/* Creates a study design for modality 0 and 1 based on designated
* split-plot design and pairing of readers and cases
* The scores do not matter. We only want the design arrays. */

public void makeDMatrices()

t0_modAB = new double[(int) Nnormal][(int) Nreader][2];
t1_modAB = new double[(int) Ndisease][(int) Nreader][2];
t0_modAA = new double[(int) Nnormal][(int) Nreader][2];
t0_modBB = new double[(int) Nnormal][(int) Nreader][2];
t1_modAA = new double[(int) Ndisease][(int) Nreader][2];
t1_modBB = new double[(int) Ndisease][(int) Nreader][2];
d0_modAA = new int[(int) Nnormal][(int) Nreader][2];
d0_modBB = new int[(int) Nnormal][(int) Nreader][2];
d0_modAB = new int[(int) Nnormal][(int) Nreader][2];
d1_modAA = new int[(int) Ndisease][(int) Nreader][2];
d1_modBB = new int[(int) Ndisease][(int) Nreader][2];
d1_modAB = new int[(int) Ndisease][(int) Nreader][2];
int NreaderPerModality, NreaderPerGroup;
int NnormalPerModality, NnormalPerGroup;
int NdiseasePerModality, NdiseasePerGroup;

SizePanel1.pairedReadersFlag == 1 ?

Yes

NreaderPerModality = (int) Nreader;

No

NreaderPerModality = (int) (Nreader / 2);
fullyCrossedA = false;
fullyCrossedB = false;
fullyCrossedAB = false;

SizePanel1.pairedNormalsFlag == 1 ?

Yes

NreaderPerModality = (int) Nnormal;

No

NreaderPerModality = (int) (Nnormal / 2);
fullyCrossedA = false;
fullyCrossedB = false;
fullyCrossedAB = false;

SizePanel1.pairedDiseasedFlag == 1 ?

Yes

NreaderPerModality = (int) Ndisease;

No

NreaderPerModality = (int) (Ndisease / 2);
fullyCrossedA = false;
fullyCrossedB = false;
fullyCrossedAB = false;

SizePanel1.numSplitPlots > 1 ?

Yes

fullyCrossedA = false;
fullyCrossedB = false;
fullyCrossedAB = false;

No

NreaderPerGroup = NreaderPerModality / SizePanel1.numSplitPlots;
NnormalPerGroup = NnormalPerModality / SizePanel1.numSplitPlots;
NdiseasePerGroup = NdiseasePerModality / SizePanel1.numSplitPlots;
int readerID_modA, caseID_modA;
int readerID_modB, caseID_modB;
int s = 0;

s < SizePanel1.numSplitPlots ?

No

End

Yes

Int i = 0;

i < NreaderPerGroup ?

Yes

readerID_modA = i + (NreaderPerGroup * s);

No

s++;

SizePanel1.pairedReadersFlag == 1

Yes

readerID_modB = readerID_modA;

No

readerID_modB = readerID_modA + NreaderPerModality;

Int j = 0;

j < NnormalPerGroup ?

Yes

caseID_modA = j + (NnormalPerGroup * s);

No

Int j = 0;

SizePanel1.pairedNormalsFlag == 1

Yes

caseID_modB = caseID_modA;

No

caseID_modB = caseID_modA + NnormalPerModality;

d0_modAA[caseID_modA][readerID_modA][0] = 1;
d0_modAA[caseID_modA][readerID_modA][1] = 1;
d0_modBB[caseID_modB][readerID_modB][0] = 1;
d0_modBB[caseID_modB][readerID_modB][1] = 1;
d0_modAB[caseID_modA][readerID_modA][0] = 1;
d0_modAB[caseID_modB][readerID_modB][1] = 1;

j++;

j < NdiseasePerGroup ?

No

caseID_modA = j + (NdiseasePerGroup * s);

SizePanel1.pairedDiseasedFlag == 1

No

caseID_modB = caseID_modA + NdiseasePerModality;

Yes

caseID_modB = caseID_modA

d1_modAA[caseID_modA][readerID_modA][0] = 1;
d1_modAA[caseID_modA][readerID_modA][1] = 1;
d1_modBB[caseID_modB][readerID_modB][0] = 1;
d1_modBB[caseID_modB][readerID_modB][1] = 1;
d1_modAB[caseID_modA][readerID_modA][0] = 1;
d1_modAB[caseID_modB][readerID_modB][1] = 1;

i++;

i++;