# SAS CODE

## FIRST STEP: DATA = W.FOOT

```
proc import datafile="pathway" out=W.foot dbms=xlsx replace;
sheet="SAS";
getnames=yes;
run;

/*Volume of fat tissue*/
data W.foot;
set W.foot;
BV1_2C_Brozek=(FM_2C_Brozek/0.948);
BV1_2C_Lohman = (FM_2C_Lohman/0.9007);
BV1_2C_Siri = (FM_2C_Siri/0.9007);
BV1_3C_Siri = (FM_3C_Siri/0.9007);
run;
/*Volume of fat-free tissue*/
data W.foot;
set W.foot;
BV0_2C_Brozek= BV- BV1_2C_Brozek;
BV0_2C_Lohman = BV- BV1_2C_Lohman;
BV0_2C_Siri = BV- BV1_2C_Siri;
BV0_3C_Siri = BV- BV1_3C_Siri;
run;
/*density of fat-free tissue*/
data W.foot;
set W.foot;
d0_2C_Brozek= (FFM_2C_Brozek/ BV0_2C_Brozek);
d0_2C_Lohman= (FFM_2C_Lohman/ BV0_2C_Lohman);
d0_2C_Siri= (FFM_2C_Siri/ BV0_2C_Siri);
d0_3C_Siri= (FFM_3C_Siri/ BV0_3C_Siri);
```

```
run;



/* SUMMARIES FOR DEFINING SPECIFIC BC CUTOFFS*/
title "summaries for setting cutoffs";
proc means data=W.foot maxdec=5 mean std min max;
where dummyt=1;
var ... ;
run;

data W.foot;
set W.foot;
study_2C_BF = (((1.0293*1.12)/d)*((0.3091)/(1.12-1.0293))-((1.0293*0.3091)/(1.12-1.0293)))*100;
run;

proc print data=W.foot (obs=10);
run;

/*LOOKING FOR VARIABLES CORRELATION*/
title "correlation between dependents variables and circumferences";
proc corr data=W.foot rank nosimple plots=none;
where dummyt=1;
var stature ...;
with BV d;
id i;
run;

title "correlation between dependents variables and skinfolds";
proc corr data=W.foot rank nosimple plots=none;
where dummyt=1;
var ...;
with BV d;
```

```
id i;

run;


title "correlation between dependents variables and BIA parameters";

proc corr data=W.foot rank nosimple plots=none;

where dummyt=1;

var ...;

with BV d;

id i;

run;


PROC freq data=W.foot;

table catage;

where dummyt=1;

run;


title "Summary statistics for measured variables";

proc means data=W.foot maxdec=2 mean std cv median skew nolabels;

where dummyt=1;

class catage;

var &measures;

run;


title "Summary statistics for Body Composition variables";

proc means data=W.foot maxdec=2 mean std cv median skew nolabels;

where dummyt=1;

class catage;

var &BF &FM &FFM &d0_ &TBW;

run;


/*VARIABLES DISTRIBUTION*/

Title "Variables distributions";
```

```
proc univariate data=W.foot;

where dummyt=1;

var &measures &BF &FM &FFM &TBW;

histogram &measures &BF &FM &FFM &TBW/ normal lognormal;

inset mean std skewness/ position=ne;

run;


title "Selecting best regressors for BV prediction: Circumferences";

proc glmselect data=W.foot plots=(criteria candidates coefficients);

where dummyt=1;

class catage/ order=internal;

model BV= catage stature &Circ/selection=stepwise select=sl slstay=0.01 slentry=0.1 stats=all
details=all stb;

run;

quit;


title "Selecting best regressors for BV prediction: SK";

proc glmselect data=W.foot plots=(criteria candidates coefficients);

where dummyt=1;

class catage/ order=internal;

model BV= catage stature bic_m tric_m sub_m sopi_m sops_m thigh_m med_m/selection=stepwise
select=sl slstay=0.01 slentry=0.1 stats=all details=all stb;

run;

quit;

/*ONE-WAY ANOVA or KRUSKAL-WALLIS: comparisons between catage*/

title "One-Way ANOVA for anthropometrical measures comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;

class catage;

id i;

model y=catage;

run;
```

```
quit;

title "One-Way ANOVA for BIA measures comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;

class catage;

id i;

model y=catage;

run;

quit;

title "One-Way ANOVA for Body composition measures comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;

class catage;

id i;

model y=catage;

run;

quit;

title "One-Way ANOVA for FM measures comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;

class catage;

id i;

model y=catage;

run;

quit;

title "One-Way ANOVA for FFM measures comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;
```

```
class catage;

id i;

model y=catage;

run;

quit;


title "One-Way ANOVA for FF tissue density comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;

class catage;

id i;

