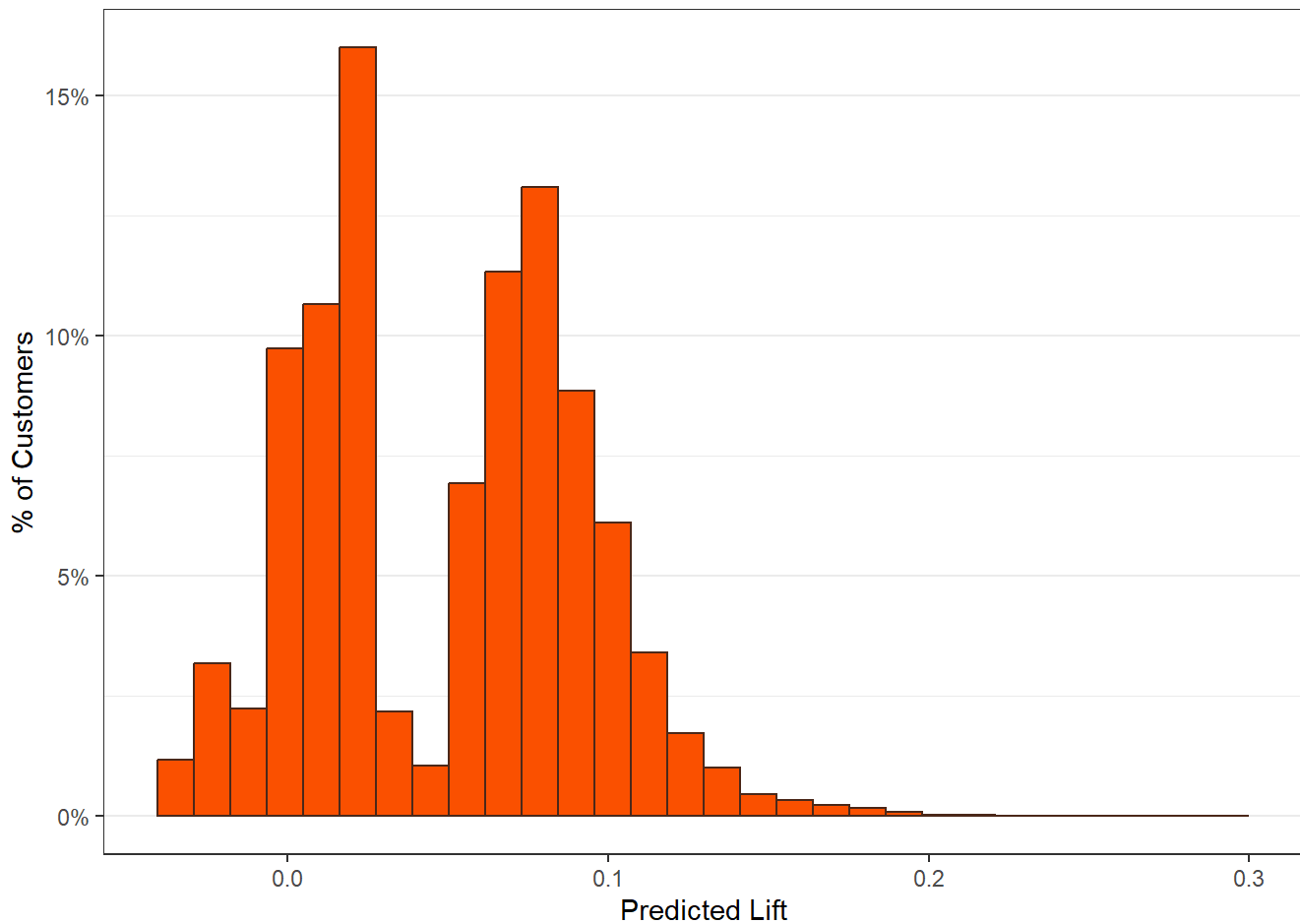
We use the `easy_liftplots()` function from the `MKT4320BGSU` package to easily create lift plots.

