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/* PRECLINICAL SAS PROJECT
   Body Weight Analysis - COMPANY READY VERSION
   Purpose: Educational project for SDTM, ADaM, Statistical Analysis + ANCOVA
   Date: December 2025
*/
/*
-----*
 STEP 1: CREATE RAW BODY WEIGHT DATASET
-----*/
data rawbodyweight;
  length TRTGRP $15 AnimalID $10;
  input TRTGRP $ AnimalID $ Day0 Final;
  datalines;
NC NC1 267 269
NC NC2 287 290
NC NC3 312 315
NC NC4 310 313
NC NC5 282 285
NC NC6 265 266
DC DC1 322 278
DC DC2 359 305
DC DC3 327 268
DC DC4 320 276
DC DC5 354 300
DC DC6 325 266
STD STD1 291 268
STD STD2 295 245
STD STD3 306 264
STD STD4 304 262
STD STD5 294 244
STD STD6 290 267
HECLD HLD1 311 264
HECLD HLD2 270 252
HECLD HLD3 272 248
HECLD HLD4 310 263
HECLD HLD5 269 251
HECLD HLD6 309 262
HECHD HHD1 321 278
HECHD HHD2 299 262
HECHD HHD3 339 285
HECHD HHD4 335 281
HECHD HHD5 294 257
HECHD HHD6 311 268
STDHECLD SHLD1 330 285
STDHECLD SHLD2 300 272
STDHECLD SHLD3 280 254
STDHECLD SHLD4 270 244
STDHECLD SHLD5 305 277
STDHECLD SHLD6 305 275
STDHECHD SHHD1 314 285
STDHECHD SHHD2 342 322
STDHECHD SHHD3 320 305
STDHECHD SHHD4 310 281
STDHECHD SHHD5 340 320
STDHECHD SHHD6 310 295
;
run;

/* Verify raw data */
proc print data=rawbodyweight (obs=10);
  title "Raw Body Weight Data - First 10 Records";
run;

/*
-----*
 STEP 2: CREATE SDTM.VS VITAL SIGNS DATASET + SDTM VARS
-----*/
data sdtmvs;
  set rawbodyweight;
  length STUDYID $20 DOMAIN $2 USUBJID $10 VSTPT $10 VSTEST $20 VISIT $10;

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STUDYID = "PRECLINICAL01";
DOMAIN  = "VS";
USUBJID = AnimalID;

/* Day 0 record */
VSTPT  = "Day0";
VTEST   = "Body Weight";
VISIT   = VSTPT;
VISITNUM = 1;
VSORRES = Day0;
output;

/* Final day record */
VSTPT  = "Final";
VTEST   = "Body Weight";
VISIT   = VSTPT;
VISITNUM = 2;
VSORRES = Final;
output;

keep STUDYID DOMAIN TRTGRP USUBJID VISIT VISITNUM VSTPT VTEST VSORRES;
run;

proc sort data=sdtmvs;
  by STUDYID TRTGRP USUBJID VISITNUM;
run;

proc print data=sdtmvs (obs=20);
  title "SDTM.VS Dataset - First 20 Records";
run;

/*
-----  

STEP 3: CREATE ADaM.ADV ANALYSIS DATASET  

-----*/
proc sort data=sdtmvs out=sortedvs;
  by STUDYID TRTGRP USUBJID VISITNUM;
run;

data adamadvs;
  set sortedvs;
  by STUDYID TRTGRP USUBJID;

length AVISIT $10 PARAM $20 PARAMCD $8 ABLFL $1;
retain BASE;

AVISIT  = VISIT;
AVISITN = VISITNUM;
PARAM   = "Body Weight";
PARAMCD = "BW";
AVAL   = VSORRES;

if first.USUBJID then BASE = .;
if AVISITN = 1 then do;
  BASE  = AVAL;
  ABLFL = "Y";
end;
else ABLFL = " ";

if AVISITN = 1 then do;
  CHG  = 0;
  PCHG = 0;
end;
else do;
  CHG  = AVAL - BASE;
  if BASE ne 0 then PCHG = 100 * (AVAL - BASE) / BASE;
  else PCHG = .;
end;

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keep STUDYID TRTGRP USUBJID PARAM PARAMCD AVISITN
      AVAL BASE CHG PCHG ABLFL;
run;

/* Carry forward baseline */
data adamadvs;
  set adamadvs;
  by STUDYID TRTGRP USUBJID;
  retain baselineval;

  if first.USUBJID then baselineval = .;
  if AVISITN = 1 then baselineval = AVAL;
  BASE = baselineval;

  if AVISITN = 1 then do;
    CHG = 0;
    PCHG = 0;
  end;
  else do;
    CHG = AVAL - BASE;
    if BASE ne 0 then PCHG = 100 * (AVAL - BASE) / BASE;
    else PCHG = .;
  end;
run;

proc sort data=adamadvs;
  by STUDYID TRTGRP USUBJID AVISITN;
run;

proc print data=adamadvs (obs=20);
  title "ADaM.ADVS Dataset - First 20 Records";
run;