model y=catage;

run;

quit;


title "One-Way ANOVA for Water measures comparisons between age categories";

proc glm data=W.foot plots=none;

where dummyt=1;

class catage;

id i;

model &p_w=catage;

run;

quit;


title "Kruskal-Wallis for non-parametric measures comparisons between age categories";

proc npar1way data=W.foot plots=none wilcoxon;

where dummyt=1;

class catage;

var y;

run;


/*MODELLING FOR BEST PREDICTORS*/
```

```
title "Selecting best regressors for BV prediction: BIA";
proc glmselect data=W.foot plots=(criteria candidates coefficients);
where dummyt=1;
class catage/ order=internal;
model BV= catage stature &BIA/selection=stepwise select=sl slstay=0.01 slentry=0.1 stats=all
details=all stb;
run;
quit;


/*MODELLING FOR BEST PREDICTORS_ polynomial models*/
title "Selecting best regressors for BV prediction: Circumferences";
proc glmselect data=W.foot plots=(criteria candidates coefficients);
where dummyt=1;
class catage/ order=internal;
model BV= catage stature stat_sq &Circ &Circ_sq/selection=stepwise select=sl slstay=0.01
slentry=0.1 stats=all details=all stb;
run;
quit;


title "Selecting best regressors for BV prediction: SK";
proc glmselect data=W.foot plots=(criteria candidates coefficients);
where dummyt=1;
class catage/ order=internal;
model BV= catage stature stat_sq bic_m tric_m sub_m sopi_m sops_m thigh_m med_m
                          bic_m_sq tric_m_sq sub_m_sq sopi_m_sq sops_m_sq thigh_m_sq
med_m_sq/selection=backward select=sl slstay=0.01 slentry=0.1 stats=all details=all stb;
run;
quit;


title "Selecting best regressors for BV prediction: BIA";
proc glmselect data=W.foot plots=(criteria candidates coefficients);
where dummyt=1;
class catage/ order=internal;
```

```
model BV= catage stature stat_sq &BIA &BIA_sq/selection=backward select=sl slstay=0.01 slentry=0.1 stats=all details=all stb;
run;
quit;
/*Generating dummy for reg procedure*/
Data W.foot;
set W.foot;
dummycat=1;
if catage=2 then dummycat=0;
run;
proc format;
value dummycat
                0 ="adult"
                1= "adolescent"
;
run;
data W.foot;
set W.foot;
format dummycat dummycat.;
run;

/*model diagnostic*/
data W.foot;
set W.foot;
d_BV_C=1;
if i=43 then d_BV_C=0;
run;

title "BV by circumferences: model diagnostic";
proc reg data=W.foot plots=(diagnostics(stats=all) dfbetas cooksd fitplot) noprint;
where dummyt=1 and d_BV_C=1;
id i;
```

```
model BV= dummycat stature arm_rel hip thigh calf/ r p b cli clm clb vif acov spec dwprob white;

output out=W.foot r=res_BV_C p=yhat_BV_C;

run;

quit;
```

## SECOND STEP: DATA = FOOT

```
proc import datafile="pathway" out=foot dbms=xls replace;
sheet="SAS";
getnames=yes;
run;
proc sort data=foot;
by t i;
run;
proc format;
value catage
            1 = "adolescent"
            2 = "adult";
run;
data foot;
set foot;
format catage catage.;
run;
/*Generating dummy for reg procedure*/
Data foot;
set foot;
dummycat=1;
if catage=2 then dummycat=0;
run;
proc format;
value dummycat
                        0 ="adult"
                        1= "adolescent"
;
run;
data foot;
set foot;
```

```
format dummycat dummycat.;
run;
proc print data=foot (obs=1);
run;

/* CORRELATIONS PLOTS*/
title "Scatter plots for circumferences over categories";
proc sgscatter data=foot datacolors=(CX98FB98) DATACONTRASTCOLORS=(black gray) datasymbols=(trianglefilled) datalinepatterns=(shortdash) pad=0;
where dummyt=1;
compare y=BV x=(arm_rel arm_str hip thigh calf)/reg=(lineattrs=(thickness=3)) group=catage nowall MARKERATTRS=(size=15);
label BV="Body Volume [L]" arm_rel= "relaxed arm" arm_str="stretched arm" catage="category" ;
run;

title "Scatter plots for skinfolds over categories";
proc sgscatter data=foot datacolors=(CX98FB98) DATACONTRASTCOLORS=(black gray) datasymbols=(trianglefilled) datalinepatterns=(shortdash) pad=0;
where dummyt=1;
compare y=BV x=(bic tric sub sopi sops thigh_1 med)/reg=(lineattrs=(thickness=3)) group=catage nowall MARKERATTRS=(size=15);
