

# BST02: Using R for Statistics in Medical Research

## Part D: Statistics with R

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24 - 28 February 2020

## In this Section

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- ▶ Common statistical tests
  - ▶ for continuous data
  - ▶ for categorical data
- ▶ (Generalized) linear regression
- ▶ Useful functions for regression models
- ▶ Modelling non-linear effects

## t-test: `t.test()`

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### One-sample t-test

- compares the **mean of one sample** with a fixed value  $\mu$

## t-test: `t.test()`

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### One-sample t-test

- ▶ compares the **mean of one sample** with a fixed value  $\mu$

### Two sample / independent samples t-test

- ▶ compares the **difference between the means** of two samples with a fixed value  $\mu$

## t-test: `t.test()`

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### Two sample / independent samples t-test

- ▶ compares the **difference between the means** of two samples with a fixed value  $\mu$

### Related samples t-test

- ▶ compares the **mean of the difference** between related observations with a fixed value  $\mu$  (same as one-sample t-test)

## Wilcoxon Test: `wilcox.test()`

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### Wilcoxon Signed Rank Test

- ▶ tests if **one sample** (or the difference between two paired samples) is **symmetric about**  $\mu$

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### Wilcoxon Rank Sum Test / Mann-Whitney test

- ▶ test for a **location shift between the distributions** of two independent samples

See also BBR Sections 7.2 & 7.3 (<http://hbiostat.org/doc/bbr.pdf>)

## Kruskal-Wallis Rank Sum Test: `kruskal.test()`

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- ▶ **extension** of the Wilcoxon rank sum test for **more than two groups**
- ▶ test for a **difference in location** of a continuous variable between multiple groups
- ▶ the **Wilcoxon rank sum test is a special case** of the Kruskal-Wallis rank sum test



## Other tests for continuous data

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- ▶ **Kolmogorov-Smirnov Test:** `ks.test()`  
tests if two samples are drawn from the same continuous distribution
- ▶ **Shapiro-Wilk Normality Test:** `shapiro.test()`
- ▶ **Friedman Rank Sum Test:** `friedman.test()`  
non-parametric test for two or more related samples
- ▶ ...

# Tests for Continuous Data

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## Demo

- ▶ Tests for Continuous Data

**R** **html**

# Tests for Categorical Data / Proportions

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## One-sample Proportion Test

- ▶ tests if the **proportion in one sample** is equal to a fixed value  $p$
- ▶ `prop.test()` and `binom.test()`

# Tests for Categorical Data / Proportions

---

## One-sample Proportion Test

- ▶ tests if the **proportion in one sample** is equal to a fixed value  $p$
- ▶ `prop.test()` and `binom.test()`

## Tests for Proportions in Multiple (independent) Groups

- ▶ tests if the **proportions in several samples** are equal
- ▶ `chisq.test()` and `fisher.test()` (when there are cells with 0)

See also BBR Sections 5.7 & 6 (<http://hbiostat.org/doc/bbr.pdf>)

# Tests for Categorical Data / Proportions

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## Related Samples: McNemar Test

- ▶ Tests for **symmetry** in a  $2 \times 2$  table
- ▶ `mcnemar.test()`

# Tests for Categorical Data / Proportions

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## Related Samples: McNemar Test

- ▶ Tests for **symmetry** in a  $2 \times 2$  table
- ▶ `mcnemar.test()`

## 3-Dimensional Contingency Table

- ▶ Cochran-Mantel-Haenszel Test
- ▶  $\chi^2$  test for **independence** of two nominal variables **within each stratum**
- ▶ `mantelhaen.test()`

# Tests for Categorical Data

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## Demo

- ▶ Tests for Categorical Data

**R** **html**

## Practical

- ▶ Statistical Tests

**html**

# Useful Functions: Statistical Tests

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## Continuous Outcomes

- ▶ `t.test()`
- ▶ `wilcox.test()`
- ▶ `kruskal.test()`
- ▶ `ks.test()`
- ▶ `friedman.test()`
- ▶ `shapiro.test()`

