

SIRE516

Basic data analyses

Disclaimer

- This is not a statistics class so I will not cover all statistical aspects behind each analysis.
- I will cover regularly used analyses.
- However, I can provide detailed explanations if time permits.

Exploratory data analysis

Understanding your data

- Before any analysis
 - Read the data dictionary
 - Consult the source (e.g. 'wet lab' people, physicians)
- Type of data
 - Transformation?
 - Type of test and analysis?

Understanding your data

- General data types
 - Categorical
 - Nominal
 - Ordinal
 - Numerical
 - Arbitrary (uniform distribution?)
 - Normal distribution
 - Other: Binomial, Poisson, Beta, etc

Histogram

```
1  ###Histogram
2  library(MASS)
3  ?iris
4
5  #Which parameter is normally distributed?
6  truehist(iris$Sepal.Length)
7  truehist(iris$Sepal.Width)
8  truehist(iris$Petal.Length)
9  truehist(iris$Petal.Width)
```

```
10
```

Quantile-Quantile plot

```
11 ▾ ##### Q-Q plot #####  
12 library(car)  
13  
14 #Which parameter is normally distributed?  
15 qqPlot(iris$Sepal.Length)  
16 qqPlot(iris$Sepal.Width)  
17 qqPlot(iris$Petal.Length)  
18 qqPlot(iris$Petal.Width)
```

Test of normality

```
20 ##### Test of Normality
21
22 #Which parameter is normally distributed?
23 shapiro.test(iris$Sepal.Length)
24 shapiro.test(iris$Sepal.Width)
25 shapiro.test(iris$Petal.Length)
26 shapiro.test(iris$Petal.Width)
```


What to do if your data is not normally distributed?

- Transformation
 - Log10: Viral load
- Non-parametric analyses
 - No transformation
 - Arbitrary values

```
28 ▾ ##### Data transformation #####
29 dat <- rnorm(100,mean = 5,sd = 2) # Generate 100 numbers with mean = 5 and sd = 2 (Normal distribution)
30 truehist(dat)
31
32 expdat <- exp(dat) #e^x ~ 2.718282^x
33 truehist(expdat)
34
35 shapiro.test(dat)
36 shapiro.test(expdat)
37
38 tdat <- log10(expdat + 1) # + 1 is important because log10(0) is undefined!
39 truehist(tdat)
40 shapiro.test(tdat)
41
```

How to present values summarizing your data

- Categorical
 - Count (Percent of count of all category)

```
42 ▾ ##### Summarize categorical value #####  
43 rows <- sample(nrow(iris),91, replace = F) # Sample 91 rows from the iris dataset  
44 IR <- iris[rows,]  
45  
46 tb <- table(IR$Species)  
47 print(tb)  
48  
49 percent <- round(100 * tb/nrow(IR),1)  
50 print(percent)  
51  
52 paste0(tb," (",percent,")")
```

How to present values summarizing your data

- Numerical
 - Mean \pm Standard deviation
 - Normal distribution only

```
54 ##### Summarize numerical value (Mean SD) #####
55 m <- round(mean(IR$Sepal.Length),1)
56 s <- round(sd(IR$Sepal.Length),1)
57 paste0(m, "  $\pm$  ", s)
58
59 lm <- round(mean(exp(IR$Sepal.Length)),1)
60 ls <- round(sd(exp(IR$Sepal.Length)),1)
61 paste0(lm, "  $\pm$  ", ls) # SD >= mean implying deviation from normal distribution
62
63 llm <- round(mean(log10(1+ exp(IR$Sepal.Length))),1)
64 lls <- round(sd(log10(1+exp(IR$Sepal.Length))),1)
65 paste0(llm, "  $\pm$  ", lls)
```

How to present values summarizing your data

- Numerical
 - Median (Interquartile range, IQR, Q25 to Q75)
 - Median (Range, Min to Max)
 - Almost always suitable for numerical data

```
67 - #### Summarize numerical value (Median) ####
68 q <- round(quantile(IR$Sepal.Length,c(0.5,0.25,0.75)),1)
69 paste0(q[1]," (",q[2],"-",q[3],")")
70 paste0(median(IR$Sepal.Length)," (",min(IR$Sepal.Length),"-",max(IR$Sepal.Length),")")
71
72 lq <- round(quantile(exp(IR$Sepal.Length),c(0.5,0.25,0.75)),1)
73 paste0(lq[1]," (",lq[2],"-",lq[3],")")
74 paste0(round(median(exp(IR$Sepal.Length)),1)," (",round(min(exp(IR$Sepal.Length)),1),
75         "- ",round(max(exp(IR$Sepal.Length)),1),")")
```