Usage:

- `easy_liftplots(x, vars = "all", pairs = NULL, ar = NULL, ci = 0.95, bins = 30, numeric_bins = 5, by_numeric_bins = 3, grid = TRUE, top = NULL, ft = TRUE)`
- where:
  - `x` is an object returned by `easy_uplift()` (must include *xall* and *xcovariates* or *xspec* covariates).
  - `vars` is a character vector of covariate names to plot. Default is "all" (uses *x* *covariates*/*xspec*\$*covariates*).
  - `pairs` is an optional list of length-2 character vectors specifying interaction-style plots to create, e.g., `list(c("recency", "zip"), c("gender", "income"))`.
  - `ar` is an optional aspect ratio passed to `theme(aspect.ratio = ar)`. Default is NULL.
  - `ci` affects the error-bar style. Use 0 for  $\pm 1$  SD error bars, or one of `c(0.90, 0.95, 0.975, 0.99)` for normal-approximation confidence intervals. Default is 0.95.
  - `bins` is an integer; number of bins for the histogram. Default is 30.
  - `numeric_bins` is an integer; number of quantile bins for numeric covariates. Default is 5.
  - `by_numeric_bins` is an integer; number of quantile bins to use for the second variable in a pair when it is numeric. Default is 3.
  - `grid` is logical; if TRUE, also return paginated cowplot grids of plots. Default is TRUE.
  - `top` is an optional integer. If provided, only the top `top` covariates (by `score_wmae`) are included in `plots_main/pages_main`. Rankings are still computed for all covariates.
  - `ft` is logical; if TRUE (default), return ranking tables as flextable objects.

A histogram is always produced, which shows the distribution of predicted uplift across customers. It is saved as `$hist`.

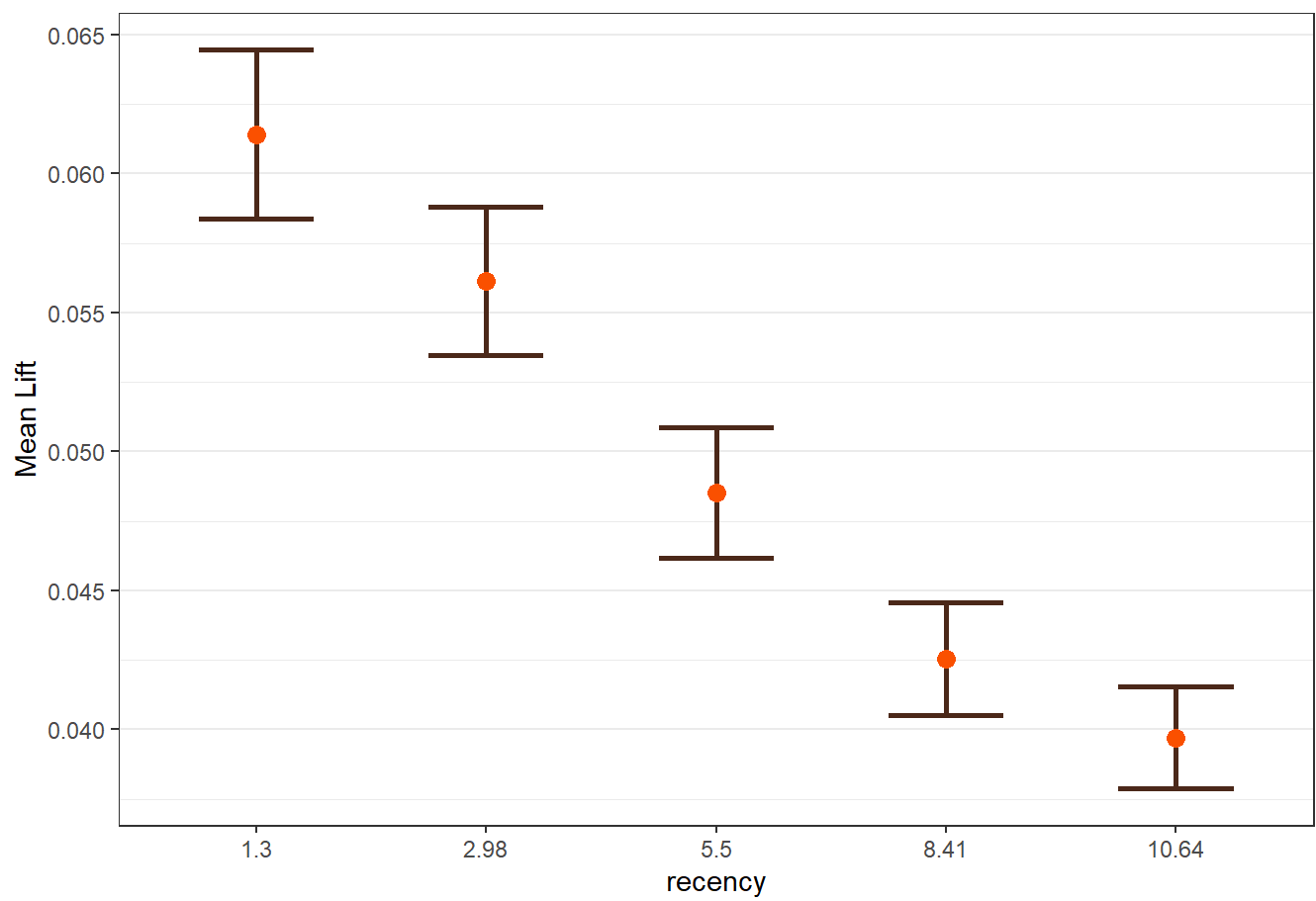
```
lift_out <- easy_liftplots(visit_uplift, vars = "all", ci = 0.99)
lift_out$hist
```



