

# Planning Data Analysis

**Tuan V. Nguyen**

**Professor and NHMRC Senior Research Fellow**

**Garvan Institute of Medical Research**

**University of New South Wales**

**Sydney, Australia**

# Plan of analysis

- **Checking data consistency**
- **Aims of analysis**
- **Set up tables and graphs**
- **Determine appropriate R packages**
- **Doing analysis and documentation**

# Checking data consistency

# Data integrity is VERY important

- **Data accuracy and integrity: extremely important**
- **Data preparation: 90%, analysis: 10%**

# Main Steps for Data Preparation

- **Create the data file.**
  - Original data
  - Interim data
  - Documentation
- **Clean the data**
- **Process the data**
- **Create an analysis-ready copy of the data**
- **Document the data**

# Some critical points to format your data set

- **Do not include header, trailer information, subtotals, or other extraneous information. For descriptive purposes you may include one row giving variable names.**

# Data layout

- All analysis software accept data in table format (data matrix)
  - For survey data, column usually represents single variable (a single question), row represents an individual case
  - Different processing for multiple-response questions

	Id	Age	Gender	Service	employed
Case 1	1	27	1	2	1
Case 2	2	19	2	1	2
Case 3	3	24	2	3	1

## Format data so that each variable is in its own single column

For example,

SubID	Time	Response
ADJ	1	183
ADJ	2	177
ADJ	3	192
BDR	1	186
BDR	2	183
BDR	3	169

and better not

SubID	Time 1 Response	Time 2 Response	Time 3 Response
ADJ	183	177	192
BDR	186	183	169

and absolutely not

SubID	Time	Response	SubID	Time	Response
ADJ	1	183	BDR	1	186
ADJ	2	177	BDR	2	183
ADJ	3	192	BDR	3	169

## Columns must be explicitly filled with data

SubID	Time	Response
ADJ	1	183
ADJ	2	177
ADJ	3	192
BDR	1	186
BDR	2	183
BDR	3	169

**and not**

SubID	Time	Response
ADJ	1	183
	2	177
	3	192
BDR	1	186
	2	183
	3	169

- **All columns must have the same number of rows and Missing data (empty cells) Use a blank space or a . to indicate missing data.**
  - Missing value cannot be treated as “0”.
- **Keep an identical field, such the subject ID.**

- If there are multiple data files, do not rely on the file names to carry variable information. For example, if separate files are used for the results of two treatments, include a column in each file containing the name of the treatment

*Filename: Anjou*

SubID	Time	Response	HeartRate
ADJ	1	183	120
ADJ	2	177	115
ADJ	3	192	101

*Filename: Bartlett*

SubID	Time	Response	HeartRate
BDR	1	186	112
BDR	2	183	115
BDR	3	169	135

# Not like these !

*Filename: Anjou*

Time	Response	HeartRate
1	183	120
2	177	115
3	192	101

*Filename: Bartlett*

Time	Response	HeartRate
1	186	112
2	183	115
3	169	135

## **Counted proportion data**

**If data consists of counted proportions,  
e.g. number of individuals responding out of total number  
of individuals,**

**do not reduce the data to percentages or proportions  
beforehand.**

**It is recommended that both numerator and denominator  
of the proportion be entered as separate columns.**

**For example,**

Dose	Total	Dead
1	90	5
2	85	30
3	93	60

**Not**

Dose	% Dead
1	5.5
2	35.3
3	64.5

**It is easy to compute proportions during the analysis if they are required, but alternative analyses such as logistic regression may be precluded if original counts are unavailable.**

- **Polytomous data.**

If data consists of numbers falling into a number of mutually exclusive classes, do not reduce to proportions or percentages beforehand, but enter the integer counts.

For example,

Red	White	Blue
10	25	2
5	50	1

not

Red	White	Blue
27.0	67.5	5.4
8.9	89.3	1.8

- **Each column has its own criteria or “meaning”.**

**Narrow the definition for each variable means to create a new variable.**

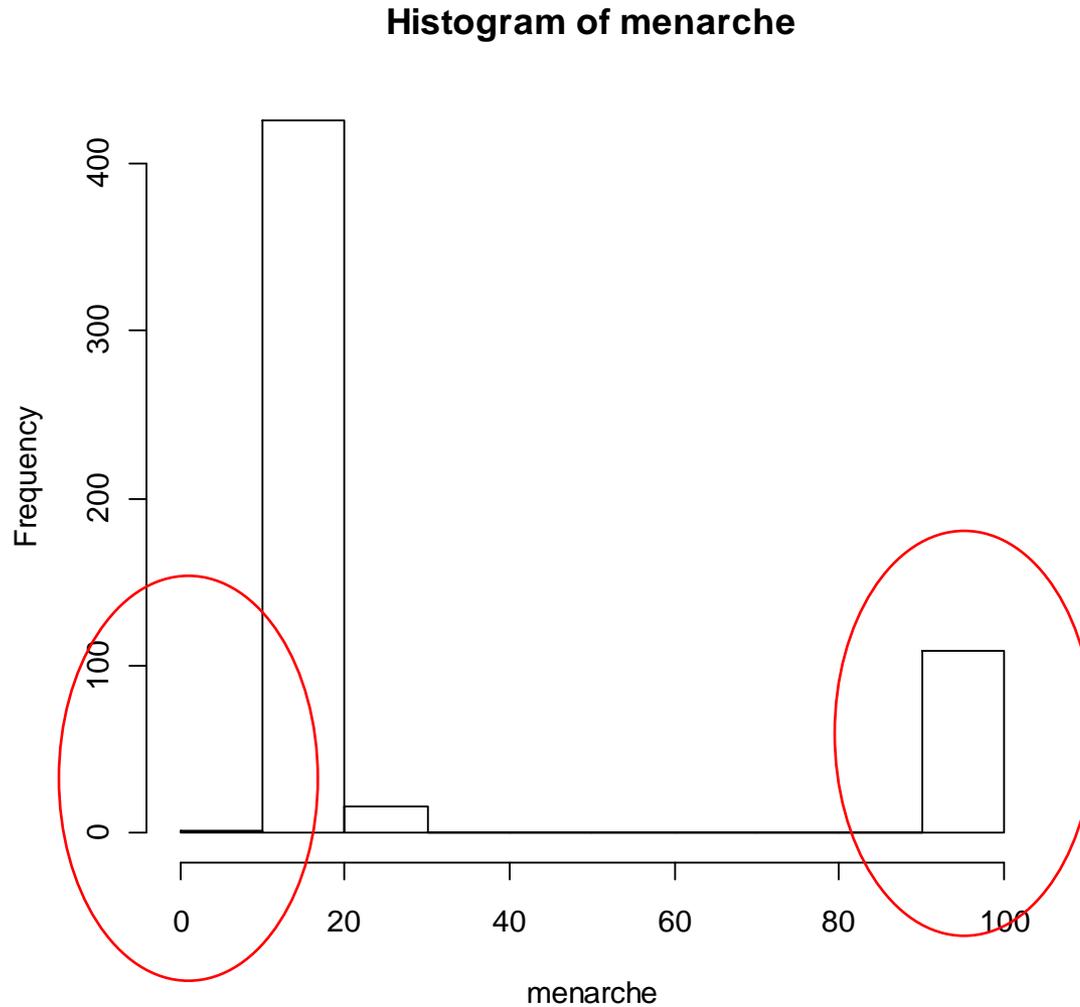
**For example,**

**gender, age → >45 year-old male**

# Checking distribution

- **Use histogram to check for distribution**
  - Are they normally distributed
- **Use scatterplot to check for abnormal data points**