Practical 1

Practical 1

- We will create a “baseline” characteristic table of the IRIS data set
- The table will contain four columns one for variable and three for each species
- The first row will be count (%) for each species

```
1 ?iris
2 summary(iris)
3 |
```

Hypothesis testing

Why?

- We cannot measure or test all existing data.
- We measure and test a small part (i.e. sample) of the data (i.e. population).
- How can we be sure the small part represents all the data?
 - Sample size → Type 1 & 2 errors
 - Hypothesis testing → Type 1 errors
- We **reject** a “Null” hypothesis
 - Sufficient evidence

Table of error types		Null hypothesis (H_0) is	
		True	False
Decision about null hypothesis (H_0)	Don't reject	Correct inference (true negative) (probability = $1-\alpha$)	Type II error (false negative) (probability = β)
	Reject	Type I error (false positive) (probability = α)	Correct inference (true positive) (probability = $1-\beta$)

One-sample testing

- Population mean or proportion was previously estimated
- We test whether the value found in our sample agrees with these values

One-sample test of proportion

- Example: Flipping a normal coin would result in a head in 50% of the trials
- You flip your coin 100 times and get a head 71 times. Is your coin normal or loaded?

```
77 ~ #### One-sample proportion test ####  
78 binom.test(x = 71, n = 100, p = 0.5) # Exact test  
79  
80 prop.test(x = 71, n = 100, p = 0.5) # Estimation  
81
```

One-sample test of mean

- Example: A survey in 2000 found that Thai male first graders had a mean height of 105 cm with a standard deviation of 5 cm.
- You conduct a similar survey in 100 first graders and found that the mean height is now 107 cm with the same standard deviation. Are the male first graders getting taller?

```
82 ▾ ##### One-sample mean test #####
83 dat <- round(rnorm(n = 100, mean = 107, sd = 5),1) # Simulate the survey data
84 truehist(dat)
85
86 t.test(dat, mu = 105) # Parametric test
87 wilcox.test(dat, mu = 105) # Non-parametric test
88
89 dat2 <- round(runif(n = 100, min = 92, max = 122 ),1) # Simulate the survey data. Not normal distribution
90 truehist(dat2)
91 mean(dat2)
92
93 t.test(dat2, mu = 105) # Parametric test
94 wilcox.test(dat2, mu = 105) # Non-parametric test
```

Test difference in proportions

- Example: Proportion of patients with cancer for two populations
- `chisq.test()` and `prop.test()` for large samples (require different inputs)
- Exact test for smaller samples → We will focus on this test in Categorical data analysis

```
96 ##### Difference in proportions #####
97 smoke <- 510
98 smoke_CA <- 400
99 non_smoke <- 540
100 non_smoke_CA <- 300
101
102 smoke_not_CA <- smoke - smoke_CA
103 non_smoke_not_CA <- non_smoke - non_smoke_CA
104
105 prop.test(x = c(non_smoke_CA, smoke_CA), n = c(non_smoke, smoke))
106
107 m <- matrix(data = c(non_smoke_CA, non_smoke_not_CA, smoke_CA, smoke_not_CA) , nrow = 2)
108 print(m)
109
110 chisq.test(m)
111 fisher.test(m)
```

Test difference in means

- Example: Heights between male and female first graders.
- Parametric test: `t.test`
- Non-parametric test: `wilcox.test`

```
112 ▾ #### Difference in means ####  
113 male <- round(rnorm(n = 100 ,mean = 107, sd = 5),1)  
114 female <- round(rnorm(n = 100, mean = 105, sd = 4.5),1)  
115  
116 truehist(male)  
117 truehist(female)  
118  
119 t.test(male,female, var.equal = F, paired = F)  
120 wilcox.test(male,female, paired = F)  
121  
122 #paired = T for dependent samples (e.g. Before-After measurements)  
...
```