label BV= "Body Volume [L]" d="Body Density [kg/L]" bic="biceps" tric="triceps" sub="subscapular" sopi="soprailiac" sops="supraspinal" thigh_1="thigh" med="medialcalf" catage="category";
run;

title "Scatter plots for BIA over categories";
proc sgscatter data=foot datacolors=(CX98FB98) DATACONTRASTCOLORS=(black gray) datasymbols=(trianglefilled) datalinepatterns=(shortdash) pad=0;
where dummyt=1;
compare y=BV x=(R Xc PhA)/reg=(lineattrs=(thickness=3)) group=catage nowall MARKERATTRS=(size=15);
label BV= "Body Volume [L]" d="Body Density [kg/L]" catage="category";
run;
```

```
title "Scatter plots for circumferences over categories";
proc sgscatter data=foot datacolors=(CX98FB98) DATACONTRASTCOLORS=(black gray)
datasymbols=(trianglefilled) datalinepatterns=(shortdash) pad=0;
where dummyt=1;
compare y=d x=(arm_rel arm_str hip thigh)/reg=(lineattrs=(thickness=3)) group=catage nowall
MARKERATTRS=(size=15);
label BV= "Body Volume [L]" d="Body Density [kg/L]" arm_rel= "relaxed arm" arm_str="stretched arm"
catage="category";
run;

title "Scatter plots for skinfolds over categories";
proc sgscatter data=foot datacolors=(CX98FB98) DATACONTRASTCOLORS=(black gray)
datasymbols=(trianglefilled) datalinepatterns=(shortdash) pad=0;
where dummyt=1;
compare y=d x=(bic tric sub sopi sops thigh_1 med)/reg=(lineattrs=(thickness=3)) group=catage nowall
MARKERATTRS=(size=15);
label BV= "Body Volume [L]" d="Body Density [kg/L]" bic="biceps" tric="triceps" sub="subscapular"
sopi="soprailiac" sops="supraspinal" thigh_1="thigh" med="medialcalf" catage="category";
run;

title "Scatter plots for BIA over categories";
proc sgscatter data=foot datacolors=(CX98FB98) DATACONTRASTCOLORS=(black gray)
datasymbols=(trianglefilled) datalinepatterns=(shortdash) pad=0;
where dummyt=1;
compare y=d x=(R Xc PhA)/reg=(lineattrs=(thickness=3)) group=catage nowall
MARKERATTRS=(size=15);
label BV= "Body Volume [L]" d="Body Density [kg/L]" catage="category";
run;

/*model diagnostic*/
data foot;
set foot;
d_BV_C=1;
if i=43 then d_BV_C=0;
run;
```

```
ods graphics on;
title "BV by circumferences: model diagnostic";
proc reg data=foot plots=(diagnostics(stats=all) dfbetas cooksd fitplot) noprint;
where dummyt=1 and d_BV_C=1;
id i;
model BV= dummycat stature arm_rel hip thigh calf/ r p b cli clm clb vif acov spec dwprob white;
output out=analysis r=res_BV_C p=yhat_BV_C;
run;
quit;

/*Fitline plot*/
proc sgplot data=analysis;
where dummyt=1 and d_BV_C=1;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
loess x=yhat_BV_C y=BV / group=dummycat markerattrs=(symbol=trianglefilled size=8)
	clm clmattrs=(clmfillattrs=(color=ltgray transparency=0.6) clmlineattrs=(color=black thickness=2)) lineattrs=(pattern=dash thickness=2);
reg x=yhat_BV_C y=BV/ nomarkers lineattrs=(color=black pattern=solid thickness=2);
yaxis label="BV by ADP" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
xaxis label="Predicted BV by circumferences" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Fit plot";
run;

/*Bland & Altman plot*/
data analysis /*generate a new work data for maintaining foot values*/;
set analysis;
diff_BV_C = BV - yhat_BV_C;
avg_BV_C = (BV + yhat_BV_C) / 2;
run;
```

```
proc sql noprint;
   select mean(diff_BV_C), std(diff_BV_C) into :mean_d_BV_C, :std_d_BV_C
   from analysis;
quit;
/* Calculate the upper and lower limits of agreement */
%let BV_C_loa_up = %sysevalf(&mean_d_BV_C + 1.96* &std_d_BV_C);
%let BV_C_loa_low = %sysevalf(&mean_d_BV_C - 1.96* &std_d_BV_C);

title "BLAND & ALTMAN PLOT FOR BV PREDICITION BY CIRCUMFERENCE";
proc sgplot data=analysis;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
scatter x=avg_BV_C y=diff_BV_C /group=dummycat markerattrs=(symbol=trianglefilled size=8);
   /* Add the Mean Difference Line */
refline &mean_d_BV_C / axis=y lineattrs=(thickness=2 color=ltgray) label="Mean Diff: %sysfunc(putn(&mean_d_BV_C, 5.2))";
   /* Add the Upper and Lower Limits of Agreement */
refline &BV_C_loa_up &BV_C_loa_low / axis=y lineattrs=(pattern=dash color=ltgray) label=("+1.96*std" "-1.96*std");