# Checking for outliers



# Aims of analysis

# Common aims of data analysis

- **Determine your aims!**
  - What do you want to do ?
- **Description of single variable**
- **Comparing between groups**
- **Finding association between variables**
- **Development of predictive models**

# Descriptive analysis of single variable

- **Continuous variables**
  - Looking for distribution (`hist`, `boxplot`, `plot`)
  - Mean, SD, median, interquartile range (`psych` package: `describe`, `describe.by`)
- **Categorical variables**
  - Proportion (`table`, `gmodels`: `CrossTable`)
  - Counts
  - 95% confidence interval

# Comparison between groups

- **Continuous variables**
  - T-test, ANOVA (`t.test`, `anova`, `lm`)
- **Categorical variables**
  - Z-test, Chi-squared analysis (`Cross.Table`, `chisq.test`, `fisher.test`)
  - Binomial test (`prop.test`)

# Finding association between variables

- **Continuous variables**
  - Simple linear regression (`lm`)
  - Multiple linear regression (`lm`)
- **Categorical variables**
  - Logistic regression model (`glm`)
  - Binomial regression (`glm`)
  - Cox's proportional regression model (`survfit`, `survdiff`, `coxph`)

# An example

# Consider the vitamin D study

- **Cross-sectional study**
- **N = 558 participants, 222 men + 336 women, aged 13 – 83 yr**
- **Aims:**
  - **Prevalence of vitamin D deficiency in Vietnamese**
  - **Risk factors for vitamin D deficiency**
  - **Determinants of vitamin D**

# Variables in dataset

## Basic demographic and clinical data

- id
- sex
- dob
- address
- region
- age
- menarche
- height
- weight
- bmi
- fracture
- alcohol, coffee, tea
- season

## Biochemical and BMD data

- estradiol
- testo
- vitd
- pth
- xlap
- fnbmd
- hipbmd
- lsbmd

# Data in Excel (.csv format)

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R
1	id	sex	address	region	age	menarche	estradiol	testo	vitd	xlap	pth	height	weight	bmi	fnbmd	hipbmd	lsbmd	fracture
2	DD 002	2	DONG DA	1	30	17.00	278.30	0.519	24.43	0.293	33.73	146	38	18	0.598	0.645	0.754	2
3	DD 018	2	DONG DA	1	29	16.00	33.41	0.097	28.38		35.67	157	50	20	0.744	0.789	1.039	1
4	DD 020	1	DONG DA	1	31	16.00	34.19	9.94	23.06	0.53	19.62	160	55	21	1.075	1.04	1.016	2
5	DD 032	1	DONG DA	1	49	99.00	38.97	9.4	28.75	0.202	18.41	175	70	23	0.742	0.925	1.079	2
6	DD 035	2	DONG DA	1	60	99.00	304.89	0.033	19.41		1.20	164	63	23	0.6	0.641	0.638	2
7	DD 039	2	DONG DA	1	75	15.00	30.25	0.264	9.77		4.02	150	44	20	0.496	0.523	0.77	2
8	DD 042	2	DONG DA	1	63	15.00	20.75	0.243	39.20		24.94	155	54	22	0.669	0.737	0.88	2
9	DD 045	1	DONG DA	1	69	99.00	33.61	8.17	35.40	0.314	21.58	157	57	23	0.603	0.767	0.851	2
10	DD 046	1	DONG DA	1	71	99.00	53.73	6.5	29.10	0.41	38.41	170	64	22	0.7	0.842	0.836	1
11	DD 047	1	DONG DA	1	65	99.00	49.51	7.13	25.21	0.277	39.96	160	55	21	0.657	0.776	0.882	2
12	DD 048	1	DONG DA	1	80	99.00	45.25	3.71	34.31	0.178	57.13	159	65	26	0.718	0.929	1.214	2
13	DD 049	1	DONG DA	1	65	16.00	36.05	4.84	16.73	0.794	32.46	169	71	25	0.888	0.979	1.113	2
14	DD 050	1	DONG DA	1	65	99.00	52.59	13.85	23.43	0.747	41.30	169	71	25	0.578	0.725	0.749	2
15	DD 051	1	DONG DA	1	70	99.00	39.90	12.41	4.00	0.721	32.56	165	61	22	0.592	0.714	0.818	2
16	DD 052	1	DONG DA	1	64	16.00	42.81	10.23	23.59	0.595	35.85	163	60	23	0.694	0.853	0.97	2
17	DD 062	2	DONG DA	1	30	99.00	75.19	0.389	18.40		22.31	155	52	22	0.742	0.807	0.979	2
18	DD 080	1	DONG DA	1	35	99.00	38.97	9.4	28.75	0.202	23.62	173	56	19	1.057	0.965	1.117	2
19	DD 086	1	DONG DA	1	34	99.00	35.40	6.6	25.11	0.768	28.83	168	59	21	0.621	0.763	0.888	2
20	DD 091	1	DONG DA	1	79	17.00	38.97	7.15	23.83	0.533	50.40	160	60	23	1.002	1.125	1.478	2
21	DD 093	1	DONG DA	1	63	99.00	30.96	8.09	23.84	0.572	31.97	165	45	17	0.587	0.679	0.761	2
22	DD 094	1	DONG DA	1	77	99.00	31.90	7.91	25.34	0.674	24.34	169	55	19	0.614	0.673	0.648	2

# Plan of analysis

- Checking *data consistency*
- Checking the *distribution* of vitamin D and hormones
- *Descriptive statistics* of all variables for men and women separately

# Plan of analysis

- Define vitamin insufficiency, deficiency – call this *def*
- Find the frequency of *def* by:
  - sex, age group, urban vs rural, season
- Find risk factors for *def*
- Find the correlation between vitamin D and PTH. Is there a threshold whereby vitamin D is stable

# Statistical methods

Checking <i>data consistency</i>	Graphical analysis
Checking the <i>distribution</i> of vitamin D and hormones	Histogram
<i>Descriptive statistics</i> of all variables for men and women separately	T-test for continuous variables and z test for categorical variables
Prevalence of vit D deficiency for men and women, and various factors	Counting, Chi square test
Find risk factors for <i>def</i>	Logistic regression
Find the correlation between vitamin D and PTH. Is there a threshold whereby vitamin D is stable	Linear regression

# What we want to have ...

Table 1. Characteristics of participants

Variable	Men	Women	P-value
Age			
Height			
Weight			
BMI			
25(OH)D			
PTH			
Etc.			