Practical 2

Practical 2

- We will perform hypothesis testing with the “Melanoma” dataset.
- We will compare between males and females for any difference in each parameter
- For ‘status’, regroup to 1 vs 2+3

```
1 library(MASS)
2
3 ?Melanoma
4
5 female <- Melanoma[which(Melanoma$sex == 0),]
6 male   <- Melanoma[which(Melanoma$sex == 1),]
```

Categorical Data Analysis

Contingency table

- Help/visualize for categorical data analysis
- Example:

	Cancer (Case)	No cancer (Control)
Smoker	400	150
Non smoker	100	320
TOTAL	500	470

Contingency table

- Create a table from counts

```
124 ▾ ##### Contingency table from counts #####
125 ctable <- matrix(c(400,150,100,320), nrow = 2 , byrow = T) # Matrix fill data by column by default
126 dimnames(ctable) <- list(c("Smoker","Non-smoker"),c("Cancer","No cancer"))
127 print(ctable)
128
129 matrix(c(400,150,100,320), nrow = 2)
```

Contingency table

- Create a table from raw data

```
131 - #### Contingency table from raw data ####
132
133 #Simulate the data
134 rawdat <- data.frame(patientID = 1:(400+150+100+320),
135                       smoking = c(rep("Smoker",400+150),rep("Non-smoker",100+320)),
136                       status = c(rep("Cancer",400),rep("No cancer",150),rep("Cancer",100),rep("No cancer",320)))
137 View(rawdat)
138 summary(rawdat)
139
140 ctable2 <- table(rawdat[,c("smoking","status")])
141 print(ctable2)
```

Test of difference proportions

- `chisq.test()` → Estimation
 - **Caution:** if >20% of cells (e.g. 1 in 4 cells of a 2x2 contingency table) is ≤ 5 , Chi-square will not be accurate.
- `fisher.test()` → Exact test
 - Can be used in most cases. But a large sample size will require intensive computation.

```
143 ▾ ##### Test of difference proportions #####
144
145  chisq.test(ctable2)
146  fisher.test(ctable2)
147
148  small <- matrix(data = c(1,39,2,20), nrow = 2, byrow = T)
149  print(small)
150
151  chisq.test(small)
152  fisher.test(small)
```

Measure of association

- Question: If you decide to start smoking, how much more likely you will get cancer?
- Relative risk (RR)
 - *** Specifically for cohort or cross-sectional study***
 - **Not** for a case-control study
 - Cases and Controls were specifically recruited
 - Cases from a “rare” disease
 - True prevalence and incidence are lost

$$RR = \frac{\Pr(Disease|Exposed)}{\Pr(Disease|Not\ exposed)}$$

Measure of association

- Odds ratio (OR)
 - Can be used with cross-sectional, cohort and case-control studies
 - Logistic regression

$$\text{Odds of an event} = \frac{\text{Pr}(\text{event will occur})}{\text{Pr}(\text{event will not occur})}$$

$$OR = \frac{\text{odds that an exposed person develops a disease}}{\text{odds that a non - exposed person develops a disease}}$$

Measure of association

	Disease	No disease	Total
Exposed	a	b	a + b
Non-exposed	c	d	c + d
TOTAL	a + c	b + d	a + b + c + d

- $RR = \frac{\frac{a}{a+b}}{\frac{c}{c+d}}$

= 1 → No association

< 1 → Negative association (protection)

> 1 → Positive association (elevation)

- $OR = \frac{\frac{a}{b}}{\frac{c}{d}}$

Measure of association

- Package “epitools”

```
143 ##### Measure of association
144 library(epitools)
145
146 #Re-arrange data to match epitools requirement
147 rawdat$status <- factor(rawdat$status, levels = c("No cancer", "Cancer"))
148 rawdat$smoking <- factor(rawdat$smoking, levels = c("Non-smoker", "Smoker"))
149
150 ctable3 <- table(rawdat[, c("smoking", "status")])
151 print(ctable3)
152
153 res <- oddsratio(ctable3, method = "wald")
154 print(res)
155
156 res2 <- riskratio(ctable3, method = "wald")
157
158 print(res2)
```