The main lift plots are saved in `$plots_main`. Lift-by-covariate plots display how average uplift varies across customer segments.

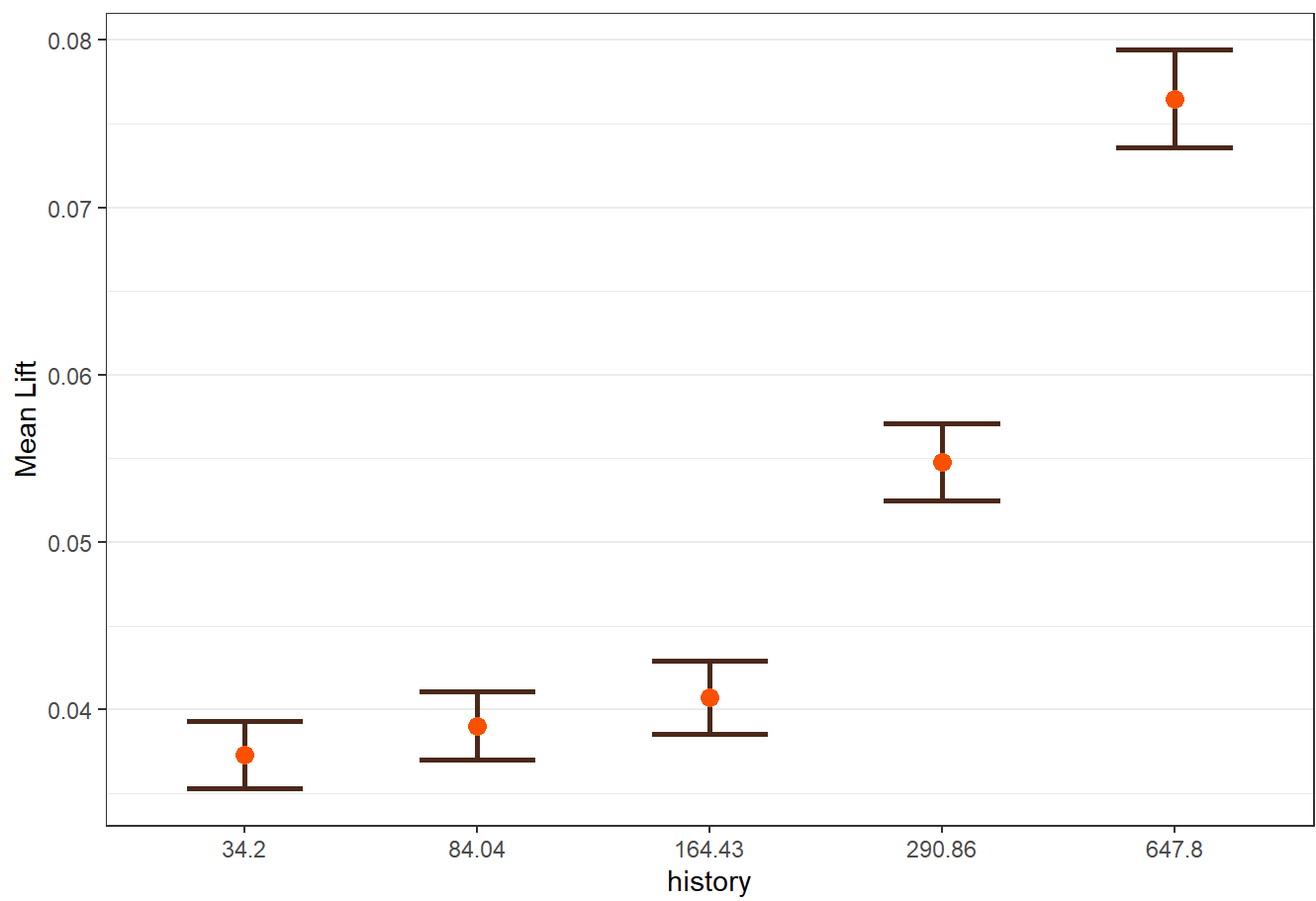
```
lift_out$plots_main
```

```
$recency
```