refline 0 / axis=y lineattrs=(pattern=dot thickness=2 color=black);
yaxis label="BV by ADP - predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold) min=-5 max=5;
xaxis label="Mean of BV by ADP and predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Bland & Altman plot: ADP vs circumferences";
run;

proc print data=analysis (obs=3);
run;

/*LIN'S CCC*/
proc corr data=analysis outp=CCC noprint;
```

```
var BV yhat_BV_C;
run;


data analysis;
set CCC(where=(_type_='CORR' and _name_='BV'));
   /* Pearson's r */
   r_BV_C = yhat_BV_C;
set CCC(where=(_type_='STD'));
   s1 = BV;
   s2 = yhat_BV_C;
set CCC(where=(_type_='MEAN'));
   m1 = BV;
   m2 = yhat_BV_C;
   /* The 'C_b' bias correction factor */
   v = s1 / s2;
   u = (m1 - m2) / sqrt(s1 * s2);
   cb_BV_C = 2 / (v + (1/v) + u**2);
   /* Lin's CCC */
   ccc_BV_C = r_BV_C * cb_BV_C;
keep r_BV_C cb_BV_C ccc_BV_C;
run;
title "Lin's Coefficient";
proc print data=CCC;
run;


/*MODEL BY SKINFOLD THICKNESSESS*/
data foot;
set foot;
d_BV_SK=1;
if i=56 then d_BV_SK=0;
run;
```

```
/*BEST MODEL*/
title "BV by SK: model diagnostic without i=56";
proc reg data=foot plots=(diagnostics(stats=all) dfbetas cooksd fitplot) noprint;
where dummyt=1 and d_BV_SK=1;
id i;
model BV= dummycat stature sub/ r p b cli clm clb vif acov spec dwprob white;
output out=analysis r=res_BV_SK p=yhat_BV_SK;
run;
quit;
/*fi plot SK*/
proc sgplot data=analysis;
where dummyt=1 and d_BV_SK=1;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
loess x=yhat_BV_SK y=BV / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8)
	clm clmattrs=(clmfillattrs=(color= ltgray transparency=0.6)) lineattrs=(pattern=dash thickness=2);
reg x=yhat_BV_SK y=BV/ nomarkers lineattrs=(color=black pattern=solid thickness=2);
yaxis label="BV by ADP" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
xaxis label="Predicted BV by SK" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Fit plot";
run;



/*Bland & Altman plot*/
data analysis /*generate a new work data for maintaining foot values*/;
set analysis;
diff_BV_SK = BV - yhat_BV_SK;
avg_BV_SK = (BV + yhat_BV_SK) / 2;
run;

proc sql noprint;
```

```
   select mean(diff_BV_SK), std(diff_BV_SK) into :mean_d_BV_SK, :std_d_BV_SK
   from analysis;
quit;
/* Calculate the upper and lower limits of agreement */
%let BV_SK_loa_up = %sysevalf(&mean_d_BV_SK + 1.96* &std_d_BV_SK);
%let BV_SK_loa_low = %sysevalf(&mean_d_BV_SK - 1.96* &std_d_BV_SK);

title1 "BLAND & ALTMAN PLOT FOR BV PREDICITION BY SK";
proc sgplot data=analysis;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
scatter x=avg_BV_SK y=diff_BV_SK / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8);
   /* Add the Mean Difference Line */
refline &mean_d_BV_SK / axis=y lineattrs=(thickness=2 color=ltgray) label="Mean Diff: %sysfunc(putn(&mean_d_BV_C, 5.2))";
   /* Add the Upper and Lower Limits of Agreement */
refline &BV_SK_loa_up &BV_SK_loa_low / axis=y lineattrs=(pattern=dash color=ltgray) label=("+1.96*std" "-1.96*std");
refline 0 / axis=y lineattrs=(pattern=dot thickness=2 color=black);
yaxis label="BV by ADP - predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold) min=-10 max=10;
xaxis label= "Mean of BV by ADP and predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Bland & Altman Plot: ADP vs SK";
run;

/*LIN'S CCC*/
proc corr data=analysis outp=CCC noprint;
var BV yhat_BV_SK;
run;

data lin_sk;
```

```
set CCC(where=(_type_='CORR' and _name_='BV'));
   /* Pearson's r */
   r_BV_SK = yhat_BV_SK;
set CCC(where=(_type_='STD'));
   s1 = BV;
   s2 = yhat_BV_SK;
set CCC(where=(_type_='MEAN'));
   m1 = BV;
   m2 = yhat_BV_SK;
   /* The 'C_b' bias correction factor */
   v = s1 / s2;
   u = (m1 - m2) / sqrt(s1 * s2);
   cb_BV_SK = 2 / (v + (1/v) + u**2);
   /* Lin's CCC */
   ccc_BV_SK = r_BV_SK * cb_BV_SK;
keep r_BV_SK cb_BV_SK ccc_BV_SK;
run;
title "Lin's Coefficient";
proc print data=CCC;
run;
proc print data=lin_sk;
run;