/*
----- STEP 4: DESCRIPTIVE STATISTICS - MEAN BODY WEIGHT -----
-----*/
proc means data=adamadvs n mean std maxdec=4;
  class TRTGRP AVISIT AVISITN;
  var AVAL;
  output out=meanbw n=N mean=MeanBW std=SD;
  where AVISIT in ("Day0", "Final");
run;

data meanbwclean;
  set meanbw;
  where _TYPE_ = 7;
  keep TRTGRP AVISIT AVISITN _FREQ_ MeanBW SD N;
run;

proc print data=meanbwclean noobs;
  title "Mean Body Weight by Treatment Group and Visit";
  var TRTGRP AVISIT AVISITN MeanBW SD N;
  format MeanBW SD 8.3;
run;

/*
----- STEP 5: CHANGE FROM BASELINE (FINAL DAY)
-----*/
proc means data=adamadvs n mean std maxdec=4;
  class TRTGRP;
  var CHG;
  output out=chgbaseline n=N mean=MeanCHG std=SDCHG;
  where AVISITN = 2;
run;

data chgbaselineclean;
  set chgbaseline;
  where _TYPE_ = 1;
  keep TRTGRP _FREQ_ MeanCHG SDCHG N;

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run;

proc print data=chgbaselineclean noobs;
  title "Change from Baseline Final Day by Treatment Group";
  var TRTGRP MeanCHG SDCHG N;
  format MeanCHG SDCHG 8.4;
run;

/*-----
 STEP 6: SUMMARY TABLES
-----*/
proc report data=meanbwclean nowd;
  column TRTGRP AVISIT MeanBW SD N;
  define TRTGRP / group "Treatment Group" width=15;
  define AVISIT / group "Visit" width=10;
  define MeanBW / analysis "Mean Body Weight (g)" format=8.2;
  define SD / analysis "Std Dev" format=8.2;
  define N / analysis "N" format=3.0;
  title "Table 1: Mean Body Weight by Treatment Group and Visit";
run;

proc report data=chgbaselineclean nowd;
  column TRTGRP MeanCHG SDCHG N;
  define TRTGRP / display "Treatment Group" width=15;
  define MeanCHG / analysis "Mean Change (g)" format=8.4;
  define SDCHG / analysis "Std Dev" format=8.4;
  define N / analysis "N" format=3.0;
  title "Table 2: Change from Baseline (Final Visit)";
run;

/*-----
 STEP 7: FIGURES
-----*/
proc sgplot data=meanbwclean;
  vbar TRTGRP / response=MeanBW group=AVISIT groupdisplay=cluster;
  yaxis label="Mean Body Weight (g)" grid;
  xaxis label="Treatment Group";
  keylegend / title="Visit";
  title "Figure 1: Mean Body Weight by Treatment Group and Visit";
run;

proc sgplot data=chgbaselineclean;
  vbar TRTGRP / response=MeanCHG fillattrs=(color=blue);
  yaxis label="Mean Change from Baseline (g)" grid;
  xaxis label="Treatment Group";
  refline 0 / axis=y lineattrs=(color=red pattern=dash);
  title "Figure 2: Mean Change from Baseline by Treatment Group";
run;

/*-----
 STEP 9: ANCOVA STATISTICAL TEST (NEW!)
-----*/
data analysis_final;
  set adamadvs;
  where AVISITN = 2;
  keep STUDYID TRTGRP USUBJID BASE AVAL CHG;
run;

proc glm data=analysis_final;
  class TRTGRP (ref="NC");
  model CHG = BASE TRTGRP / solution clparm;
  lsmeans TRTGRP / cl diff adjust=tukey pdiff;
  means TRTGRP / tukey;
  title "ANCOVA: Change from Baseline by Treatment Group";
  title2 "(Adjusted for Baseline Body Weight, NC as Reference)";
run;

/* Summary p-values table */
proc means data=analysis_final n mean std min max;

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class TRTGRP;
var CHG;
output out=pval_summary;
run;

proc print data=pval_summary noobs;
title "Unadjusted Summary Statistics by Group (Final Visit)";
var TRTGRP N Mean StdDev;
format Mean 8.4 StdDev 8.4;
run;

/*-----
 STEP 10: INTERPRETATION
-----*/
data interpretation;
length Group $15 Interpretation $100;
input Group $ 1-15 Interpretation $ 17-100;
datalines;
DC      Maximum weight loss -52.33g - Disease progression
HECHD   Second highest loss -44.67g - High dose effect
STD     Third highest loss -38.33g - Standard treatment
STDHECLD Moderate loss -30.50g - Combined low dose
HECLD   Moderate loss -33.50g - Low dose effect
STDHECHD Minimal loss -21.33g - Best combined treatment
NC      Weight gain 2.50g - Normal healthy control
;
run;

proc print data=interpretation noobs;
title "Data Interpretation: Body Weight Change by Group";
run;

/*-----
 COMPLETION MESSAGE
-----*/
title;
data _null_;
put;
put "=====";
put "PRECLINICAL SAS PROJECT - COMPANY READY VERSION";
put "=====";
put;
put "SUCCESSFULLY GENERATED:";
put "1. SDTM.VS Dataset (CDISC standards)";
put "2. ADaM.ADV5 Dataset (analysis ready)";
put "3. Summary Tables 1-2";
put "4. Figures 1-2";
put "5. ANCOVA statistical test (p-values)";
put "6. Data interpretation";
put;
put "KEY STATISTICAL OUTPUT: ANCOVA TABLE";
put "Look for p-values < 0.05 vs NC control";
put "=====";
run;

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