**Appendices**

Appendix 1**.** Intra-rater agreement (first rater) with row and column percentages and

 Intra-rater agreement (second rater) with row and column percentages

Appendix 2. R code for AC calculation

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Appendix 5. Output from Agreestat for various measures of agreement

|  |  |
| --- | --- |
| **First rater Gestalt****Impression** |  **First rater Impression after examining**  |
|  | **Not ill Appearing****(%)** | **Not Sure (%)** | **Ill****Appearing****(%)** | **Total****(%)** |
| **Not ill Appearing** | 113 | (92) | 3 | (33) | 2 |  (7) | 118 | (74) |
| (96) | (3) | (2) | (101\*) |
| **Not Sure** | 8 | (7) | 4 | (44) |  2 |  (7) | 14 | (9) |
| (57) | (29) | (14) | (100) |
| **Ill Appearing** | 2 | (11) | 2 | (22) | 23 | (85) | 27 | (17) |
| (7) | (7) | (85) | (98\*) |
| **Total** | 123 | (100) |  9 | (100) | 26 |  (100) | 159 | (100) |
|  |  |  |  |
| (77) | (6) | (16) | (99\*) |

**Appendix 1**

**Table 4 A.** Intra-rater agreement (first rater) with row and column percentages. (\* Totals not 100% due rounding error)

**Appendix 1**

|  |  |
| --- | --- |
| **Second rater Gestalt****Impression** |  **Second rater Impression after examining**  |
|  | **Not ill Appearing****(%)** | **Not Sure****(%)** | **Ill Appearing****(%)** | **Total****(%)** |
| **Not ill Appearing** | 113 | (90) | 3 | (38) |  4 |  (15) | 120 | (75) |
| (94) | (3) | (3) | (100) |
| **Not Sure** | 9 | (7) | 5 | (63) |  2 |  (8) | 16 | (10) |
| (56) | (31) | (13) | (100) |
| **Ill Appearing** | 3 | (2) | 0 | (0) | 20 |  (77) | 23 | (14) |
| (13) | (0) | (87) | (100) |
| **Total** | 125 | (100) |  8 | (100) | 26 | (100) | 159 | (100) |
| (79) | (5) | (16) | (100) |

**Table 4 B.** Intra-rater agreement (second rater) with row and column percentages.

**Appendix 2. Selected R code to calculate AC1 (Not peer reviewed)**

# Input data

data\_forR <- read.csv("~/PIRS/data\_forR.csv")

#The original author was Dr. Pedro Emmanuel A. A. do Brasilemail: pedro.brasil@ipec.fiocruz.bremail: emmanuel.brasil@gmail.com

# The credit is all his, the errors all mine

# originally posted at https://stat.ethz.ch/pipermail/r-sig-epi/attachments/20120503/7c03297b/attachment.pl

AC1 <- function(table,conflev=0.95,N=Inf,print=TRUE){

 if(dim(table)[1] != dim(table)[2]){

 stop('The table should have the same number of rows and columns!')

 }

 n <- sum(table)

 f <- n/N

 pa <- sum(diag(table))/n # formula 18

 q <- ncol(table) # number of categories

 pkk <- diag(table)/n

 pak <- sapply(1:q,function(i)sum(table[i,]))/n

 pbk <- sapply(1:q,function(i)sum(table[,i]))/n

 pik <- (pak + pbk)/2

 pegama <- (sum(pik\*(1-pik)))/(q-1)

 gama <- (pa - pegama)/(1 - pegama) # AC1 statistics

 # 2 raters special case variance

 pkl <- table/n

 soma <- 0;

 for(k in 1:q){

 for(l in 1:q){

 soma <- soma + (pkl[k,l]\*((1-(pik[k]+pik[l])/2)^2))