# What we want to have ...

Table 2. Prevalence of vitamin D deficiency

Risk factor	N	Prevalence	95% CI
Sex Men Women			
Age <20 20-29 30-39 40-49 50-59 60+			
Season Winter Non-winter			
Residence Rural Urban			

# What we want to have ...

Table 3. Risk factors for vitamin D deficiency

Risk factor	Odds ratio	95% CI	P-value
Age			
Sex			
BMI			
Season			
Residence			
Etc.			

**Which determinants are statistically significant ?**

**How much variance of vit D deficiency can be explained by these risk factors?**

**Which one is important?**

# What we want to have ...

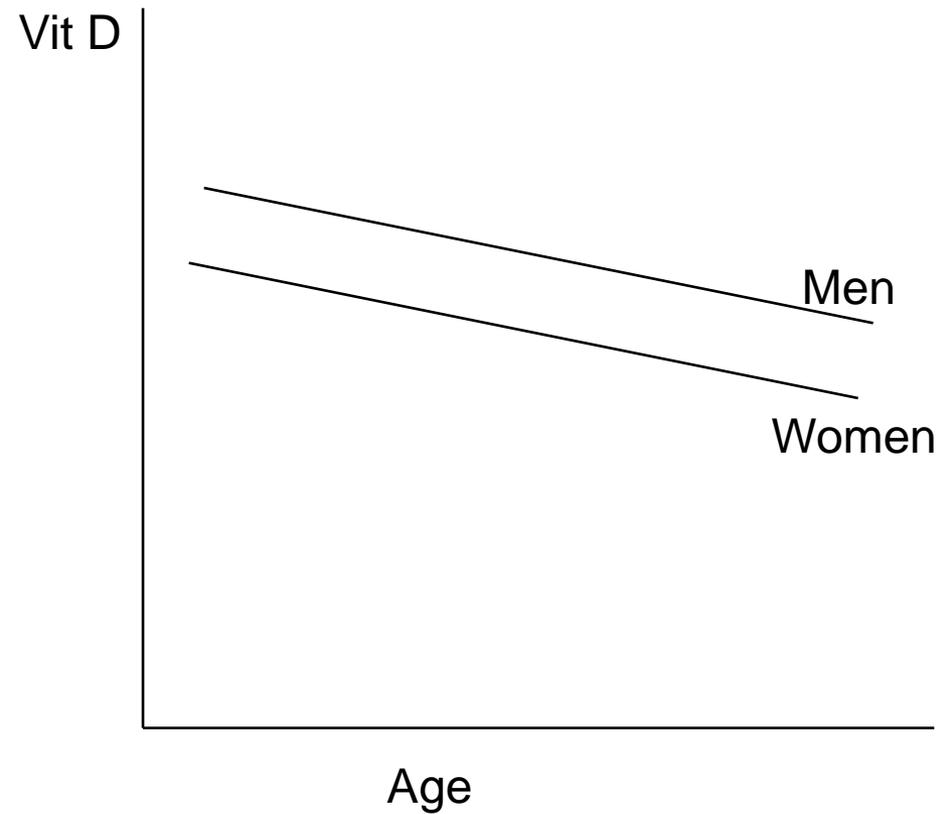
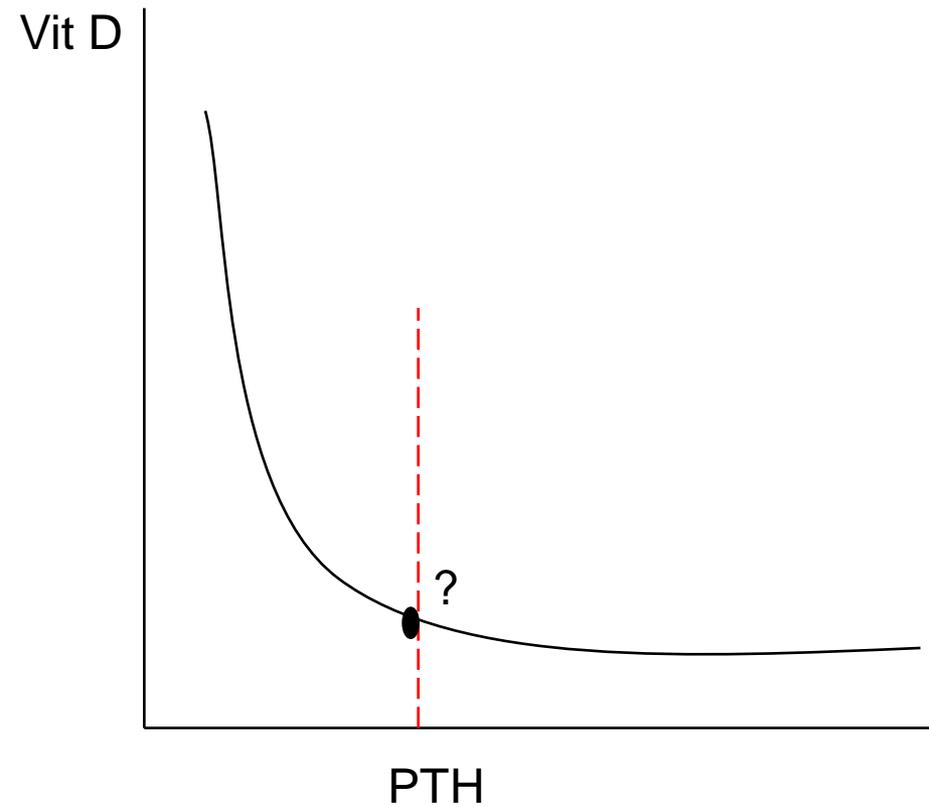
Table 4. Determinants of 25(OH) levels

Determinant	Unit	Regression coefficient	P-value
Age			
Sex			
BMI			
Season			
Residence			
Etc.			