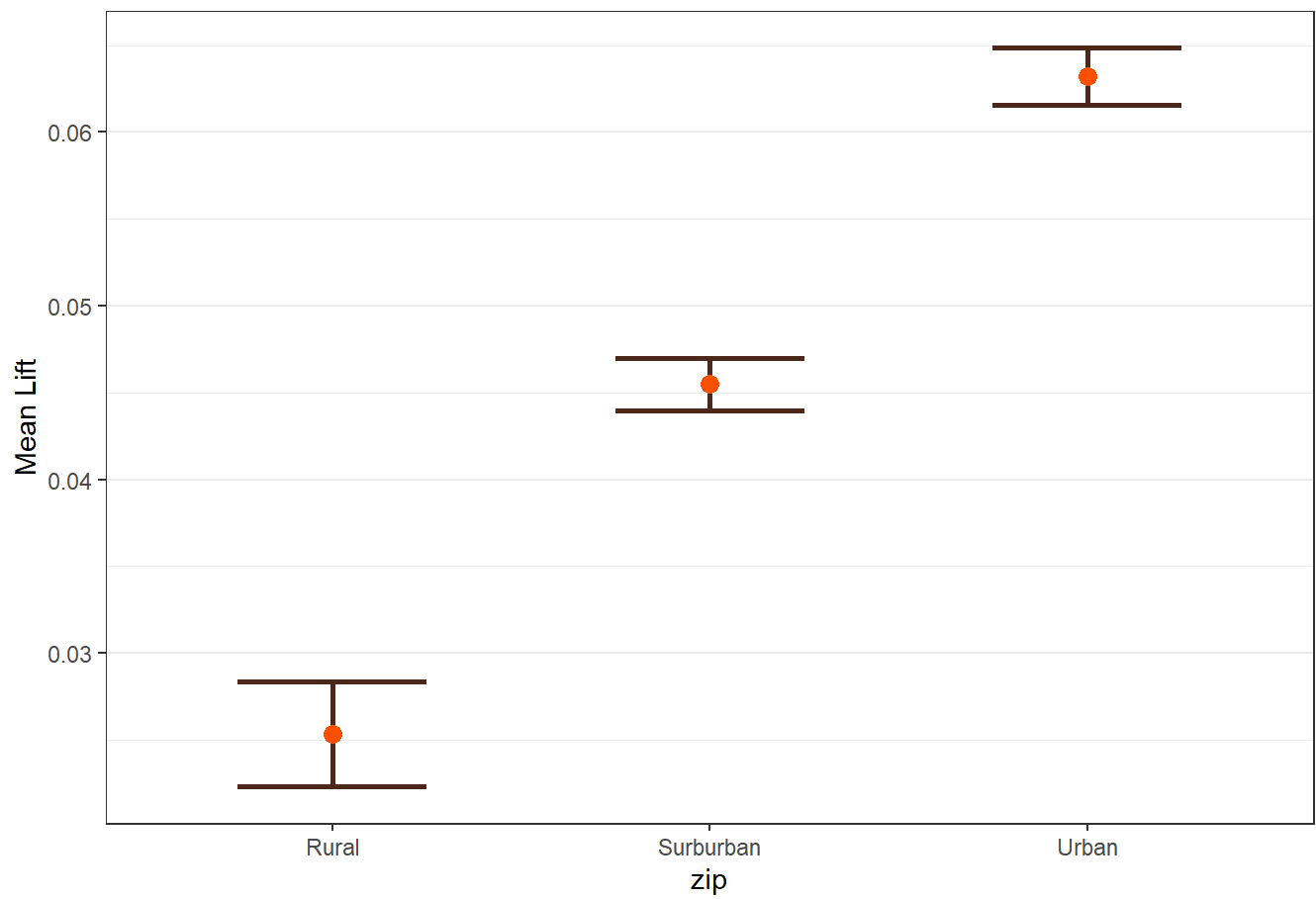


\$history

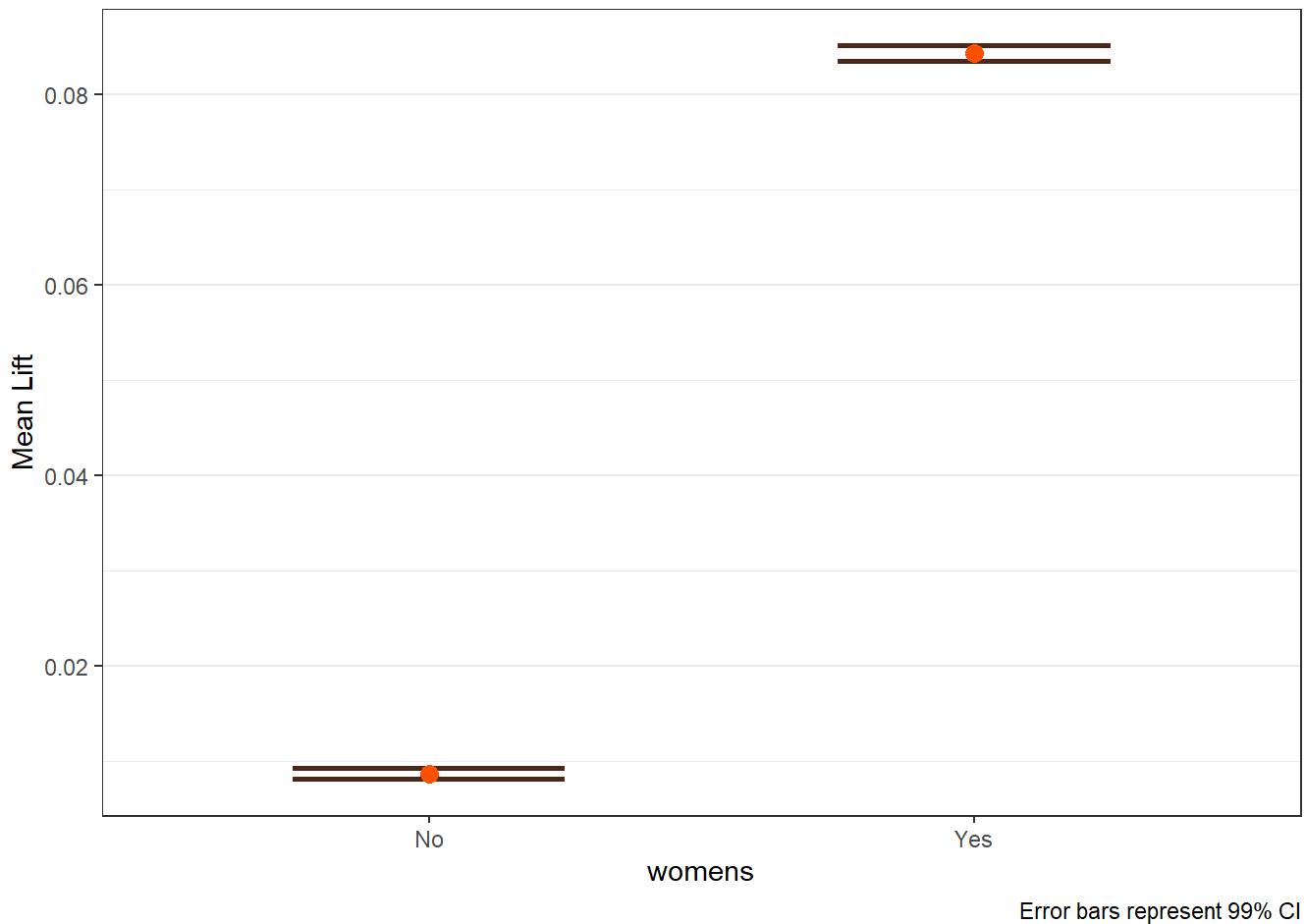




\$zip



\$womens

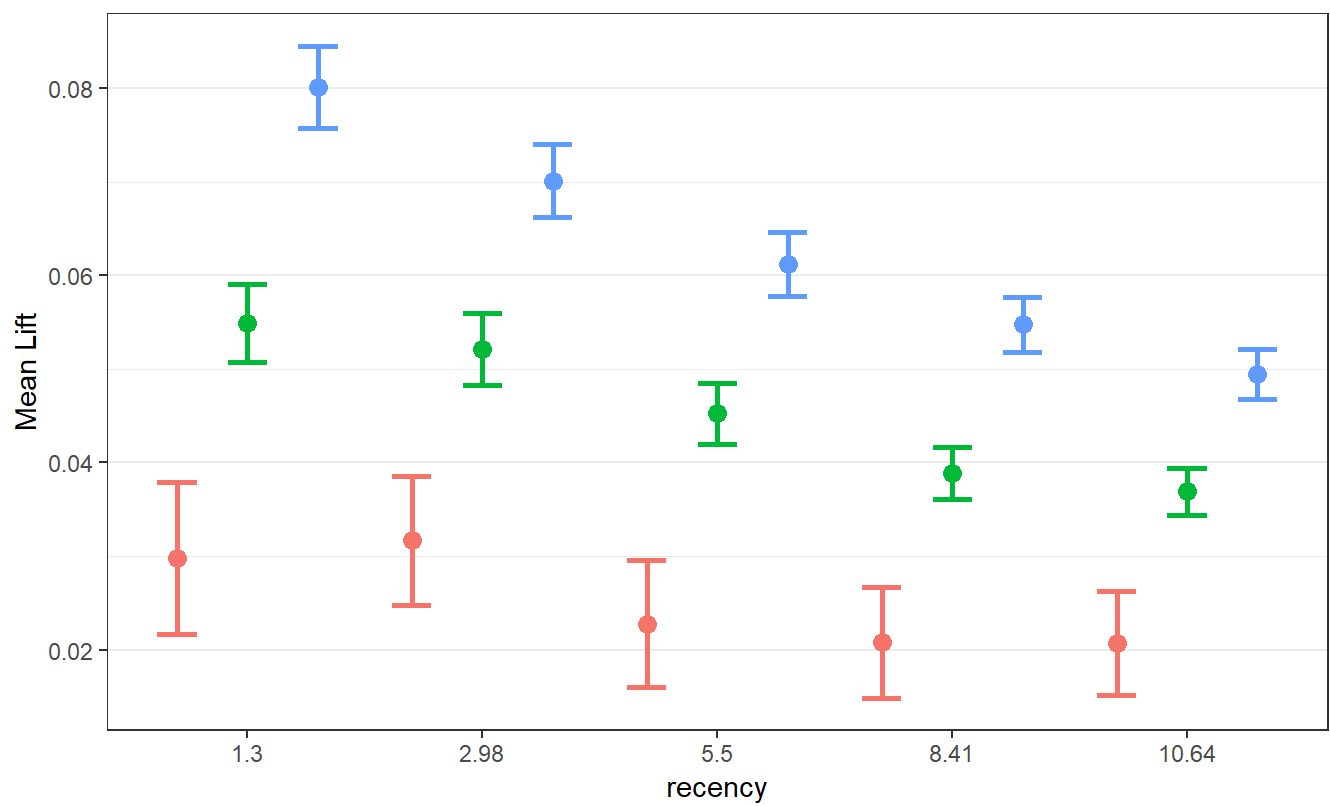


The `pairs` option is extremely valuable when known interactions are included in the model. The option can also be useful to help identify if an interaction may be warranted. If `pairs` is provided, the plots are saved in `plots_pairs`.

```
lift_out_pairs <- easy_liftplots(visit_uplift, vars = "all",
                                pairs = list(c("recency", "zip"),
                                              c("history", "womens")),
                                ci = 0.99)

lift_out_pairs$plots_pairs
```