 }

 }

 vgama <- ((1-f)/(n\*(1-pegama)^2)) \* (pa\*(1-pa) - 4\*(1-gama)\*((1/(q-1))\*sum(pkk\*(1-pik)) - pa\*pegama) + 4\*((1-gama)^2) \*((1/((q-1)^2))\*soma - pegama^2))

 epgama <- sqrt(vgama)# AC1 standard error

 lcb <- max(0,gama - epgama\*qnorm(1-(1-conflev)/2,0,1)) # lower confidencebound

 ucb <- min(1,gama + epgama\*qnorm(1-(1-conflev)/2,0,1)) # upper confidence bound

 if(print==TRUE){

 cat('Raw agreement:',pa,'Chance-independent agreement:',pegama,'\n')

 cat('Agreement coeficient (AC1):',gama,'AC1 standard error:',epgama,'\n')

 cat(conflev\*100,'% Confidence Interval (AC1): (',lcb,',',ucb,')\n')

 }

 invisible(c(pa,pegama,gama,epgama,lcb,ucb))

 }

 inter1 <-table(impression1, impression3)

 AC1(inter1)

 x <- AC1(inter1,print=F)

 print(x)

 inter2 <-table(impression2 ,impression4)

 x1 <- AC1(inter2,print=F)

 print(x1)

 intra1 <-table(impression1 ,impression2)

 x2<- AC1(intra1, print=F)

 print(x2)

 intra2 <-table(impression3, impression4)

 x3<-AC1(intra2 ,print=F)

 print(x3)

**Appendix 3. Selected Stata code for data management and generating graphs (Not peer reviewed)**

//

//

//Sacramento

//

//PIRS

//

//clear all

import delimited C:\Users\8core\Downloads\pirs.mer, varnames(1) asdouble clear

format %12.0f accountnumber

sort accountnumber

gen id2 =\_n

isid id2

rename stexamtime firststexamtime

rename ndexamtime secondndexamtime

// code to correct data entry errors ommitted

gen time1 =date1 + firststexamtime

gen time2 =date2 + secondndexamtime

gen double t1 = clock(time1 , "MDYhm")

gen double t2 = clock(time2 , "MDYhm")

gen interval = (t2-t1) /60000

label var t1 "time/date first exam"

label var t2 "time/date second exam"

label var interval " Minutes between two exams"

gen dob = date(dateofbirth , "MDY" )

format %td dob

list dateofbirth dob

label var dob "DoB"

label var initialimpression4 "Second MD Impression after exam"

label var initialimpression3 "Second MD Gestalt Impression"

label var initialimpression1 "First MD Gestalt Impression"

label var initialimpression2 "First MD Impression after exam"

label var tylenolbeforeexam "Any antipyretic before first exam"

label var tylenolintermediate "Any antipyretic after first and before second exam"

//Check for discrepancies

list acc if interval >240

list acc if interval <0

list acc if disposition ==""

duplicates tag studyid , gen(tag)

list accountnumber studyid if(tag) ,sepby(studyid )

duplicates tag mrec ,gen(tag2)

sort mrec

list accountnumber mrec studyid if (tag2) ,sepby (mrec)

list accountnumber if tylenolbeforeexam ==""

list accountnumber date1 firststexamtime date2 secondndexamtime if tylenolintermediate ==""

// Turning string to labelled coded variables as needed

gen admit =.

replace admit =1 if disposition =="Admit"

replace admit =0 if disposition =="Discharge"

label var admit "Admitted =1"

label def dispo 0 "Discharged" 1 "Admitted"

//

gen dos =date(date,"MDY")

format %td dos

label var dos "Date of Service"