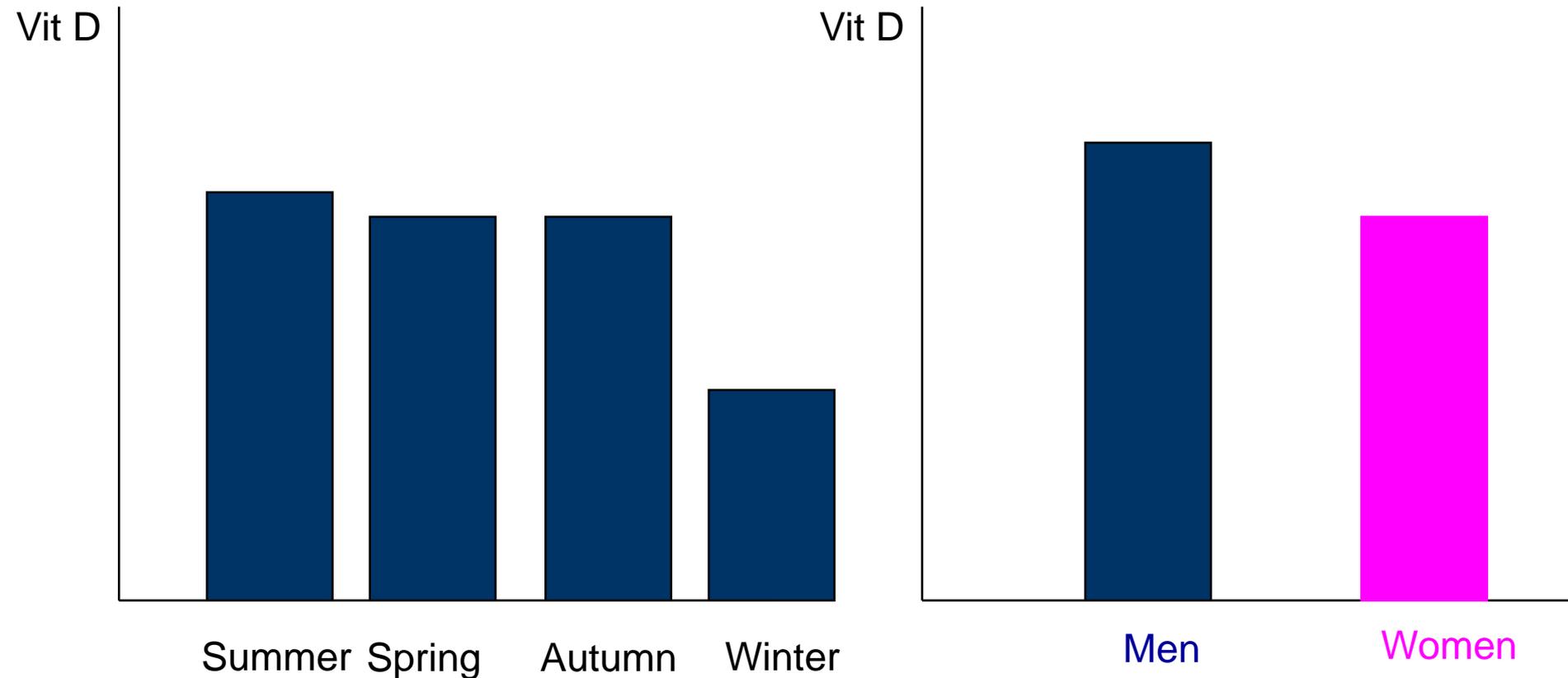
**Which determinants are statistically significant ?**

**How much variance of vit D can be explained by these determinants?**

# What we want to have ...



# What we want to have ...



# Procedures of analysis

- Arrange data in Excel
- Use R packages to analysis
  - `psych` (for descriptive analyses)
  - `rms` (for logistic regression analysis)
  - `Hmisc` (for data manipulation)
  - `xtab` (for contingency tables)

# Read-in data

```
# Tell R where the data are stored
setwd("C:/Documents and Settings/Tuan/My Documents/_Current
      Projects/_Vietnam/Huong/Vitamin D")

# Reading the data into a dataset called vd
vd = read.csv("vitaminD.csv", header=T, na.strings=" ")

# What variables are in vd
names(vd)

# Tell R that we will work on vd from now on
attach(vd)
```

# Checking data consistency

```
# Let's get some basic statistics for all variables
```

```
# First, we load the package psych
```

```
library(psych)
```

```
# then get statistics
```

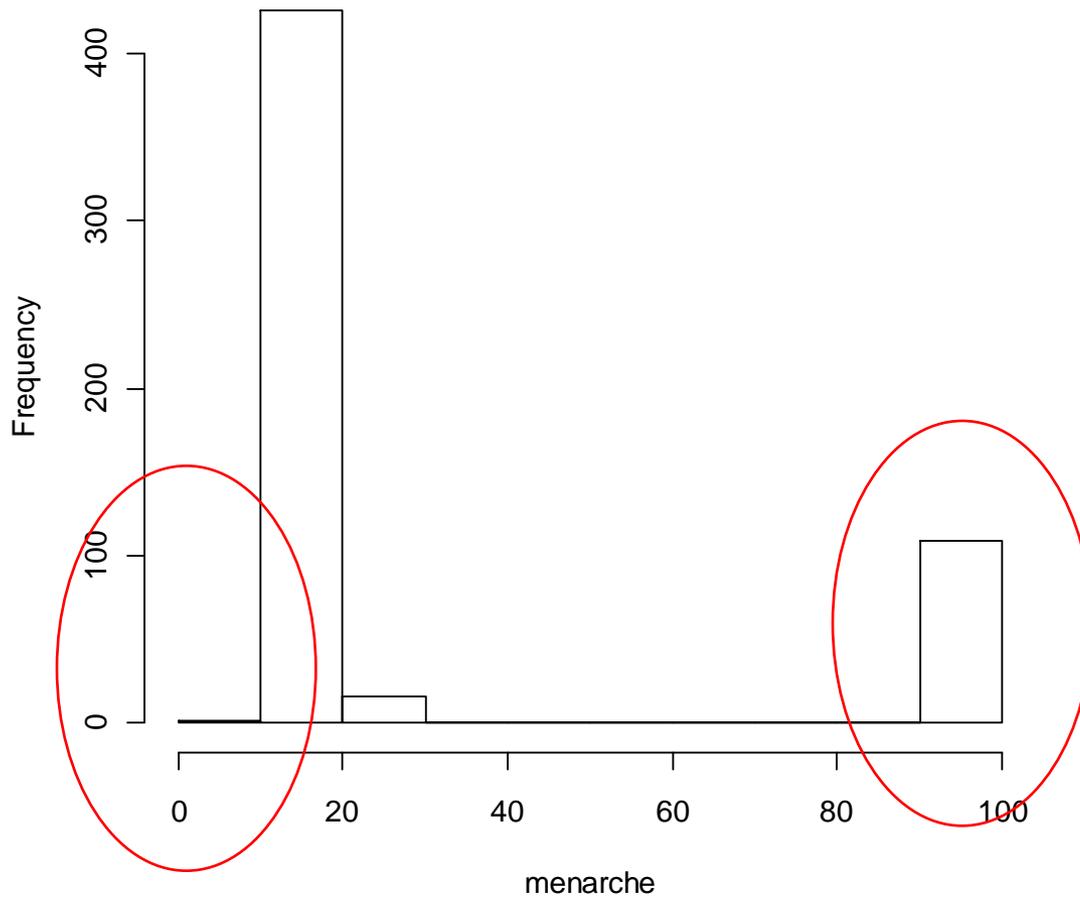
```
describe(vd)
```

```
> describe(vd, skew=FALSE)
```