Practical 3

Practical 3

- We will calculate odds ratios for alcohol and tobacco consumption in the “esoph” dataset
- Alcohol consumption → 0-39g/day versus ≥ 40 g/day
- Tobacco consumption → 0-9g/day versus ≥ 10 g/day

```
1 library(MASS)
2 library(epitools)
3
4 ?esoph
5 esoph$alc <- factor(esoph$alcgp, levels(esoph$alcgp), labels = c("0-39g/day", rep(">=40g/day", 3)))
6 esoph$tob <- factor(esoph$tobgp, levels(esoph$tobgp), labels = c("0-9g/day", rep(">=10g/day", 3)))
```

Linear Regression

Correlation between two numerical variables

- By knowing $X \rightarrow$ Estimate Y
- Parametric: Pearson (default)
- Non-parametric: Spearman and Kendall

```
160 - #### Correlation between numerical variables ####
161 ?iris
162
163 cor.test(iris$Sepal.Length,iris$Petal.Width) #Paired values
164 cor.test(~Sepal.Length + Petal.Width, iris) #Data.frame
165
166 cor.test(iris$Sepal.Length,iris$Petal.Width, method = "s") #Non-parametric
167 cor.test(iris$Sepal.Length,iris$Petal.Width, method = "k") #Non-parametric
```

Correlation between two numerical variables

- P-value:
 - Null hypothesis: the coefficient of correlation = 0
- Interpretation of the coefficient of correlation

Correlation Coefficient Value	Direction and Strength of Correlation
−1.0	Perfectly negative
−0.8	Strongly negative
−0.5	Moderately negative
−0.2	Weakly negative
0.0	No association
+0.2	Weakly positive
+0.5	Moderately positive
+0.8	Strongly positive
+1.0	Perfectly positive

By knowing $X \rightarrow$ Estimate Y

- Simple linear regression: $y = \alpha + \beta x + \varepsilon$
 - α = intercept
 - β = slope
 - ε = error (mean of $\varepsilon = 0$)
 - $\hat{y} = \alpha + \beta x$

```
169 ##### Simple linear regression #####  
170  
171 m <- lm(Sepal.Length ~ Petal.Width , iris)  
172 print(m)  
173 summary(m)
```

Interpreting regression result

Intercept (α)

Slope (β)

```
> summary(m)

Call:
lm(formula = Sepal.Length ~ Petal.Width, data = iris)

Residuals:
    Min       1Q   Median       3Q      Max
-1.38822 -0.29358 -0.04393  0.26429  1.34521

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)  4.77763    0.07293   65.51  <2e-16 ***
Petal.Width  0.88858    0.05137   17.30  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.478 on 148 degrees of freedom
Multiple R-squared:  0.669,    Adjusted R-squared:  0.6668
F-statistic: 299.2 on 1 and 148 DF,  p-value: < 2.2e-16
```

P-values:

Test whether any coefficient = 0

*Normally, the intercept is kept regardless of p-value

$R^2 \rightarrow$ % of Y explained (predicted) by your model
Used adjusted R^2 for multivariate regression

Multivariate linear regression

- Add more independent variables for prediction
- Categorical variables can be added
 - R does not need recoding of categorical variables for regression

```
175 ▾ ##### Multivariate linear regression #####  
176  
177 mm <- lm(Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width + Species , iris)  
178 print(mm)  
179 summary(mm)
```


Multivariate linear regression

```
> summary(mm)

Call:
lm(formula = Sepal.Length ~ Sepal.Width + Petal.Length + Petal.Width +
    Species, data = iris)

Residuals:
    Min       1Q   Median       3Q      Max
-0.79424 -0.21874  0.00899  0.20255  0.73103

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    2.17127    0.27979   7.760 1.43e-12 ***
Sepal.Width     0.49589    0.08607   5.761 4.87e-08 ***
Petal.Length    0.82924    0.06853  12.101 < 2e-16 ***
Petal.Width    -0.31516    0.15120  -2.084  0.03889 *
Speciesversicolor -0.72356    0.24017  -3.013  0.00306 **
Speciesvirginica -1.02356    0.33373  -3.067  0.00258 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.3068 on 144 degrees of freedom
Multiple R-squared:  0.8673,    Adjusted R-squared:  0.8627
F-statistic: 188.3 on 5 and 144 DF,  p-value: < 2.2e-16
```