## Categorical Outcomes

- ▶ `prop.test()`
- ▶ `binom.test()`
- ▶ `chisq.test()`
- ▶ `fisher.test()`
- ▶ `mcnemar.test()`
- ▶ `mantelhaen.test()`

## Pairwise tests

- ▶ `pairwise.prop.test()`
- ▶ `pairwise.t.test()`
- ▶ `pairwise.wilcox.test()`

## Variance and Correlation

- ▶ `cor.test()`
- ▶ `bartlett.test()`
- ▶ `var.test()`

## Multiple Testing Adjustment

- ▶ `p.adjust()`



# Linear Regression

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A standard linear regression model has the form

$$y = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p + \varepsilon \quad \text{with} \quad \varepsilon \sim N(0, \sigma^2)$$

where

- ▶  $y$  is the **outcome** variable ("dependent variable")
- ▶  $x_1, \dots, x_p$  are the **covariates** ("independent variables")
- ▶  $\beta_0, \dots, \beta_p$  are the **regression coefficients**
  - ▶  $\beta_0$  is the intercept
  - ▶  $\beta_1, \dots, \beta_p$  estimate the effects of the covariates
- ▶  $\varepsilon$  is a vector of **residuals**, which we assume to be (approximately) normally distributed.

# Linear Regression

---

To fit a **linear regression** in R we use the function `lm()`.

The most important arguments are

- ▶ **formula:**  
a formula object
- ▶ **data:**  
a `data.frame` (optional, but usually needed)
- ▶ **subset:**  
a vector specifying which observations should be used (optional)  
(works like the `subset` argument of the function `subset()`)

# Model Formula

---

A `formula` object has the form

```
outcome ~ linear predictor
```

for example

```
y ~ x1 + x2 + x3
```

# Model Formula

---

A `formula` object has the form

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for example

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y ~ x1 + x2 + x3
```

- ▶ Variables are separated by "+" signs.
- ▶ An intercept is automatically included.
- ▶ One-sided formulas (omitting the outcome) are possible (used for random effects specification).

## Model Formula: Interactions

---

Interaction terms are written using ":" or "\*".

"\*" includes the main effects and interaction terms, i.e.,

```
y ~ x1 * x2
```

is equivalent to

```
y ~ x1 + x2 + x1:x2
```

## Model Formula: Interactions

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y ~ x1 * x2
```

is equivalent to

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y ~ x1 + x2 + x1:x2
```

Interactions between multiple variables can be written using "()", i.e.,

```
y ~ x1 * (x2 + x3)
```

is equivalent to

```
y ~ x1 * x2 + x1 * x3
```

## Model Formula: Interactions

---

To specify a **higher level interaction** “^” is used.

For example:

```
y ~ (x1 + x2 + x3)^3
```

will create all interactions up to 3-way and is equivalent to

```
y ~ x1 * x2 * x3
```

and equivalent to

```
y ~ x1 + x2 + x3 + x1:x2 + x1:x3 + x2:x3 + x1:x2:x3
```

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and equivalent to

```
y ~ x1 + x2 + x3 + x1:x2 + x1:x3 + x2:x3 + x1:x2:x3
```

and

```
y ~ (x1 + x2 + x3)^2
```

will create all two-way interactions and is equivalent to

```
y ~ x1 + x2 + x3 + x1:x2 + x1:x3 + x2:x3
```



## Model Formula: Removing terms

---

The “-” sign can be used to remove terms from a model formula.

For example

```
y ~ x1 * x2 * x3 - x2 - x1:x3
```

is equivalent to

```
y ~ x1 + x3 + x1:x2 + x2:x3 + x1:x2:x3
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The “-” sign can be used to remove terms from a model formula.