	var	n	mean	sd	median	trimmed	mad	min	max	range	se
id*	1	558	278.37	159.85	279.50	278.58	204.60	1.00	554.00	553.00	6.77
sex	2	558	1.60	0.49	2.00	1.63	0.00	1.00	2.00	1.00	0.02
address*	3	558	4.65	2.17	4.50	4.68	3.71	1.00	8.00	7.00	0.09
region	4	558	2.60	1.30	2.50	2.63	2.22	1.00	4.00	3.00	0.05
age	5	558	46.63	17.79	49.00	46.82	20.76	13.00	83.00	70.00	0.75
menarche	6	552	32.61	33.04	17.00	26.84	2.97	0.00	99.00	99.00	1.41
estradiol	7	558	67.57	74.74	41.35	51.03	25.69	5.00	476.10	471.10	3.16
testo	8	558	2.67	3.26	0.50	2.19	0.68	0.02	13.85	13.83	0.14
vitd	9	558	25.69	8.62	25.83	25.64	7.31	4.00	59.87	55.87	0.36
xlap	10	244	0.39	0.27	0.31	0.35	0.21	0.02	1.57	1.55	0.02
pth	11	558	30.62	12.65	29.04	29.52	11.79	1.20	93.53	92.33	0.54
height	12	558	157.71	7.92	157.00	157.60	7.41	134.00	181.00	47.00	0.34
weight	13	558	50.70	8.08	50.00	50.23	7.41	32.00	85.00	53.00	0.34
bmi	14	558	20.33	2.63	20.00	20.18	2.97	14.00	31.00	17.00	0.11
fnbmd	15	558	0.72	0.12	0.71	0.72	0.12	0.39	1.11	0.72	0.01
hipbmd	16	558	0.81	0.12	0.81	0.81	0.11	0.29	1.17	0.88	0.01
lsbmd	17	554	0.86	0.15	0.87	0.86	0.15	0.42	1.48	1.05	0.01
fracture	18	558	4.90	16.70	2.00	2.00	0.00	1.00	99.00	98.00	0.71
alcohol	19	557	2.63	9.19	2.00	1.82	0.00	1.00	99.00	98.00	0.39
coffee	20	552	1.87	0.34	2.00	1.96	0.00	1.00	2.00	1.00	0.01
tea	21	552	1.61	0.49	2.00	1.64	0.00	1.00	2.00	1.00	0.02
ruralurban	22	558	1.69	0.46	2.00	1.74	0.00	1.00	2.00	1.00	0.02
location	23	558	0.31	0.46	0.00	0.26	0.00	0.00	1.00	1.00	0.02
season	24	558	2.18	0.81	2.00	2.22	1.48	1.00	3.00	2.00	0.03

```
> hist(menarche)
```

Histogram of menarche



# Descriptive analysis by sex

```
describe.by (vd, sex, skew=F, interp=FALSE)
```

group: 1

	var	n	mean	sd	median	trimmed	mad	min	max	range	se
id*	1	222	296.79	166.79	302.50	301.37	197.19	3.00	554.00	551.00	11.19
sex	2	222	1.00	0.00	1.00	1.00	0.00	1.00	1.00	0.00	0.00
address*	3	222	4.85	2.06	5.00	4.94	2.97	2.00	7.00	5.00	0.14
region	4	222	2.72	1.25	3.00	2.77	1.48	1.00	4.00	3.00	0.08
age	5	222	46.67	19.30	49.00	46.57	25.20	14.00	83.00	69.00	1.30
menarche	6	220	53.99	40.85	20.00	53.31	7.41	12.00	99.00	87.00	2.75
estradiol	7	222	42.76	12.46	41.33	42.19	10.90	8.95	92.33	83.38	0.84
testo	8	222	6.24	2.25	6.05	6.16	2.16	0.84	13.85	13.01	0.15
vitd	9	222	28.57	8.94	28.29	28.45	8.46	4.00	59.87	55.87	0.60
xlap	10	100	0.45	0.31	0.35	0.41	0.26	0.02	1.57	1.55	0.03
pth	11	222	31.76	13.50	29.69	30.29	12.34	8.63	93.53	84.90	0.91
height	12	222	164.20	6.03	164.00	164.07	5.93	148.00	181.00	33.00	0.40
weight	13	222	54.46	8.44	53.00	54.06	7.41	35.00	85.00	50.00	0.57
bmi	14	222	20.13	2.72	20.00	19.96	2.97	15.00	31.00	16.00	0.18
fnbmd	15	222	0.76	0.12	0.76	0.75	0.12	0.39	1.11	0.72	0.01
hipbmd	16	222	0.85	0.12	0.84	0.85	0.12	0.29	1.17	0.88	0.01
lsbmd	17	220	0.90	0.14	0.91	0.90	0.14	0.53	1.48	0.94	0.01
fracture	18	222	4.14	14.43	2.00	2.00	0.00	1.00	99.00	98.00	0.97
alcohol	19	222	1.88	6.57	1.00	1.43	0.00	1.00	99.00	98.00	0.44
coffee	20	221	1.79	0.41	2.00	1.86	0.00	1.00	2.00	1.00	0.03