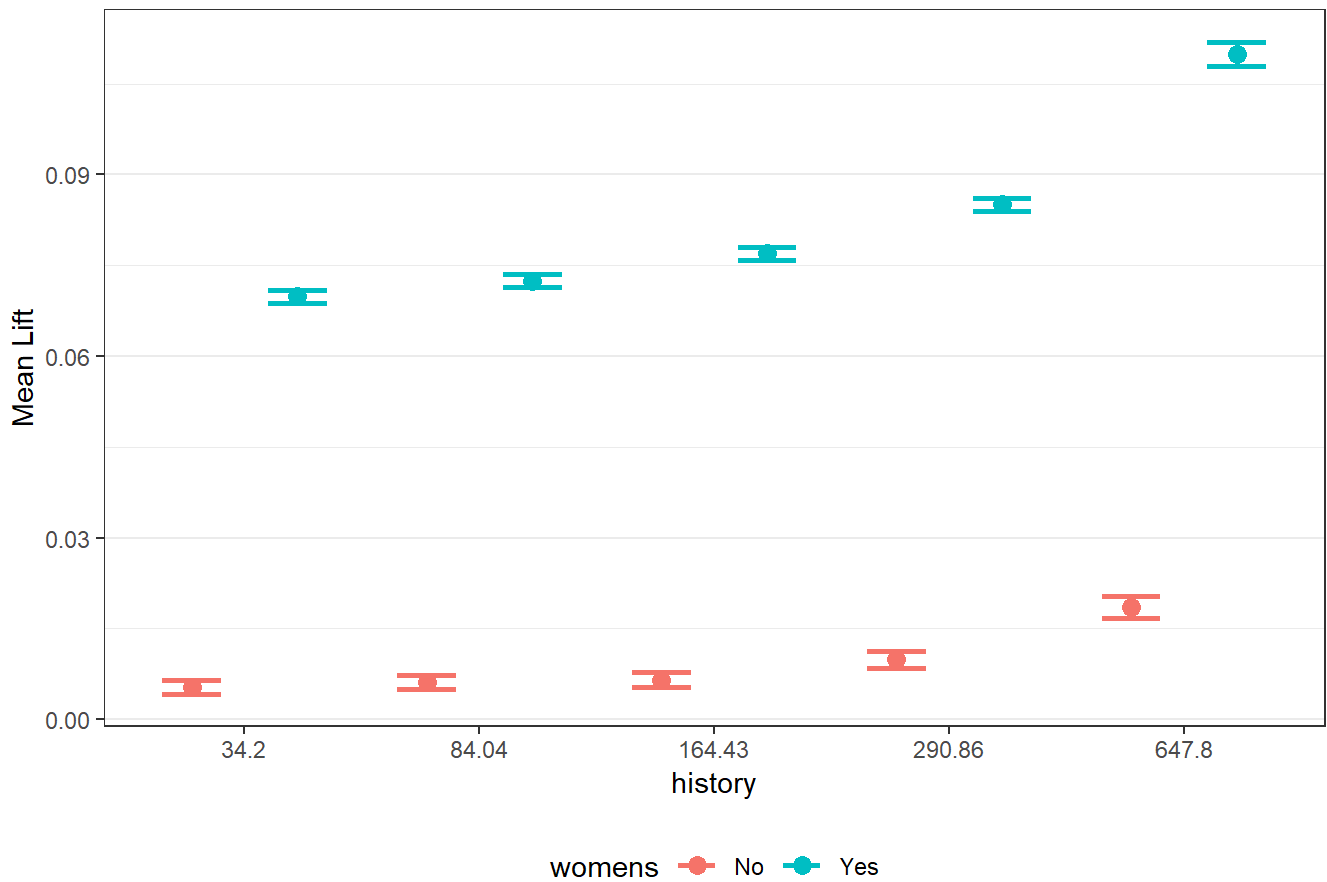
```
$`recency × zip`
```



zip Rural Suburban Urban

Error bars represent 99% CI

```
$`history` × womens`
```



Error bars represent 99% CI

## 12.8 From Analysis to Action

Uplift modeling enables smarter targeting strategies:

- Send promotions only to customers with positive uplift.
- Prioritize customers in the highest uplift deciles.
- Avoid over-targeting customers unlikely to respond.

These strategies can improve campaign profitability and customer experience.

## 12.9 Summary

In this chapter, you learned how to:

- validate randomization in A/B tests,
- estimate average treatment effects,
- move beyond averages using uplift modeling,
- interpret uplift diagnostics for targeting decisions.

A/B testing answers *whether* a campaign works. Uplift modeling answers *for whom* it works.

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## 12.10 What's Next

In many real-world marketing problems, managers face a different challenge: customers are not choosing between respond and not respond, but among multiple competing alternatives.

Examples include:

- Which brand a customer purchases
- Which product variant is selected
- Which service tier is chosen

In the next chapter, we introduce standard multinomial logistic regression, a workhorse model for analyzing and predicting choice among more than two options. You will learn how to:

- Model customer choice across multiple alternatives
- Interpret coefficients and predicted choice probabilities
- Evaluate model fit and classification performance
- Use multinomial logit models for applied marketing decisions

This next step shifts our focus from experimental treatment effects to choice modeling, setting the foundation for more advanced models of consumer decision-making used throughout marketing analytics and research.