//

///

// CREATING THE DATASET FOR FIGURE 1, PATIENT FLOW

//

//

cap drop agedays

cap drop age

gen agedays =(dos-dob)

label var agedays "Age in days"

gen age =(dos-dob)/30.25

label var age "Age in months"

cap drop tag1

drop if agedays >730

duplicates tag mrec , gen(tag1)

tab tag1

duplicates drop mrec ,force

isid mrec

//

// Para1 1 infant characteristics /age/gender/dispostion

//Table 1 Provider Range in years, range in time

//

//para1

tabstat age ,stat(med iqr p25 p75)

tab sex

tab admit

// Table 1 list of diagnoses

// Provider pairs

cap drop pair\_type1

gen pair\_type1 =0

replace pair\_type1 =1 if regexm(providertype, "Attending" )==1 & regexm(providertype2, "Attending" )==1

replace pair\_type1 =1 if regexm(providertype, "Attending" )==1 & regexm(providertype2, "R4" )==1

replace pair\_type1 =1 if regexm(providertype, "Attending" )==1 & regexm(providertype2, "PA-C" )==1

replace pair\_type1 =1 if regexm(providertype2, "Attending" )==1 & regexm(providertype, "PA-C" )==1

replace pair\_type1 =1 if regexm(providertype2, "Attending" )==1 & regexm(providertype, "R4" )==1

replace pair\_type1 =1 if regexm(providertype2, "PA-C" )==1 & regexm(providertype, "R4" )==1

replace pair\_type1 =1 if regexm(providertype, "PA-C" )==1 & regexm(providertype2, "R4" )==1

label var pair\_type1 "Both observers were Attending R4 or PA-C"

cap drop pair\_type2

gen pair\_type2 =0

replace pair\_type2 =1 if regexm(providertype,"R1") ==1 & regexm(providertype2,"R4")==1

replace pair\_type2 =1 if regexm(providertype,"R2") ==1 & regexm(providertype2,"Attending")==1

replace pair\_type2 =1 if regexm(providertype,"R1") ==1 & regexm(providertype2 ,"PA-C")==1

replace pair\_type2 =1 if regexm(providertype,"R3") ==1 & regexm(providertype2,"Attending")==1

replace pair\_type2 =1 if regexm(providertype2,"R1") ==1 & regexm(providertype ,"R4")==1

replace pair\_type2 =1 if regexm(providertype2,"R2") ==1 & regexm(providertype ,"Attending")==1

replace pair\_type2 =1 if regexm(providertype2,"R1") ==1 & regexm(providertype ,"PA-C")==1

replace pair\_type2 =1 if regexm(providertype2,"R3") ==1 & regexm(providertype,"Attending")==1

label var pair\_type2 "Difference >2 yrs in experience between raters"

//

gen antipyretic\_home = .

replace antipyretic\_home =1 if tylenolbeforeexam =="Yes"

replace antipyretic\_home =0 if tylenolbeforeexam =="No"

gen antipyretic\_between = .

replace antipyretic\_between =1 if tylenolintermediate =="Yes"

replace antipyretic\_between =0 if tylenolintermediate =="No"

label var antipyretic\_home "Antipyretic before presentation"

label var antipyretic\_between "Antipyretic between exams"

cap label drop yesno

label def yesno 0 "No" 1 "Yes"

label val antipyretic\_home yesno

label val antipyretic\_between yesno

cap label drop appear

label def appear 0 "Well Appearing" 1 "Not Sure" 2 "Ill Appearing"

forval a=1(1)4 {

cap drop impression`a'

gen impression`a' =.

replace impression`a' = 0 if initialimpression`a' =="Well Appearing"

replace impression`a' = 1 if initialimpression`a' =="Not Sure or Equivocal"

replace impression`a' = 2 if initialimpression`a' =="Ill Appearing"

label val impression`a' appear

}

label var impression1 "First MD Gestalt Impression"

label var impression2 "First MD Impression after exam"

label var impression3 "Second MD Gestalt Impression"

label var impression4 "Second MD Impression after exam"