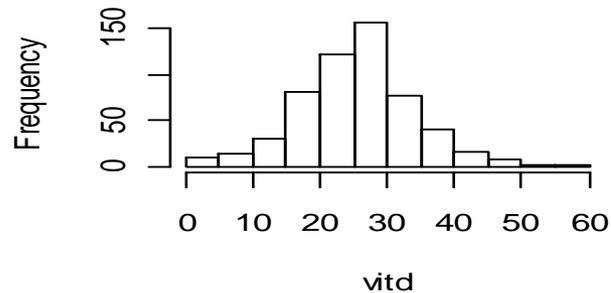
group: 2

	var	n	mean	sd	median	trimmed	mad	min	max	range	se
id*	1	336	266.19	154.14	266.00	264.52	202.37	1.00	551.00	550.00	8.41
sex	2	336	2.00	0.00	2.00	2.00	0.00	2.00	2.00	0.00	0.00
address*	3	336	4.51	2.23	4.00	4.51	2.97	1.00	8.00	7.00	0.12
region	4	336	2.53	1.33	2.00	2.53	1.48	1.00	4.00	3.00	0.07
age	5	336	46.60	16.74	49.00	47.04	19.27	13.00	82.00	69.00	0.91
menarche	6	332	18.44	14.42	16.00	16.00	2.97	0.00	99.00	99.00	0.79
estradiol	7	336	83.96	92.24	41.74	65.28	36.46	5.00	476.10	471.10	5.03
testo	8	336	0.32	0.59	0.20	0.23	0.19	0.02	7.91	7.89	0.03
vitd	9	336	23.79	7.86	24.26	23.93	7.10	4.00	59.60	55.60	0.43
xlap	10	144	0.34	0.24	0.28	0.31	0.19	0.06	1.26	1.20	0.02
pth	11	336	29.87	12.03	28.56	29.03	11.32	1.20	92.87	91.67	0.66
height	12	336	153.42	5.82	154.00	153.53	5.93	134.00	168.00	34.00	0.32
weight	13	336	48.21	6.78	48.00	47.94	7.41	32.00	74.00	42.00	0.37
bmi	14	336	20.46	2.56	20.00	20.33	2.97	14.00	30.00	16.00	0.14
fnbmd	15	336	0.70	0.11	0.69	0.70	0.12	0.39	1.00	0.60	0.01
hipbmd	16	336	0.78	0.12	0.79	0.78	0.11	0.48	1.10	0.62	0.01
lsbmd	17	334	0.83	0.15	0.85	0.84	0.16	0.42	1.22	0.80	0.01
fracture	18	336	5.40	18.04	2.00	2.00	0.00	1.00	99.00	98.00	0.98
alcohol	19	335	3.12	10.56	2.00	2.00	0.00	1.00	99.00	98.00	0.58
coffee	20	331	1.92	0.28	2.00	2.00	0.00	1.00	2.00	1.00	0.02
tea	21	331	1.80	0.40	2.00	1.87	0.00	1.00	2.00	1.00	0.02
ruralurban	22	336	1.65	0.48	2.00	1.69	0.00	1.00	2.00	1.00	0.03
location	23	336	0.35	0.48	0.00	0.31	0.00	0.00	1.00	1.00	0.03
season	24	336	2.16	0.85	2.00	2.20	1.48	1.00	3.00	2.00	0.05

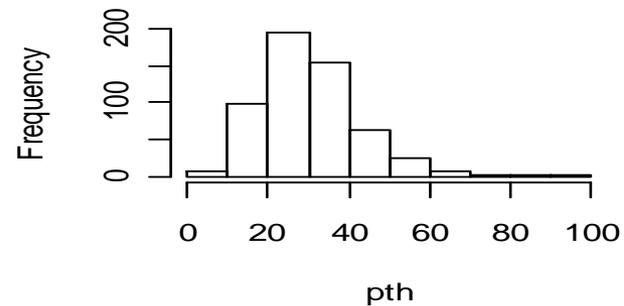
# Distribution of some continuous data

```
par(mfrow=c(2,2))  
hist(vitd); hist(pth); hist(bmi); hist(age)
```

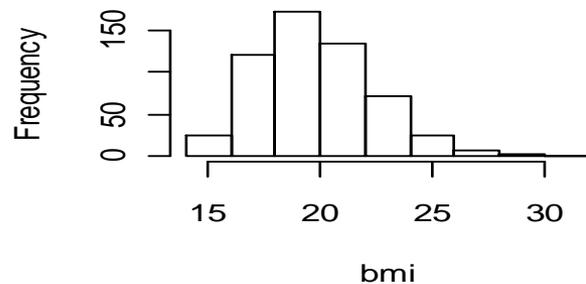
**Histogram of vitd**



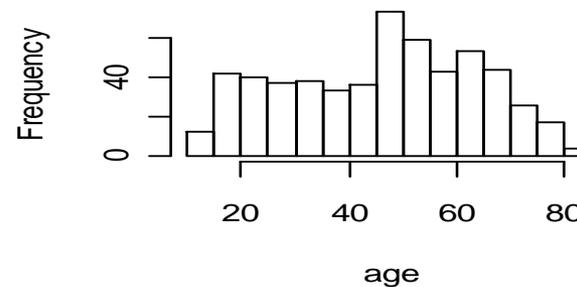
**Histogram of pth**



**Histogram of bmi**



**Histogram of age**



# Defining vitamin D insufficiency

```
library(Hmisc)
insuff = cut2(vitd, 30)

def = vitd
def = replace(def, vitd < 20.0, 1)
def = replace(def, vitd >= 20, 0)

library(gmodels)
CrossTable(def, sex, digits=3, chisq=T, fisher=T)
CrossTable(def, season, digits=3, chisq=T, fisher=T)
CrossTable(def, location, digits=3, chisq=T, fisher=T)
```

# Vitamin deficiency by sex

Total Observations in Table: 558

sex	def		Row Total
	0	1	
1	187	35	222
	1.988	6.290	
	0.842	0.158	0.398
	0.441	0.261	
	0.335	0.063	
2	237	99	336
	1.313	4.156	
	0.705	0.295	0.602
	0.559	0.739	
	0.425	0.177	
Column Total	424	134	558
	0.760	0.240	

# Vitamin deficiency by sex: test

Statistics for All Table Factors

Pearson's Chi-squared test

-----  
Chi<sup>2</sup> = 13.74685      d.f. = 1      p = 0.0002091717

Pearson's Chi-squared test with Yates' continuity correction

-----  
Chi<sup>2</sup> = 13.00639      d.f. = 1      p = 0.0003104303

Fisher's Exact Test for Count Data

-----  
Sample estimate odds ratio: 2.22876

Alternative hypothesis: true odds ratio is not equal to 1

p = 0.0001784270

95% confidence interval: 1.427180 3.540137

# Vitamin deficiency by season

season	def		Row Total
	0	1	
1	77	64	141
	8.479	26.828	
	0.546	0.454	0.253
	0.182	0.478	
	0.138	0.115	
2	147	30	177
	1.163	3.679	
	0.831	0.169	0.317
	0.347	0.224	
	0.263	0.054	
3	200	40	240
	1.705	5.396	
	0.833	0.167	0.430
	0.472	0.299	
	0.358	0.072	
Column Total	424	134	558
	0.760	0.240	

# Risk factors for vitamin D deficiency: univariate analysis

```
library(epicalc)
```

```
logistic.display(glm(def ~ sex, family=binomial))
```

```
logistic.display(glm(def ~ location, family=binomial))
```

	OR (95%CI)	P (Wald's test)	P (LR-test)
<b>sex (cont. var.)</b>	<b>2.23 (1.45,3.43)</b>	<b>&lt; 0.001</b>	<b>&lt; 0.001</b>

Log-likelihood = -300.4421

No. of observations = 558

AIC value = 604.8842

	OR (95%CI)	P (Wald's test)	P (LR-test)
<b>location: 1 vs 0</b>	<b>3.71 (2.47,5.58)</b>	<b>&lt; 0.001</b>	<b>&lt; 0.001</b>

Log-likelihood = -287.407

No. of observations = 558

AIC value = 578.8139

# Risk factors for vitamin D deficiency: univariate analysis

```
logistic.display(glm(def ~ bmi, family=binomial))
```

```
logistic.display(glm(def ~ factor(season), family=binomial))
```