/*BIA MODEL DIAGNOSTIC*/
title "BV by BIA: model diagnostic";
proc reg data=foot plots=(diagnostics(stats=all) dfbetas cooksd fitplot) noprint;
where dummyt=1;
id i;
model BV= dummycat stature R / r p b cli clm clb vif acov spec dwprob white;
output out=analysis r=res_BV_BIA p=yhat_BV_BIA;
run;
quit;
```

```
/*fit plot BIA*/

proc sgplot data=analysis;

where dummyt=1;

styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);

loess x=yhat_BV_BIA y=BV / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8)

		clm clmattrs=(clmfillattrs=(color= ltgray transparency=0.6)) lineattrs=(pattern=dash
thickness=2);

reg x=yhat_BV_BIA y=BV/ nomarkers lineattrs=(color=black pattern=solid thickness=2);

yaxis label="BV by ADP" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);

xaxis label="Predicted BV by BIA" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);

keylegend / title="" position=bottom valueattrs=(size=12);

title "Fit plot";

run;


/*Bland & Altman plot*/

data analysis /*generate a new work data for maintaining foot values*/;

set analysis;

diff_BV_BIA = BV - yhat_BV_BIA;

avg_BV_BIA = (BV + yhat_BV_BIA) / 2;

run;


proc sql noprint;

   select mean(diff_BV_BIA), std(diff_BV_BIA) into :mean_d_BV_BIA, :std_d_BV_BIA

   from analysis;

quit;

/* Calculate the upper and lower limits of agreement */

%let BV_BIA_loa_up = %sysevalf(&mean_d_BV_BIA + 1.96* &std_d_BV_BIA);

%let BV_BIA_loa_low = %sysevalf(&mean_d_BV_BIA - 1.96* &std_d_BV_BIA);


title1 "BLAND & ALTMAN PLOT FOR BV PREDICITION BY BIA";

proc sgplot data=analysis;
```

```
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);

scatter x=avg_BV_BIA y=diff_BV_BIA / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8);

   /* Add the Mean Difference Line */

refline &mean_d_BV_BIA / axis=y lineattrs=(thickness=2 color=ltgray) label="Mean Diff: %sysfunc(putn(&mean_d_BV_C, 5.2))";

   /* Add the Upper and Lower Limits of Agreement */

refline &BV_BIA_loa_up &BV_BIA_loa_low / axis=y lineattrs=(pattern=dash color=ltgray) label=("+1.96*std" "-1.96*std");

refline 0 / axis=y lineattrs=(pattern=dot thickness=2 color=black);

yaxis label="BV by ADP - predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold) min=-10 max=10;

xaxis label="Mean of BV by ADP and predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);

keylegend / title="" position=bottom valueattrs=(size=12);

title "Bland & Altman Plot: ADP vs BIA";

run;


/*LIN'S CCC*/

proc corr data=analysis outp=CCC noprint;

var BV yhat_BV_BIA;

run;


data lin_bia;

set CCC(where=(_type_='CORR' and _name_='BV'));

   /* Pearson's r */

   r_BV_BIA = yhat_BV_BIA;

set CCC(where=(_type_='STD'));

   s1 = BV;

   s2 = yhat_BV_BIA;

set CCC(where=(_type_='MEAN'));

   m1 = BV;

   m2 = yhat_BV_BIA;
```

```
   /* The 'C_b' bias correction factor */
   v = s1 / s2;
   u = (m1 - m2) / sqrt(s1 * s2);
   cb_BV_BIA = 2 / (v + (1/v) + u**2);
   /* Lin's CCC */
   ccc_BV_BIA = r_BV_BIA * cb_BV_BIA;
keep r_BV_BIA cb_BV_BIA ccc_BV_BIA;
run;
title "Lin's Coefficient";
proc print data=CCC;
run;
proc print data=lin_bia;
run;

title "BV by circumferences: model diagnostic";
/*TEST-RETEST FOR MODEL RELIABILITY*/
/*SAVING MODEL PREDICTION ON foot*/
data foot;
set foot;
BVhat_ANT= -102.45967+(1.10793*dummycat)+(0.35439*stature)+(0.51682*arm_rel)+(0.57547*hip)+(0.51166*thigh)+(0.54422*calf);
BVhat_SK= -49.56459+(-1.51037*dummycat)+(0.56847*stature)+(1.45497*sub);
BVhat_BIA= -43.47204+(1.36433*dummycat)+(0.76056*stature)+(-0.04875*R);
run;

data foot;
set foot;
FFM_2C_Study=BM-FM_2C_Study;
run;

PROC PRINT DATA=foot (obs=3);
```

```
run;

proc sort data=foot;
by t dummycat;
run;

title "descriptive statistic of predictions by time";
proc means data=foot n mean std cv maxdec=2;
by t dummycat;
var BVhat_ANT BVhat_SK BVhat_BIA BV FM_2C_Brozek FM_2C_Lohman FM_2C_Pace FM_2C_Siri FM_3C_Siri FM_2C_study BF_2C_Brozek BF_2C_Lohman BF_2C_Pace BF_2C_Siri BF_3C_Siri BF_2C_Study FFM_2C_Brozek FFM_2C_Lohman FFM_2C_Pace FFM_2C_Siri FFM_3C_Siri FFM_2C_Study ;