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y ~ x1 * x2 * x3 - x2 - x1:x3
```

is equivalent to

```
y ~ x1 + x3 + x1:x2 + x2:x3 + x1:x2:x3
```

The **intercept** can be removed from a formula by using “-1” or “+0”, i.e.

```
y ~ x1 + x2 - 1
```

```
y ~ x1 + x2 + 0
```

# Generalized Linear Regression (GLM)

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A **generalized linear regression** model has the form

$$g(\mathbb{E}(y)) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

where  $g(\ )$  is a link function and  $y$  is from the exponential family.

# Generalized Linear Regression (GLM)

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$$g(\mathbb{E}(y)) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

where  $g(\cdot)$  is a link function and  $y$  is from the exponential family.

For example **logistic regression** for binary  $y$ :

$$\log \left( \frac{P(y = 1)}{1 - P(y = 1)} \right) = \beta_0 + \beta_1 x_1 + \beta_2 x_2 + \dots + \beta_p x_p$$

$\log \left( \frac{p}{1-p} \right)$  is the **logit** link.

# Generalized Linear Regression (GLM)

---

To fit a **GLM** in R we use the function `glm()`.

The most important arguments are

- ▶ **formula:**  
a formula object
- ▶ **family:**  
a family object or name of the family function, describing the error distribution and link function
- ▶ **data:**  
a `data.frame` (optional, but usually needed)
- ▶ **subset:**  
a vector specifying which observations should be used (optional)

## Families and Link Functions

---

Common families & available links in R:

(see also ?family)

family	link
binomial	logit, probit, cauchit, log, cloglog
gaussian	identity, log, inverse
Gamma	inverse, identity, log
poisson	log, identity, sqrt

# Families and Link Functions

Common families & available links in R:

(see also `?family`)

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binomial	logit, probit, cauchit, log, cloglog
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The `family` argument in `glm()` can be specified in the following ways:

- ▶ `binomial(link = "logit")`
- ▶ `binomial()`
- ▶ `binomial`
- ▶ `"binomial"`

# Families and Link Functions

Common families & available links in R:

(see also `?family`)

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The `family` argument in `glm()` can be specified in the following ways:

- ▶ `binomial(link = "logit")`
- ▶ `binomial()`
- ▶ `binomial`
- ▶ `"binomial"`

## Note:

When the link is not explicitly specified (i.e. options 2-4), the default link is used.



# Regression

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## Demo

- ▶ Regression Basics

**R**

**html**

## Practical

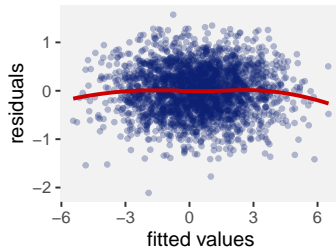
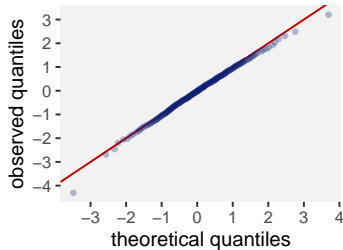
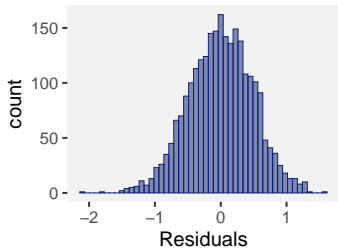
- ▶ Linear Regression **html**

# Model Evaluation

## Linear model:

Evaluate the **assumptions** of a linear regression model visually, for example:

- ▶ Histogram of residuals
- ▶ Normal QQ-plot of residuals
- ▶ Scatterplot residuals vs fitted values



# Model Comparison

---

## Nested models:

- ▶ model is a **special case** of the other, i.e.,
- ▶ model B is a special case of model A when B can be obtained by setting some regression coefficients in A to zero

Comparison using a **likelihood ratio (LR) test**, for example:

```
anova(modelA, modelB)
```

```
anova(modelA, modelB, test = "LRT") # for a glm
```

# Model Comparison

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Comparison using a **likelihood ratio (LR) test**, for example:

```
anova(modelA, modelB)
anova(modelA, modelB, test = "LRT") # for a glm
```

## Non-nested models:

Comparison using information criteria, e.g.