	OR (95%CI)	P (Wald's test)	P (LR-test)
<b>bmi (cont. var.)</b>	<b>1.05 (0.98,1.13)</b>	<b>0.174</b>	<b>0.176</b>
Log-likelihood = -306.6787			
No. of observations = 558			
AIC value = 617.3574			

	OR	lower95ci	upper95ci	Pr (> Z )
<b>factor(season)2</b>	<b>0.2455357</b>	<b>0.1468710</b>	<b>0.4104812</b>	<b>8.506640e-08</b>
<b>factor(season)3</b>	<b>0.2406250</b>	<b>0.1497158</b>	<b>0.3867354</b>	<b>4.002872e-09</b>

# Risk factors for vitamin D deficiency: multivariable analysis

```
logistic.display(glm(def ~ age+sex+bmi+location+factor(season),  
family=binomial))
```

	OR	lower95ci	upper95ci	Pr (> Z )
<b>age</b>	0.9821236	0.9698786	0.9945232	<b>0.004833844</b>
<b>sex</b>	1.9543516	1.2394551	3.0815883	<b>0.003927809</b>
<b>bmi</b>	0.9878399	0.9038924	1.0795839	0.787155190
<b>location</b>	2.4925512	0.9452428	6.5727150	<b>0.064872828</b>
<b>factor (season) 2</b>	0.5482407	0.2237126	1.3435448	0.188766835
<b>factor (season) 3</b>	0.5817646	0.1990562	1.7002735	0.322202383

# Risk factors for vitamin D deficiency: binomial regression

```
library(MASS)
summary(glm.nb(def ~ age+sex+location, data=vd))
```

## Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-2.060883	0.411777	-5.005	5.59e-07	***
age	-0.013404	0.004877	-2.748	0.0060	**
sex	0.503312	0.198337	2.538	0.0112	*
location	0.938540	0.175347	5.352	8.68e-08	***

# Determinants of vitamin D: multivariable analysis

```
library(leaps)
library(car)
library(MASS)
library(relaimpo)
# stepwise regression
fit = lm(vitd~age+bmi+sex+factor(season), data=vd)
step = stepAIC(fit, direction="both")
step$anova

# All Subsets Regression
fit2 = regsubsets(vitd~age+bmi+sex+factor(season), data=vd, nbest=5)
summary(fit2)
plot(fit2, scale="r2")
subsets(fit2, statistic="rsq")
```

# Determinants of vitamin D : multivariable analysis

```
# Calculate Relative Importance for Each Predictor
```

```
library(relaimpo)
```

```
fit = lm(vitd~age+bmi+sex+factor(season), data=vd)
```

```
calc.relimp(fit, rela=TRUE)
```

```
# Bootstrap Measures of Relative Importance (1000  
samples)
```

```
library(boot)
```

```
boot = boot.relimp(fit, b = 1000), rank = TRUE,  
diff=TRUE, rela=TRUE)
```

```
booteval.relimp(boot)
```

```
# print result
```

```
plot(booteval.relimp(boot, sort=TRUE)) # plot result
```

Relative importance metrics:

	lmg
factor(season)	0.48695621
age	0.06065485
bmi	0.02030591
sex	0.43208303

Average coefficients for different model sizes:

	1group	2groups	3groups	4groups
age	0.04504289	0.05004166	0.04961454	0.04470275
bmi	-0.23392346	-0.14266033	-0.05454423	0.03080951
sex	-4.77558719	-4.61454708	-4.46527769	-4.34587273
`factor(season)`2	5.45826902	5.18184506	4.86820278	4.52678038
`factor(season)`3	5.93707270	5.90083953	5.81691391	5.69611558

# Determinants of vitamin D: stepwise regression

```
> fit = lm(vitd~age+bmi+sex+factor(season), data=vd)
> step = stepAIC(fit, direction="both")
```

Start: AIC=2322.88

```
vitd ~ age + bmi + sex + factor(season)
```

	Df	Sum of Sq	RSS	AIC
- bmi	1	3	35095	2321
<none>			35092	2323
- age	1	324	35416	2326
- sex	1	2425	37517	2358
- factor(season)	2	2616	37708	2359

Step: AIC=2320.93

```
vitd ~ age + sex + factor(season)
```

	Df	Sum of Sq	RSS	AIC
<none>			35095	2321
+ bmi	1	3	35092	2323
- age	1	371	35466	2325
- sex	1	2422	37517	2356
- factor(season)	2	2895	37989	2361

# Determinants of vitamin D: stepwise regression

```
> step$anova  
Stepwise Model Path  
Analysis of Deviance Table
```

Initial Model:

```
vitd ~ age + bmi + sex + factor(season)
```

Final Model:

```
vitd ~ age + sex + factor(season)
```

	Step	Df	Deviance	Resid. Df	Resid. Dev	AIC
	1			552	35091.86	2322.882
	2 - bmi	1	2.975332	553	35094.83	2320.929

# Determinants of vitamin D: “final model”

```
fit = lm(vitd ~ age+sex+factor(season), data=vd)
summary(fit)
```

## Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	26.66091	1.64606	16.197	< 2e-16	***
age	0.04591	0.01899	2.418	0.0159	*
sex	-4.33997	0.70246	-6.178	1.26e-09	***
factor(season)2	4.47858	0.91536	4.893	1.31e-06	***
factor(season)3	5.62941	0.84679	6.648	7.14e-11	***

