

# Manual R function prevFV

**Authors:** Olga W. Souverein, Hendriek C. Boshuizen  
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## **Introduction**

The R function `predFV` has been developed to predict the intake of fruit and vegetables based on several biomarkers and subject characteristics for intervention groups in an intervention study. It is possible to predict fruit, vegetable and juice intake as well as fruit and vegetable intake excluding juices.

The model on which the function is based has been described in the paper: "Prediction of fruit and vegetable intake from biomarkers using individual participant data of diet-controlled intervention studies", which will appear in the *British Journal of Nutrition*.

## Requirements to the data

### Aim of the function

The aim of the function is to predict the mean fruit and vegetable intake in an intervention group after an intervention to increase fruit and vegetable by advice or counselling. The predicted fruit and vegetable intake is based on objective measures such as biomarkers and subject characteristics.

### Data requirements

Table 1 indicates which data is needed for the prediction model included in the function.

Table 1. Required data

Data	Fruit, vegetables and juice intake	Fruit and vegetable intake (excluding juices)
Carotenoids measured in plasma after intervention in $\mu\text{mol/l}$		
$\alpha$ -carotene	+	+
$\beta$ -carotene	-	+
Lycopene	-	+
Cryptoxanthin	-	+
Lutein+zeaxanthin	+	+
Folate measured in plasma after intervention in $\text{nmol/l}$	+	+
Vitamin C measured in plasma after intervention in $\mu\text{mol/l}$	-	+
Age	+	+
BMI	-	+
Gender	+	+
Smoking status	+	+

The biomarkers are used as continuous variables in the model. Carotenoids and vitamin C should be measured in  $\mu\text{mol/l}$  and folate should be measured in  $\text{nmol/l}$ . Table 2 gives possible conversion factors for carotenoids measured in  $\mu\text{g/ml}$  or folate measured in  $\mu\text{g/L}$ .

Table 2. Possible conversion factors for the biomarkers

Biomarker	Conversion	Conversion factor
$\alpha$ -carotene, $\beta$ -carotene and lycopene	from $\mu\text{g/ml}$ to $\mu\text{mol/l}$	multiply by 1.863
lutein and zeaxanthin	from $\mu\text{g/ml}$ to $\mu\text{mol/l}$	multiply by 1.758
$\beta$ -cryptoxanthin	from $\mu\text{g/ml}$ to $\mu\text{mol/l}$	multiply by 1.810
plasma/serum folate	from $\mu\text{g/L}$ to $\text{nmol/L}$	divide by 0.4415011

## How to use the function

### Load the test data

To import the test data set, run the next syntax after changing the directory to the directory where you unzipped predFV.zip:

```
test.data <- read.table(file=" C:\\\\pathname\\Testdata2.csv",
sep=",", header=TRUE)
```

### Load the function

To load the function, run the next syntax after changing the directory to the directory where you unzipped predFV.zip:

```
source("C:\\\\pathname\\predFV.R")
source("C:\\\\pathname\\print.predFV.R")
source("C:\\\\pathname\\plot.predFV.R")
source("C:\\\\pathname\\predFV.default.R")
source("C:\\\\pathname\\FVJ.R")
source("C:\\\\pathname\\FV.R")
source("C:\\\\pathname\\summary.predFV.R")
source("C:\\\\pathname\\print.summary.predFV.R")
```

### To run the function

To predict only "FVJ" (=fruit, vegetable and juice intake):

```
test <- predFV(data=test.data, AC="ACAROT2", BC="BCAROT2",
LY="LYCOP2", LZ="LUTZEAX2", CR="CRYPT2", FO="FOLATE2", VC="VITC2",
gender="GENDER", smoking="SMOKING", BMI="BMI", age="AGE",
group="INTERV", type="FVJ")
```

To display some results in a basic way

```
print(test)
```

To plot the results (plots a histogram per group of the predictions

```
plot(test)
```

To display results a little more sophisticated

```
summary(test)
```

To predict only "FV" (=fruit and vegetable intake)

```
test.1 <- predFV(data=test.data, AC="ACAROT2", BC="BCAROT2",  
LY="LYCOP2", LZ="LUTZEAX2", CR="CRYPT2", FO="FOLATE2", VC="VITC2",  
gender="GENDER", smoking="SMOKING", BMI="BMI", age="AGE",  
group="INTERV", type="FV")
```

To display some results in a basic way

```
print(test.1)
```

To plot the results (plots a histogram per group of the predictions

```
plot(test.1)
```

To display results a little more sophisticated

```
summary(test.1)
```

To predict both "FVJ" and "FV"

```
test.2 <- predFV(data=test.data, AC="ACAROT2", BC="BCAROT2",  
LY="LYCOP2", LZ="LUTZEAX2", CR="CRYPT2", FO="FOLATE2", VC="VITC2",  
gender="GENDER", smoking="SMOKING", BMI="BMI", age="AGE",  
group="INTERV", type="BOTH")
```

To display some results in a basic way

```
print(test.2)
```

To plot the results (plots a histogram per group of the predictions

```
plot(test.2)
```

To display results a little more sophisticated

```
summary(test.2)
```