 //

 // Differences

 //

cap drop dif\_inter\_gestalt

cap drop dif\_inter\_after

cap drop dif intra\*

cap label drop agree

label def agree 0 "Agree" 1 "Rater 1 one categories more ill" 2" Rater 1 two categories more ill" -1 "Rater1 one categories less ill" -2" Rater1 two categories less ill"

gen dif\_inter\_gestalt = impression1 - impression3

label var dif\_inter\_gestalt "Difference in Gestalt assessment"

gen dif\_inter\_after = impression2- impression4

label var dif\_inter\_after "Difference in assessment after full exam"

gen dif\_intra1 = impression1-impression2

gen dif\_intra2 = impression3-impression4

label val dif\_inter\_after agree

label val dif\_inter\_gestalt agree

//

//

// Variables for looking at things that affect agreement

//

cap drop s\_gestalt

cap drop s\_after

gen s\_gestalt = 0

replace s\_gestalt =1 if dif\_inter\_gestalt==0

gen s\_after =0

replace s\_after =1 if dif\_inter\_after==0

label var s\_after "1 if agreed after examining otherwise 0 "

label var s\_gestalt "1 if agreed Gestalt otherwise 0"

cap drop agelt2

gen agelt2 =0

replace agelt2 =1 if age <=2

//

//

cap drop dx

cap drop dx2

cap drop dx\_simple

cap label drop dx

cap label drop dxs

gen dx =.

label def dx 1 "Pneumonia" 2" UTI/Pyelonephritis" 3 "Bronchiolitis" 4 "Otitis media" 5 " Croup" 6 "Gastroenteritis" 7 "Cellulitis" 8 "Sepsis No focus" 9 "URI" 10 "Herpangina" 12 "Febrile illness NOS" 13 "Bacteremia" 14 "Varicella" 15 "Febrile Seizure" 20 "Non infective" 22 "Other Febrile illnesses" 11 "Pharyngitis"

replace diagnosis=lower(diagnosis)

replace dx = 1 if regexm(diagnosis , "pneum")

replace dx = 2 if regexm(diagnosis , "UTI") | regexm(diagnosis,"uti") | regexm(diagnosis,"pyel")

replace dx = 3 if regexm(diagnosis , "bronchiolitis")

replace dx = 4 if regexm(diagnosis , "media")

replace dx = 5 if regexm(diagnosis , "croup")

replace dx = 6 if regexm(diagnosis , "gastroenteritis") |regexm(diagnosis, "enteritis" )| regexm(diagnosis, "age")

replace dx = 7 if regexm(diagnosis , "cellulitis") |regexm(diagnosis ,"sepsis")

replace dx= 7 if regexm(diagnosis,"lower lip infection") |regexm(diagnosis, "skin infection")

replace dx = 8 if regexm(diagnosis , "croup")

replace dx =3 if regexm(diagnosis, "upper respiratory infection, with bronchospasm")

replace dx =9 if regexm(diagnosis,"uri")

replace dx=9 if regexm(diagnosis, "upper respiratory inpression")

replace dx =10 if regexm(diagnosis, "herpang" )

replace dx = 12 if regexm(diagnosis , "febrile illness") |regexm(diagnosis , "viral illness") |regexm(diagnosis ,"viral syndrome") & dx ==.

replace dx =12 if diagnosis=="fever." |diagnosis =="fever"

replace dx = 9 if regexm(diagnosis,"upper respiratory infection")

replace dx =11 if regexm(diagnosis, "pharyngitis")

replace dx =13 if regexm(diagnosis,"bacteremia")

replace dx=14 if regexm(diagnosis, "varicella")

replace dx=15 if regexm(diagnosis, "seizure")

replace dx =3 if diagnosis=="reactive airway disease." |diagnosis =="rsv."

replace dx=20 if diagnosis=="diaper rash."|regexm(diagnosis, "well child visit")|regexm(diagnosis, "factitious")

replace dx=6 if regexm(diagnosis, "gi infection")

replace dx =22 if dx==.