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

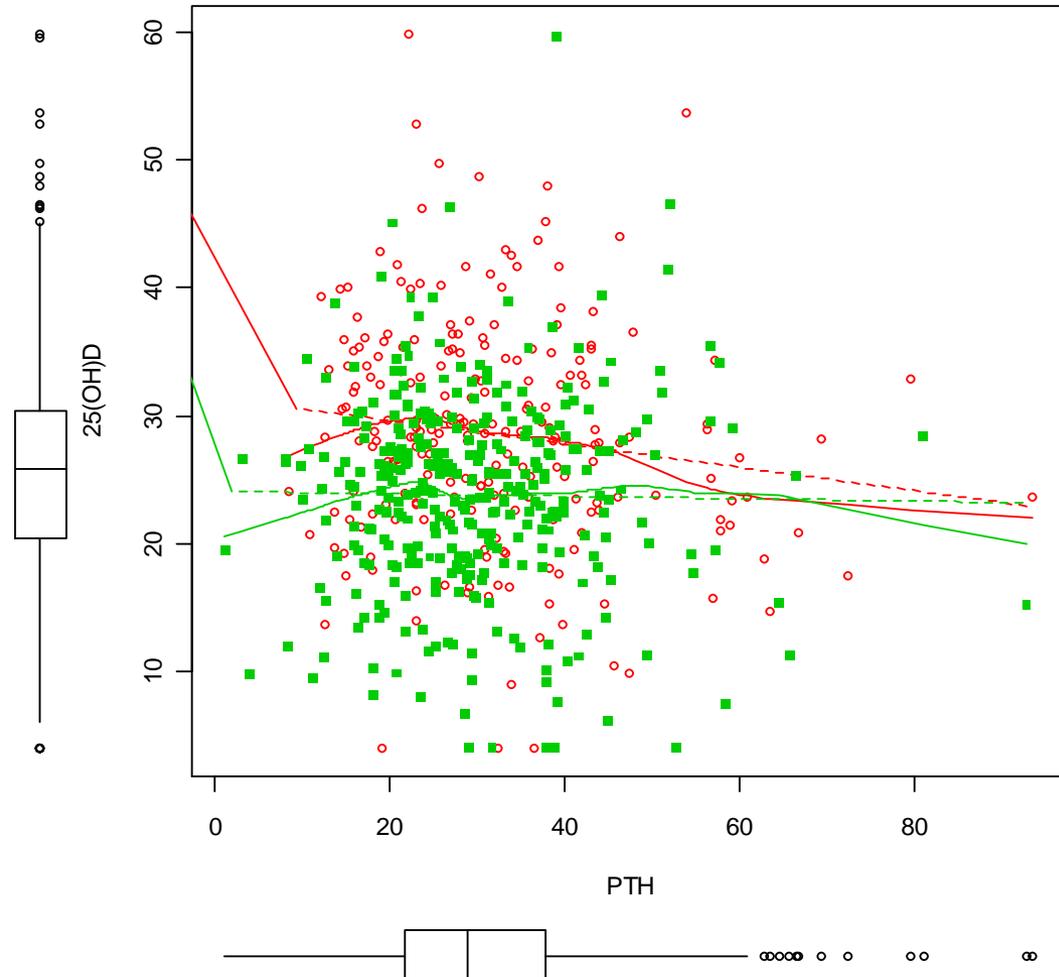
Residual standard error: 7.966 on 553 degrees of freedom

Multiple R-squared: 0.1521, Adjusted R-squared: 0.146

F-statistic: 24.81 on 4 and 553 DF, p-value: < 2.2e-16

# Relationship between vitamin D and PTH

```
library(car)
scatterplot(vitd ~ pth | sex, pch=c(1, 15),
           xlab="PTH", ylab="25(OH)D")
```



# Relationship between vitamin D and PTH

```
> fit = lm(vitd ~ pth, data=vd)
> summary(fit)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	26.70950	0.95613	27.935	<2e-16	***
pth	-0.03329	0.02886	-1.153	0.249	

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.618 on 556 degrees of freedom

Multiple R-squared: 0.002387, Adjusted R-squared: 0.0005927

F-statistic: 1.33 on 1 and 556 DF, p-value: 0.2492

# Relationship between vitamin D and PTH

```
> fit = lm(vitd ~ pth+sex+pth:sex, data=vd)
> summary(fit)
```

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	38.82787	3.09515	12.545	< 2e-16	***
pth	-0.17214	0.09074	-1.897	0.0583	.
sex	-7.36461	1.86973	-3.939	9.23e-05	***
pth:sex	0.08091	0.05586	1.448	0.1481	

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

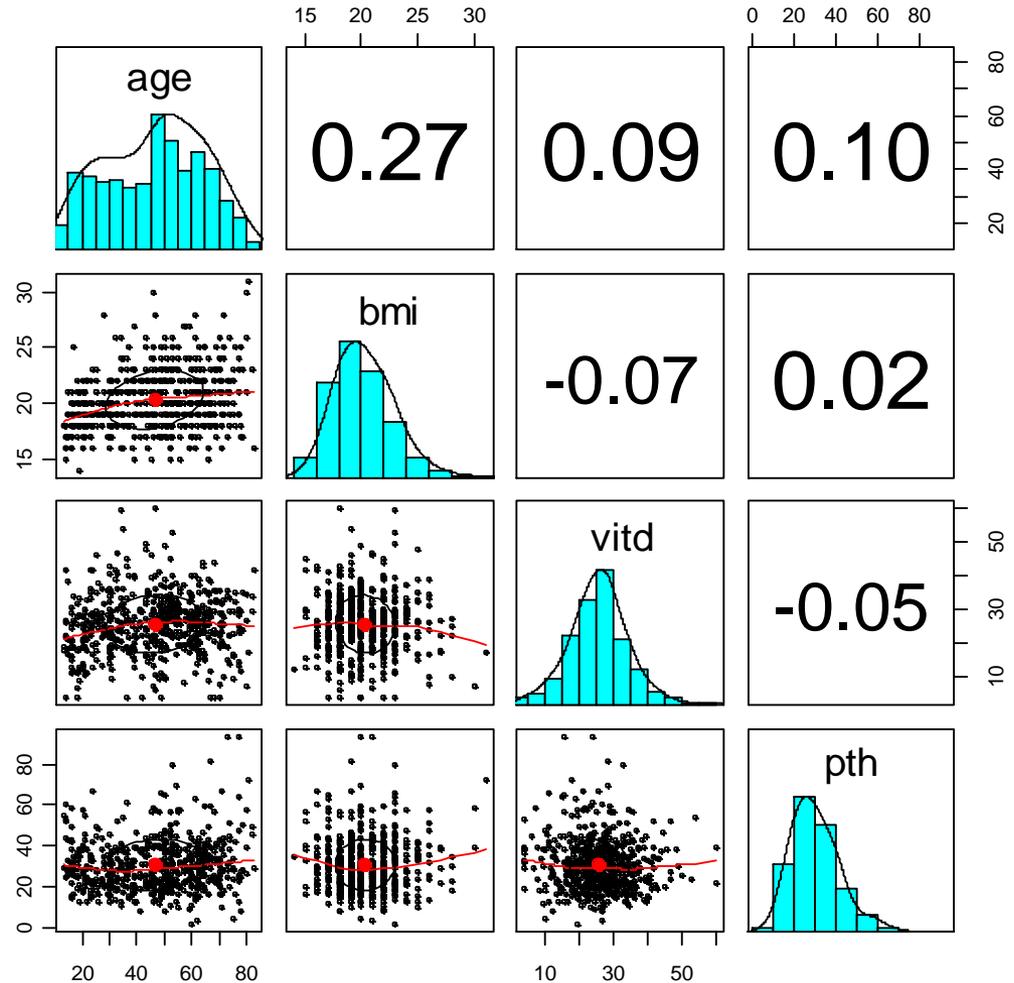
Residual standard error: 8.282 on 554 degrees of freedom

Multiple R-squared: 0.08187, Adjusted R-squared: 0.0769

F-statistic: 16.47 on 3 and 554 DF, p-value: 2.907e-10

# Let's have an overall picture

```
library(psych)  
dd = cbind(age, bmi, vitd, pth)  
pairs.panels(dd)
```



# Error plot

```
error.bars.by(vitd, sex, bars=TRUE, labels=c("Men",  
"Women"), ylab = "25(OH)D", xlab=" ", ylim=c(0,30))
```