-0.723 is added, if and only if,
species = versicolor

-1.023 is added, if and only if,
species = virginica

These values are not added
if species = setosa
(i.e. setosa is set as a reference)

Inhibit Interpretation/Conversion of Objects

- Function `I()` in the regression formula allows you to modify/calculate a variable before being fed into the model

```
181 ▾ ##### Inhibit Interpretation/Conversion of Objects #####  
182 mlog <- lm(Sepal.Length ~ I(log10(1+Petal.Width)), iris)  
183 print(mlog)  
184 summary(mlog)  
185  
186 msq <- lm(Sepal.Length ~ I(Petal.Width^2), iris) # Quadratic model  
187 print(msq)  
188 summary(msq)
```

Interaction

- Interaction between variables could be added to the model
- For example: male and female might have difference slope of height ~ weight
- Any interaction must be determined whether it is important or relevant first. Do not rely solely on statistics/statisticians!
- If a interaction is kept in the model, all interacting variables must also be kept regardless of p-values.

```
190 ▾ ##### Interaction #####  
191 mint <- lm(Sepal.Length ~ Petal.Width*Species, iris)  
192 print(mint)  
193 summary(mint)
```

Model selection

- Keep adding variables with limited improvement in performance is not optimal.
 - Simplest model with optimal performance
- Akaike's An Information Criterion (AIC) measures a trade-off between adding variables and performance improvement

```
195 ▾ ##### Model selection #####  
196   library(MASS)  
197  
198   sm <- stepAIC(mint)  
199   print(sm)  
200   summary(sm)
```

Model selection

- ANOVA could be used to compare two models whether a sufficient improvement is observed in the more complex model.
- $P < 0.05 \rightarrow$ Improvement

```
202 ▾ ##### Model selection ANOVA #####  
203  
204 anova(m, mint)  
205 anova(m, mm)  
---
```

Prediction with linear regression

- New dataset must have the identical structure as the training dataset

```
218 ▾ ##### Prediction with linear regression #####  
219 newdat <- iris[4:9,]  
220 print(newdat)  
221  
222 predict(mm, newdata = newdat)
```

Practical 4

Practical 4

- We will perform multivariate regression analysis on the “Davis” dataset
- We will determine how sex, height and interaction between sex and height affect the weight
- Select your best model

```
1 library(car)
2
3 ?Davis
4
5 #Correct errors in the dataset
6 print(Davis[10:13,])
7
8 nDavis <- Davis
9 nDavis[12,2:3] <- Davis[12,3:2]
10
11 #Use nDavis dataset, not Davis|
```


Logistic Regression

Binary outcomes

- Linear regression \rightarrow numerical outcome
- Logistic regression \rightarrow binary outcome (e.g. cancer vs no cancer)
- Regression results in $(-\infty, \infty)$
- Probability of binary outcome is $[0,1]$
- Convert probability to a real number scale
 - Log of odds \rightarrow Logit

Binary outcomes

- Convert probability to a real number scale
 - Log of odds → Logit

```
207 ▾ ##### Logit #####  
208 library(ggplot2)  
209  
210 pt <- 10^4 #Try changing number of point  
211  
212 dat <- data.frame(id = 1:pt, prob = seq(0,1,length.out = pt))  
213 ggplot(dat,aes(x = id, y = prob))+  
214   geom_line()  
215  
216 dat$odds <- dat$prob/(1-dat$prob)  
217 ggplot(dat,aes(x = id, y = odds))+  
218   geom_line()  
219  
220 dat$logit <- log(dat$odds)  
221 ggplot(dat,aes(x = id, y = logit))+  
222   geom_line()
```