run;

/*PAIRED T-TEST FOR COMPLETE VALIDATION*/
title "Paired student test for model reliability";
proc ttest data=foot sides=2 plots(unpack)=summary;
class t;
var BVhat_ANT BVhat_SK BVhat_BIA BV;
run;

title "Paired student test for model reliability";
proc ttest data=foot sides=2 plots(unpack)=summary;
by dummycat;
class t;
var BVhat_ANT BVhat_SK BVhat_BIA BV;
run;

title "Paired student test for model accuracy and precision";
proc ttest data=foot sides=2 plots=(histogram boxplot agreement);
paired (BVhat_ANT BVhat_SK BVhat_BIA)* BV;
```

```
label BVhat_ANT="predicted BV by ANT" BVhat_SK="predicted BV by SK" BVhat_BIA="predicted BV by BIA" BV="Body Volume by ADP";
run;


/*LIN CCC at retest*/
ods graphics on;
title "BV by circumferences: model re-test diagnostic";
proc reg data=foot plots=diagnostic noprint;
where t=2;
id i;
model BV= dummycat stature arm_rel hip thigh calf;
output out=analysis r=res_BV_C_post p=yhat_BV_C_post;
run;
quit;
/*Fitline plot*/
proc sgplot data=analysis;
where t=2;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
loess x=yhat_BV_C_post y=BV / group=dummycat markerattrs=(symbol=trianglefilled size=8)
	clm clmattrs=(clmfillattrs=(color=ltgray transparency=0.6) clmlineattrs=(color=black thickness=2)) lineattrs=(pattern=dash thickness=2);
reg x=yhat_BV_C_post y=BV/ nomarkers lineattrs=(color=black pattern=solid thickness=2);
yaxis label="BV by ADP" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
xaxis label="Predicted BV by circumferences" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Fit plot at retest";
run;

/*Bland & Altman plot*/
data analysis /*generate a new work data for maintaining foot values*/;
set analysis;
```

```
diff_BV_C_post = BV - yhat_BV_C_post;
avg_BV_C_post = (BV + yhat_BV_C_post) / 2;
run;

proc sql noprint;
   select mean(diff_BV_C_post), std(diff_BV_C_post) into :mean_d_BV_C_post, :std_d_BV_C_post
   from analysis;
quit;
/* Calculate the upper and lower limits of agreement */
%let BV_C_loa_up_post = %sysevalf(&mean_d_BV_C_post + 1.96* &std_d_BV_C_post);
%let BV_C_loa_low_post = %sysevalf(&mean_d_BV_C_post - 1.96* &std_d_BV_C_post);

title "BLAND & ALTMAN PLOT FOR BV PREDICITION BY CIRCUMFERENCE at retest";
proc sgplot data=analysis;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
scatter x=avg_BV_C_post y=diff_BV_C_post / group=dummycat markerattrs=(symbol=trianglefilled size=8);
   /* Add the Mean Difference Line */
refline &mean_d_BV_C_post / axis=y lineattrs=(thickness=2 color=ltgray) label="Mean Diff: %sysfunc(putn(&mean_d_BV_C_post, 5.2))";
   /* Add the Upper and Lower Limits of Agreement */
refline &BV_C_loa_up_post &BV_C_loa_low_post / axis=y lineattrs=(pattern=dash color=ltgray) label=("+1.96*std" "-1.96*std");
refline 0 / axis=y lineattrs=(pattern=dot thickness=2 color=black);
yaxis label="BV by ADP - predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold) min=-5 max=5;
xaxis label="Mean of BV by ADP and predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Bland & Altman plot: ADP vs circumferences at retest";
run;

/*LIN'S CCC*/
```

```
proc corr data=analysis outp=CCC noprint;
var BV yhat_BV_C_post;
run;

data analysis;
set CCC(where=(_type_='CORR' and _name_='BV'));
   /* Pearson's r */
   r_BV_C_post = yhat_BV_C_post;
set CCC(where=(_type_='STD'));
   s1 = BV;
   s2 = yhat_BV_C_post;
set CCC(where=(_type_='MEAN'));
   m1 = BV;
   m2 = yhat_BV_C_post;
   /* The 'C_b' bias correction factor */
   v = s1 / s2;
   u = (m1 - m2) / sqrt(s1 * s2);
   cb_BV_C_post = 2 / (v + (1/v) + u**2);
   /* Lin's CCC */
   ccc_BV_C_post = r_BV_C_post * cb_BV_C_post;
keep r_BV_C_post cb_BV_C_post ccc_BV_C_post;
run;
title "Lin's CCC";
proc print data=CCC;
run;
proc print data=analysis;
run;

/*MODEL BY SKINFOLD THICKNESSESS*/
title "BV by SK: model diagnostic at retest";
proc reg data=foot plots=diagnostics noprint;
where t=2;
```

```
id i;
model BV= dummycat stature sub;