label val dx dx

gen dx\_simple = dx

replace dx\_simple = 12 if dx\_simple ==22

replace dx\_simple = 8 if dx\_simple ==13

label def dxs 1 "Pneumonia" 2" UTI/Pyelonephritis" 3 "Bronchiolitis" 4 "Otitis media" 5 " Croup" 6 "Gastroenteritis" 7 "Cellulitis" 8 "Sepsis/Bacteremia" 9 "URI" 10 "Herpangina" 12 "Febrile illness NOS" 13 "Bacteremia" 14 "Varicella" 15 "Febrile Seizure" 20 "Non infective" 22 "Other Febrile illnesses" 11 "Pharyngitis"

label val dx\_simple dxs

//

//

cap drop prvd1

cap drop prvd2

cap label drop prvd

gen prvd1 =.

replace prvd1 =1 if providertype =="R1" |providertype=="Rotating Resident"

replace prvd1 = 2 if providertype=="R2"

replace prvd1 = 3 if providertype=="R3"

replace prvd1 = 4 if providertype=="R4"

replace prvd1 = 5 if providertype=="PA-C"

replace prvd1 = 5 if providertype=="PA-C/NP"

replace prvd1 = 6 if providertype=="Attending Phys."

gen prvd2 =.

replace prvd2 =1 if providertype2 =="R1" |providertype=="Rotating Resident"

replace prvd2 = 2 if providertype2=="R2"

replace prvd2 = 3 if providertype2=="R3"

replace prvd2 = 4 if providertype2=="R4"

replace prvd2 = 5 if providertype2=="PA-C"

replace prvd2 = 5 if providertype2=="PA-C/NP"

replace prvd2 = 6 if providertype2=="Attending Phys."

label def prvd 1 "Intern/rotator" 2 " EM-R2" 3 "EM-R3" 4 "EM-R4" 5 "PA-C" 6 "Attending"

label val prvd1 prvd

label val prvd2 prvd

//

// Figure 2

sunflower prvd1 prvd2 , binar(2.25) binwidth(0.25) scheme(s2mono) // in editor us grey16 for background and manully add labels

//Figure 3 after executing command try runnnng macro to automate graph cleanup

catplot dif\_inter\_gestalt ,percent scheme(s1mono)

catplot dif\_inter\_after ,percent scheme(s1mono)

gen interval10 = interval /10

label var interval10 "Number of 10 minute intervals between evaluations"

// create data for intrarater graph

//Sacramento 7/10/13

import delimited C:\Users\8core\Documents\PIRS\data\_for\_single\_intra\_graph.csv ,clear

save i\_graph1.dta, replace

append using i\_graph1.dta

drop dif\_intra2

rename dif\_intra1 intra\_dif

cap label drop agree

label def agree 0 "Agree" 1 "Rater 1 one categories more ill" 2" Rater 1 two categories more ill" -1 "Rater1 one categories less ill" -2" Rater1 two categories less ill"

label val intra\_dif agree

catplot intra\_dif ,percent scheme(s1mono)

//

// import main file, export rating and provider

use C:\Users\8core\Documents\PIRS\pirs.dta

export delimited mrec age interval impression1 prvd1 using "C:\Users\8core\Documents\PIRS\data\_seniority\_gestalt\_A.csv",nolabel replace

export delimited mrec age interval impression3 prvd2 using "C:\Users\8core\Documents\PIRS\data\_seniority\_gestalt\_B.csv",nolabel replace

clear

import delimited C:\Users\8core\Documents\PIRS\data\_seniority\_gestalt\_A.csv, clear

rename impression1 imp\_G

save gestalt\_A.dta, replace

clear

import delimited C:\Users\8core\Documents\PIRS\data\_seniority\_gestalt\_B.csv, clear

rename impression3 imp\_G

save gestalt\_B.dta, replace

use gestalt\_A.dta

append using gestalt\_B.dta

cap label drop appear

label def appear 0 "Well Appearing" 1 "Not Sure" 2 "Ill Appearing"

label val imp\_G appear

cap drop pv

cap label drop prvd

gen pv =prvd1

replace pv = prvd2 if pv==.

label def prvd 1 "Intern/rotator" 2 " EM-R2" 3 "EM-R3" 4 "EM-R4" 5 "PA-C" 6 "Attending"

label val pv prvd

drop prvd1 prvd2

save data\_for\_seniority\_effect\_graph.dta, replace

 gr bar cat0 cat1 cat2 ,stack over(pv) legend(row(1)) scheme(s1mono) intensity(80)

**Appendix 4.**

This simulates what would have happened if the first rater had been the second rater and vice versa.