Setting logistic regression model

- Setting and selecting logistic regression models are similar to linear regression
- The difference is the interpretation of the result

```
235 ▾ ##### Setting a logistic regression model #####
236 #From https://towardsdatascience.com/how-to-do-logistic-regression-in-r-456e9cfec7cd
237 library(AER)
238 data(Affairs)
239 ?Affairs
240
241 Affairs$ynaffair[Affairs$affairs > 0] <- 1
242 Affairs$ynaffair[Affairs$affairs == 0] <- 0
243 Affairs$ynaffair <- factor(Affairs$ynaffair, levels=c(0,1), labels=c("No", "Yes"))
244 table(Affairs$ynaffair)
245
246 lgm <- glm(ynaffair ~ gender + age + yearsmarried + children
247           + religiousness + education + occupation + rating,
248           data=Affairs, family="binomial")
249 print(lgm)
250 summary(lgm)
```

Setting logistic regression model

- The difference is the interpretation of the result

```
> summary(lgm)
```

```
Call:
```

```
glm(formula = ynaffair ~ gender + age + yearsmarried + children +  
     religiousness + education + occupation + rating, family = "binomial",  
     data = Affairs)
```

```
Deviance Residuals:
```

```
      Min       1Q   Median       3Q      Max  
-1.5713  -0.7499  -0.5690  -0.2539   2.5191
```

```
Coefficients:
```

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	1.37726	0.88776	1.551	0.120807
gendermale	0.28029	0.23909	1.172	0.241083
age	-0.04426	0.01825	-2.425	0.015301 *
yearsmarried	0.09477	0.03221	2.942	0.003262 **
childrenyes	0.39767	0.29151	1.364	0.172508
religiousness	-0.32472	0.08975	-3.618	0.000297 ***
education	0.02105	0.05051	0.417	0.676851
occupation	0.03092	0.07178	0.431	0.666630
rating	-0.46845	0.09091	-5.153	2.56e-07 ***

```
---
```

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

```
(Dispersion parameter for binomial family taken to be 1)
```

```
Null deviance: 675.38  on 600  degrees of freedom  
Residual deviance: 609.51  on 592  degrees of freedom  
AIC: 627.51
```

```
Number of Fisher Scoring iterations: 4
```

For reporting,
coefficients must be
converted to odds ratio

P-values are still used to
determine the significance of
each variable

Reporting odds ratio from regression results

```
252 ▾ ##### Reporting odds ratio from regression results #####  
253  
254 exp(cbind(OR = coef(lgm), confint(lgm)))
```

	OR	2.5 %	97.5 %
(Intercept)	3.9640180	0.7013467	22.9148790
gendermale	1.3235091	0.8294178	2.1209988
age	0.9567099	0.9223032	0.9908864
yearsmarried	1.0994093	1.0326203	1.1718726
childrenyes	1.4883560	0.8451473	2.6584834
religiousness	0.7227292	0.6049441	0.8605325
education	1.0212740	0.9254481	1.1284991
occupation	1.0314027	0.8964089	1.1884105
rating	0.6259691	0.5227302	0.7470069

Prediction with logistic regression

- New dataset must have the identical structure as the training dataset
- Use type = “response” argument to predict a probability of the event

```
256 ▾ ##### Logistic regression prediction #####  
257  
258 newdat <- Affairs[c(4,5,9,10),]  
259 predict(lgm, newdata = newdat, type = "response")  
260
```

Practical 5

Practical 5

- We will analyze “Affairs” dataset
- Select the best logistic regression model that predict an affair (e.g. anova, stepAIC)
- If needed, format the type of each variable (e.g. factor, numeric) before fitting a model

```
1 #From https://towardsdatascience.com/how-to-do-logistic-regression-in-r-456e9cfec7cd
2 library(AER)
3 data(Affairs)
4 ?Affairs
5
6 Affairs$ynaffair[Affairs$affairs > 0] <- 1
7 Affairs$ynaffair[Affairs$affairs == 0] <- 0
8 Affairs$ynaffair <- factor(Affairs$ynaffair, levels=c(0,1), labels=c("No", "Yes"))
9 table(Affairs$ynaffair)
```

In-class assignment

Early Stage Diabetes Risk Prediction

- Dataset from: <https://doi.org/10.24432/C5VG8H>
- Create and select the best logistic regression model that predict diabetes
- Report odds ratios from the selected model
- **Challenge:** Using the selected model to predict the “diabetes probability” (i.e. 0 – 1) of a 45-year-old male with sudden weight loss, visual blurring and obesity.