```
AIC(modelA, modelB)
BIC(modelA, modelB)
```

The model with the **smaller** AIC (or BIC) has the **better** fit.

# Model Evaluation

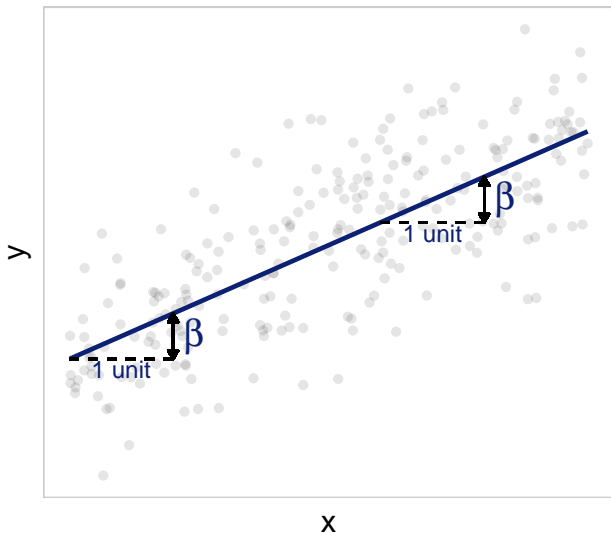
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## Demo

▶ Model Evaluation **R** **html**

# Non-linear Effects

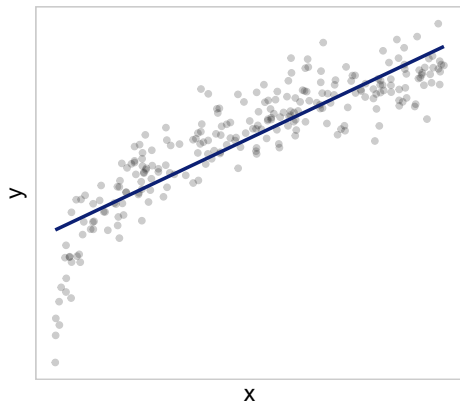
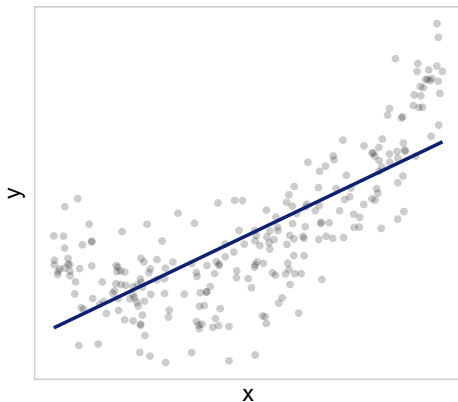
Default assumption: **linear effect**, i.e.,  $x \rightarrow y \rightarrow x + 1 \rightarrow y + \beta$ ,  $\forall x$



# Non-linear Effects

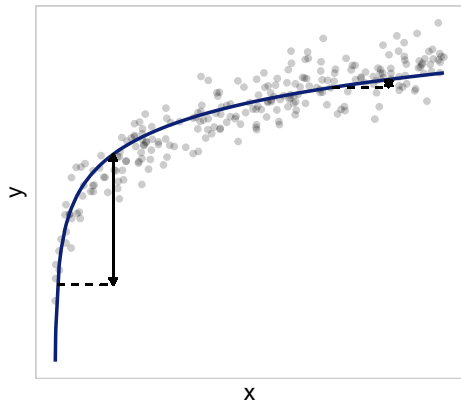
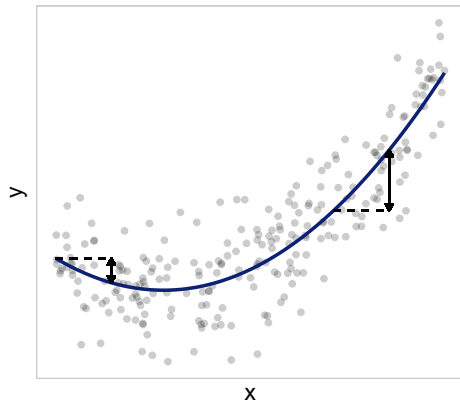
Default assumption: **linear effect**, i.e.,  $x \rightarrow y \Rightarrow x + 1 \rightarrow y + \beta, \quad \forall x$

This may not always be the case:



# Non-linear Effects

Here, we would like to allow the **effect** of a one-unit increase **of  $x$**  to **change with the value of  $x$** :





# Non-linear Effects

Sometimes, we can use

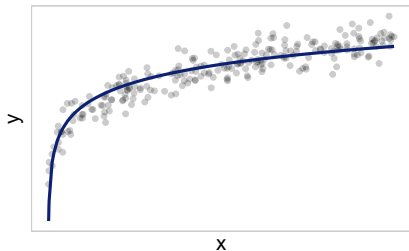
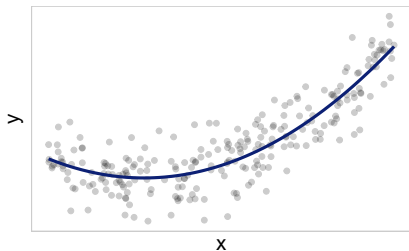
- ▶ a **transformation of x**, or
- ▶ x as well as a **polynomial** of x (or a transformation).

For example:

$$y \sim x + I(x^2)$$

or

$$y \sim \log(x)$$



## Non-linear Effects: $I()$

---

The function  $I()$  is needed to distinguish between operators that need to be interpreted as

- ▶ arithmetic operators and
- ▶ formula operators

## Non-linear Effects: `I()`

The function `I()` is needed to distinguish between operators that need to be interpreted as

- ▶ arithmetic operators and
- ▶ formula operators

Example:

```
y ~ I(a + b)
```

would be the same as

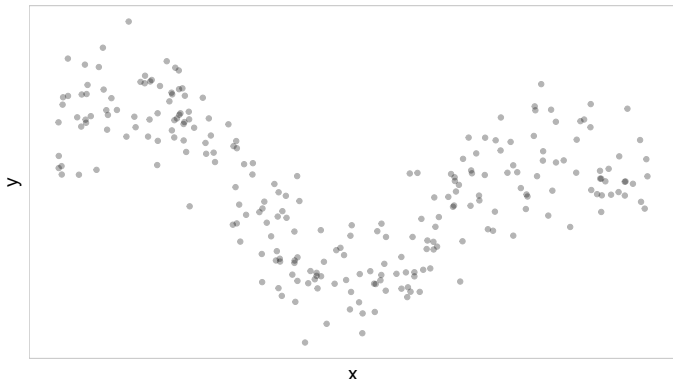
```
z <- a + b  
y ~ z
```

but not the same as

```
y ~ a + b
```

# Complex Non-linear Effects

Non-linear effects may be **more complex** than can be modelled with a simple transformation or polynomial.



**Also:** the shape may depend on other covariates in the model

➔ we do not always know the shape in advance

➔ **Regression Splines / B-Splines**

# B-Splines

---

A **B-Spline** is a linear combination of a set of **basis functions**.

These basis functions are defined so that they are

- ▶ a **polynomial functions** inside a given interval, and
- ▶ zero outside that interval.

The intervals are defined by a set of **knots**.

The polynomial function have a certain **degree** (i.e., constant, linear, quadratic, ...)

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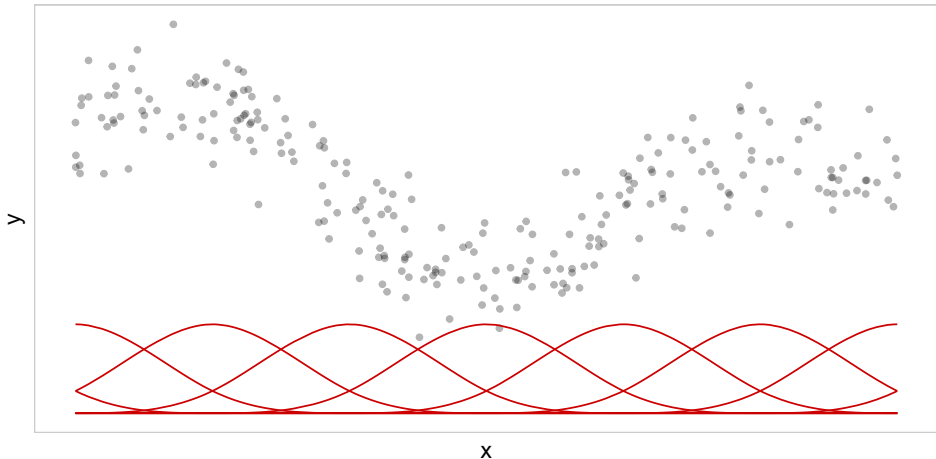
## B-Splines in R

The R package **splines** provides the functions

- ▶ **bs()**: B-splines