//Sacramento

//Permutation testing

//

//

cap drop random\_\*

cap drop R\_imp\*

cap drop minK

cap drop maxK

cap drop kappa\*

forval i =1(1)500{

set seed `i'`i'

gen random\_`i' =2\*(runiform())

list random\_`i' in 1

gen R\_imp\_first\_`i' = impression1 if random\_`i' <=1

gen R\_imp\_second\_`i' = impression1 if R\_imp\_first\_`i'==.

replace R\_imp\_first\_`i' = impression3 if R\_imp\_first\_`i' ==.

replace R\_imp\_second\_`i' =impression3 if R\_imp\_second\_`i'==.

kap R\_imp\_first\_`i' R\_imp\_second\_`i' , w(w2)

gen kappa\_`i' =r(kappa)

}

egen minK= rowmin(kappa\_\*)

egen maxK= rowmax(kappa\_\*)

**Appendix 5.**  Additional measures of agreement demonstrating the number of results that could be obtained in an inter rater reliability study. (Expanded Table 5) Output from Agreestat.

|  |  |  |
| --- | --- | --- |
| **Inter rater Gestalt**  |  |  |
| Unweighted | Linear weighting | Quadratic weighting  |
| Cohen’s κ 0.118AC1 0.550Scott’s π 0.118Krippendorf’s α 0.120Brennan-Prediger 0.462Percent 64.1%  | Cohen’s κ s 0.177AC2 0.601Scott’s π 0.177Krippendorf’s α f 0.179Brennan-Prediger 0.406Percent 73.6 | Cohen’s κ s 0.220AC2 0.6345Scott’s π 0.2197Krippendorf’s α 0.2221Brennan-Prediger 0.3491Percent 78.3 |
| **Inter rater after exam**  |  |  |
| Unweighted  | Linear weighting | Quadratic weighting  |
| Cohen’s κ 0.235AC1 0.6546Scott’s π 0.2163Krippendorf’s α 0.2188Brennan-Prediger 0.5754Percent 71.7% | Cohen’s κ 0.2609AC2 0.6716Scott’s π 0.2608Krippendorf’s α 0.263Brennan-Prediger 0.4834Percent 77.0 | Cohen’s κ 0.2891AC2 0.6825Scott’s π 0.28896Krippendorf’s α 0.2912Brennan-Prediger 0.33915Percent 79.7 |
| **First rater with self** |  |  |
| Unweighted  | Linear weighting | Quadratic weighting  |
| Cohen’s κ 0.695AC1 0.851Scott’s π 0.6948Krippendorf’s α 0.6958Brennan-Prediger 0.8208Percent 88.1 | Cohen’s κ 0.7773AC-2 0.8926Scott’s π 0.7771Krippendorf’s α 0.7778Brennan-Prediger0.8373Percent 92.8 | Cohen’s κ 0.8325AC-2 0.91988Scott’s π 0.8325Krippendorf’s α 0.8329Brennan-Prediger 0.85377Percent 95.1 |
| **Second rater with self**  |  |  |
| Unweighted | Linear weighting | Quadratic weighting  |
| Cohen’s κ 0.6717AC1 0.8386Scott’s π 0.6709Krippendorf’s α 0.67193Brennan-Prediger 0.80555Percent 87.0 | Cohen’s κ 0.7346AC-2 0.8713Scott’s π 0.7343Krippendorf’s α 0.7351Brennan-Prediger 0.8055Percent 91.3 | Cohen’s κ 0.7773AC-2 0.8931Scott’s π 0.7773Krippendorf’s α 0.77797Brennan-Prediger 0.8056Percent 93.5 |