output out=analysis r=res_BV_SK p=yhat_BV_SK;
run;
quit;
/*Fitline plot*/
proc sgplot data=analysis;
where t=2;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
loess x=yhat_BV_SK y=BV / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8)
        clm clmattrs=(clmfillattrs=(color=ltgray transparency=0.6) clmlineattrs=(color=black
thickness=2)) lineattrs=(pattern=dash thickness=2);
reg x=yhat_BV_SK y=BV/ nomarkers lineattrs=(color=black pattern=solid thickness=2);
yaxis label="BV by ADP" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
xaxis label="Predicted BV by SK" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Fit plot at retest";
run;


/*Bland & Altman plot*/
data analysis /*generate a new work data for maintaining foot values*/;
set analysis;
diff_BV_SK = BV - yhat_BV_SK;
avg_BV_SK = (BV + yhat_BV_SK) / 2;
run;


proc sql noprint;
   select mean(diff_BV_SK), std(diff_BV_SK) into :mean_d_BV_SK, :std_d_BV_SK
   from analysis;
quit;
/* Calculate the upper and lower limits of agreement */
%let BV_SK_loa_up = %sysevalf(&mean_d_BV_SK + 1.96* &std_d_BV_SK);
```

```
%let BV_SK_loa_low = %sysevalf(&mean_d_BV_SK - 1.96* &std_d_BV_SK);


title1 "BLAND & ALTMAN PLOT FOR BV PREDICITION BY SK at retest";
proc sgplot data=analysis;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
scatter x=avg_BV_SK y=diff_BV_SK / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8);
   /* Add the Mean Difference Line */
refline &mean_d_BV_SK / axis=y lineattrs=(thickness=2 color=ltgray) label="Mean Diff: %sysfunc(putn(&mean_d_BV_SK, 5.2))";
   /* Add the Upper and Lower Limits of Agreement */
refline &BV_SK_loa_up &BV_SK_loa_low / axis=y lineattrs=(pattern=dash color=ltgray) label=("+1.96*std" "-1.96*std");
refline 0 / axis=y lineattrs=(pattern=dot thickness=2 color=black);
yaxis label="BV by ADP - predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold) min=-10 max=10;
xaxis label="Mean of BV by ADP and predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Bland & Altman Plot : ADP vs SK at retest";
run;


/*LIN'S CCC*/
proc corr data=analysis outp=CCC noprint;
var BV yhat_BV_SK;
run;


data lin_sk;
set CCC(where=(_type_='CORR' and _name_='BV'));
   /* Pearson's r */
   r_BV_SK = yhat_BV_SK;
set CCC(where=(_type_='STD'));
   s1 = BV;
```

```
   s2 = yhat_BV_SK;
set CCC(where=(_type_='MEAN'));
   m1 = BV;
   m2 = yhat_BV_SK;
   /* The 'C_b' bias correction factor */
   v = s1 / s2;
   u = (m1 - m2) / sqrt(s1 * s2);
   cb_BV_SK = 2 / (v + (1/v) + u**2);
   /* Lin's CCC */
   ccc_BV_SK = r_BV_SK * cb_BV_SK;
keep r_BV_SK cb_BV_SK ccc_BV_SK;
run;
title "Lin's Coefficient";
proc print data=CCC;
run;
proc print data=lin_sk;
run;

/*BIA MODEL DIAGNOSTIC*/
title "BV by BIA: model diagnostic at re-test";
proc reg data=foot plots=diagnostics noprint;
where t=2;
id i;
model BV= dummycat stature R;
output out=analysis r=res_BV_BIA p=yhat_BV_BIA;
run;
quit;
/*Fitline plot*/
proc sgplot data=analysis;
where t=2;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
loess x=yhat_BV_BIA y=BV / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8)
```

```
        clm clmattrs=(clmfillattrs=(color=ltgray transparency=0.6) clmlineattrs=(color=black thickness=2)) lineattrs=(pattern=dash thickness=2);
reg x=yhat_BV_BIA y=BV/ nomarkers lineattrs=(color=black pattern=solid thickness=2);
yaxis label="BV by ADP" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
xaxis label="Predicted BV by BIA" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Fit plot at retest";
run;

/*Bland & Altman plot*/
data analysis /*generate a new work data for maintaining foot values*/;
set analysis;
diff_BV_BIA = BV - yhat_BV_BIA;
avg_BV_BIA = (BV + yhat_BV_BIA) / 2;
run;

proc sql noprint;
   select mean(diff_BV_BIA), std(diff_BV_BIA) into :mean_d_BV_BIA, :std_d_BV_BIA
   from analysis;
quit;
/* Calculate the upper and lower limits of agreement */
%let BV_BIA_loa_up = %sysevalf(&mean_d_BV_BIA + 1.96* &std_d_BV_BIA);
%let BV_BIA_loa_low = %sysevalf(&mean_d_BV_BIA - 1.96* &std_d_BV_BIA);