- ▶ **ns()**: natural cubic (B-)splines

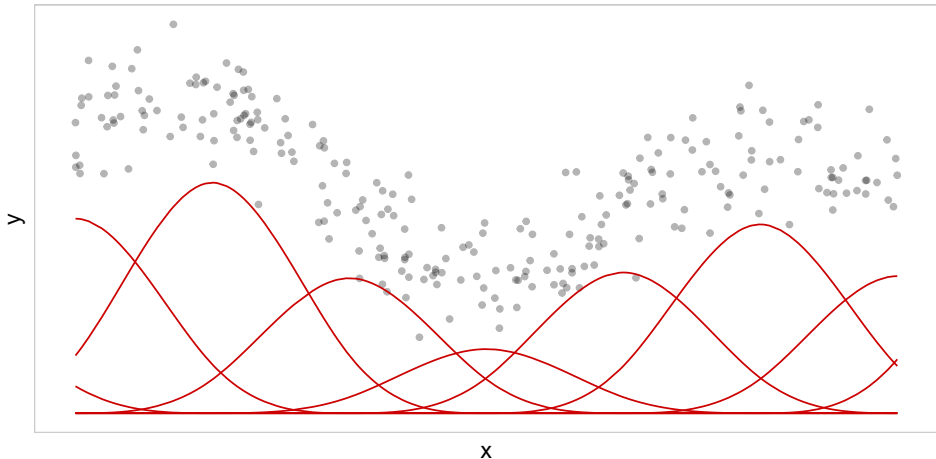
# B-Splines

Instead of  $y \sim \beta_0 + \beta_1 x + \dots$  we assume  $y \sim \beta_0 + \sum_{\ell=1}^d \beta_{\ell} B_{\ell}(x) + \dots$



# B-Splines

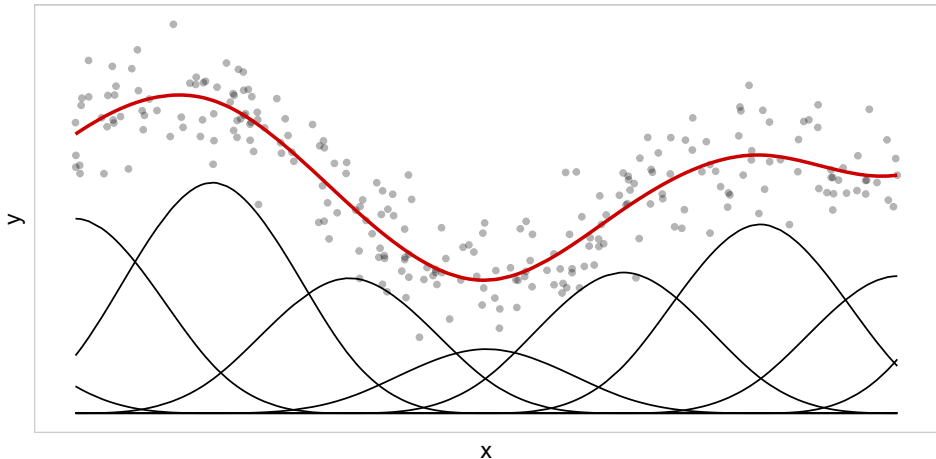
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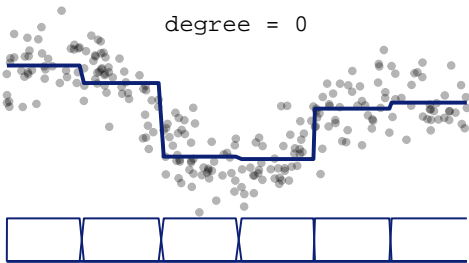
# B-Splines

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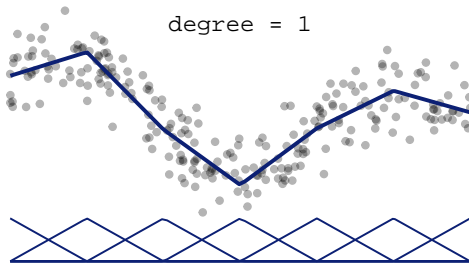


# B-Splines: degree

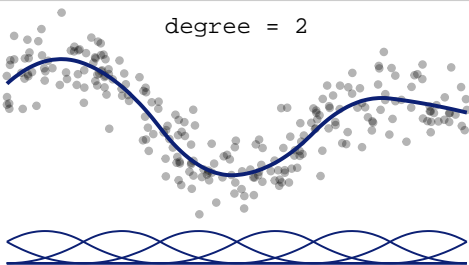
degree = 0



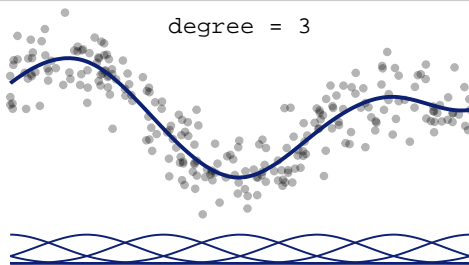
degree = 1



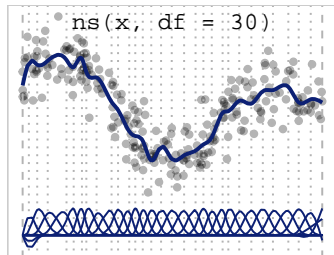
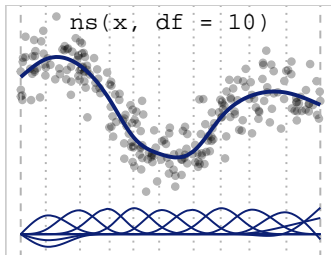
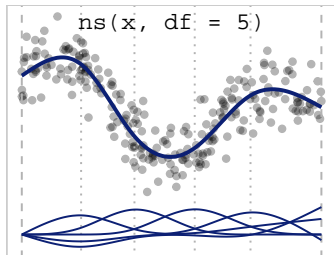
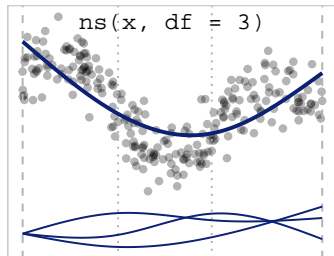
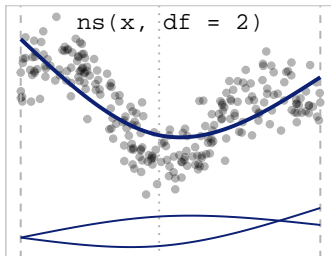
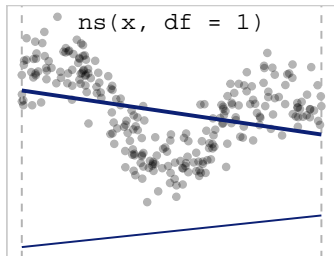
degree = 2



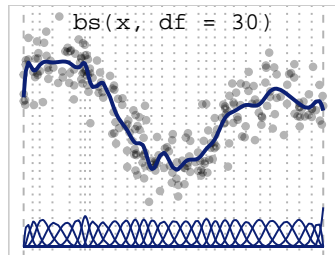
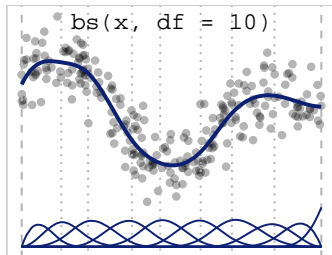
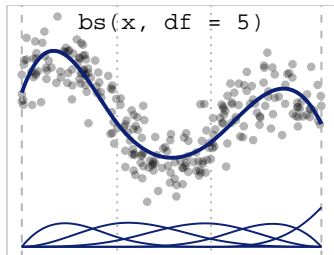