title1 "BLAND & ALTMAN PLOT FOR BV PREDICITION BY BIA at re-test";
proc sgplot data=analysis;
styleattrs axisextent=data backcolor=white wallcolor=white datacontrastcolors=(black gray);
scatter x=avg_BV_BIA y=diff_BV_BIA / group=dummycat/*NEW*/ markerattrs=(symbol=trianglefilled size=8);
   /* Add the Mean Difference Line */
refline &mean_d_BV_BIA / axis=y lineattrs=(thickness=2 color=ltgray) label="Mean Diff: %sysfunc(putn(&mean_d_BV_BIA, 5.2))";
   /* Add the Upper and Lower Limits of Agreement */
```

```
refline &BV_BIA_loa_up &BV_BIA_loa_low / axis=y lineattrs=(pattern=dash color=ltgray) label=("+1.96*std" "-1.96*std");
refline 0 / axis=y lineattrs=(pattern=dot thickness=2 color=black);
yaxis label="BV by ADP - predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold) min=-10 max=10;
xaxis label="Mean of BV by ADP and predicted BV" labelattrs=(size=14 weight=bold) valueattrs=(size=10 weight=bold);
keylegend / title="" position=bottom valueattrs=(size=12);
title "Bland & Altman Plot : ADP vs BIA at retest";
run;

/*LIN'S CCC*/
proc corr data=analysis outp=CCC noprint;
var BV yhat_BV_BIA;
run;

data lin_bia;
set CCC(where=(_type_='CORR' and _name_='BV'));
   /* Pearson's r */
   r_BV_BIA = yhat_BV_BIA;
set CCC(where=(_type_='STD'));
   s1 = BV;
   s2 = yhat_BV_BIA;
set CCC(where=(_type_='MEAN'));
   m1 = BV;
   m2 = yhat_BV_BIA;
   /* The 'C_b' bias correction factor */
   v = s1 / s2;
   u = (m1 - m2) / sqrt(s1 * s2);
   cb_BV_BIA = 2 / (v + (1/v) + u**2);
   /* Lin's CCC */
   ccc_BV_BIA = r_BV_BIA * cb_BV_BIA;
keep r_BV_BIA cb_BV_BIA ccc_BV_BIA;
```

```
run;
title "Lin's Coefficient";
proc print data=CCC;
run;
proc print data=lin_bia;
run;

proc print data=foot (obs=1);
run;

proc sort data=foot;
by t catage;
run;
/*PAIRED T-TEST BETWEEN BC MODELS*/
title "Paired student test for BC models comparisons";
proc ttest data=foot sides=2 plots=(boxplot agreement);
where t=1;
paired BF_2C_Study*(BF_2C_Brozek BF_2C_Lohman BF_2C_Pace BF_2C_Siri BF_3C_Siri);
run;

title "Paired student test for BC models comparisons: by categories";
proc ttest data=foot sides=2 plots=(boxplot agreement);
by catage;
where t=1;
paired BF_2C_Study*(BF_2C_Brozek BF_2C_Lohman BF_2C_Pace BF_2C_Siri BF_3C_Siri);
run;

title "One-Way ANOVA for BC models comparisons within categories";
proc glm data=foot plot=meanplot(clband);
where t=1;
class dummycat;
model BF_2C_Brozek BF_2C_Lohman BF_2C_Pace BF_2C_Siri BF_3C_Siri = dummycat BF_2C_study;
```

```
lsmeans dummycat / cl pdiff=anom adjust=nelson plot=anom;
run;
quit;

/*MONTE CARLO FOR MODELS ERROR*/
data monte_carlo;
do sim = 1 to 10000;
int_A = -102.45967 + 5.27906 * rannor(123);
stat = 165.316 + 6.194 * rannor(123);
arm = 26.506 + 2.020 * rannor(123);
hip = 70.106 + 3.734 * rannor(123);
thigh = 52.828 + 3.352 * rannor(123);
calf = 35.669 + 2.229 * rannor(123);

int_B = -49.56459 + 11.76384 * rannor(123);
sub = 9.173 + 1.980 * rannor(123);

int_C = -43.47204 + 12.98293 * rannor(123);
R = 527.038 + 59.145 * rannor(123);

/* coefficients */
c_stat_A = 0.35439;
c_arm = 0.51682;
c_hip = 0.57547;
c_thigh = 0.51166;
c_calf = 0.54422;
c_cat_A = 1.10793;
/*SK*/
c_stat_B = 0.56847;
c_sub = 1.45497;
c_cat_B = -1.51037;
/*BIA*/
```

```
c_stat_C = 0.76056;
c_R = -0.04875;
c_cat_C=1.36433;

ANT = int_A + (stat*c_stat_A) + (arm*c_arm) + (hip*c_hip) + (thigh*c_thigh) + (calf*c_calf) + c_cat_A;
SK = int_B + (stat*c_stat_B) + (sub*c_sub) + c_cat_B;
BIA = int_C + (stat*c_stat_C) + (R*c_R) + c_cat_C;
ANT_noint = (stat*c_stat_A) + (arm*c_arm) + (hip*c_hip) + (thigh*c_thigh) + (calf*c_calf) + c_cat_A;
SK_noint = (stat*c_stat_B) + (sub*c_sub) + c_cat_B;
BIA_noint = (stat*c_stat_C) + (R*c_R) + c_cat_C;
output;
end;
run;

PROC UNIVARIATE DATA=monte_carlo;
var ANT;
histogram ANT/normal;
var SK;
histogram SK/normal;
var BIA;
histogram BIA/normal;
var ANT_noint;
histogram ANT_noint/normal;
var SK_noint;
histogram SK_noint/normal;
var BIA_noint;
histogram BIA_noint/normal;
run;
```