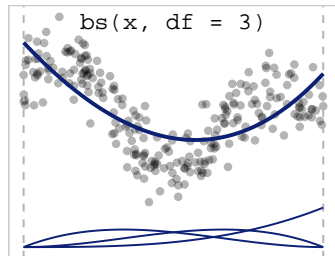
degree = 3



# B-Splines: df



# B-Splines: df



## B-Splines in R: `bs()` & `ns()`

---

Important arguments of `ns()` and `bs()` are:

### degree

- ▶ degree of the polynomial in each of the basis functions
- ▶ in `bs()`: default is 3
- ▶ in `ns()`: always 3 (“cubic”)

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### df

- ▶ degrees of freedom, i.e., “number of regression coefficients” used
- ▶ for `bs()`: has to be  $\geq$  degree

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### degree

- ▶ degree of the polynomial in each of the basis functions
- ▶ in `bs()`: default is 3
- ▶ in `ns()`: always 3 (“cubic”)

### knots

- ▶ position of (inner) knots
- ▶ if unspecified:
  - ▶ `df`-degree knots are used
  - ▶ positioned at equally spaced quantiles

### df

- ▶ degrees of freedom, i.e., “number of regression coefficients” used
- ▶ for `bs()`: has to be  $\geq$  degree

## B-Splines in R: `bs()` & `ns()`

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- ▶ for `bs()`: has to be  $\geq$  degree

### knots

- ▶ position of (inner) knots
- ▶ if unspecified:
  - ▶ df-degree knots are used
  - ▶ positioned at equally spaced quantiles

### Boundary.knots

- ▶ by default: `range(x)`
- ▶ outside the `Boundary.knots` the fit is extrapolated



# Non-linear Effects

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## Demo

- ▶ Splines [R](#) [html](#)

## Practicals

- ▶ Logistic Regression & More [html](#)
- ▶ Logistic Regression II [html](#)
- ▶ Custom Model Summary Function [html](#)

# Regression

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## Regression Models

- ▶ `lm()`
- ▶ `glm()`

## Regression Results

- ▶ `summary()`
- ▶ `coef()`, `confint()`
- ▶ `fitted()`, `residuals()`,  
`rstandard()`
- ▶ `AIC()`, `BIC()`
- ▶ `anova()`

## Plots

- ▶ `plot()`
- ▶ `qqnorm()`, `qqline()`, `qqplot()`

## Formulas

- ▶ Formula operators: `+`, `-`, `*`, `:`, `^`
- ▶ `ns()`, `bs()`, `I()`
- ▶ `all.vars()`
- ▶ `update()`
- ▶ `as.formula()`