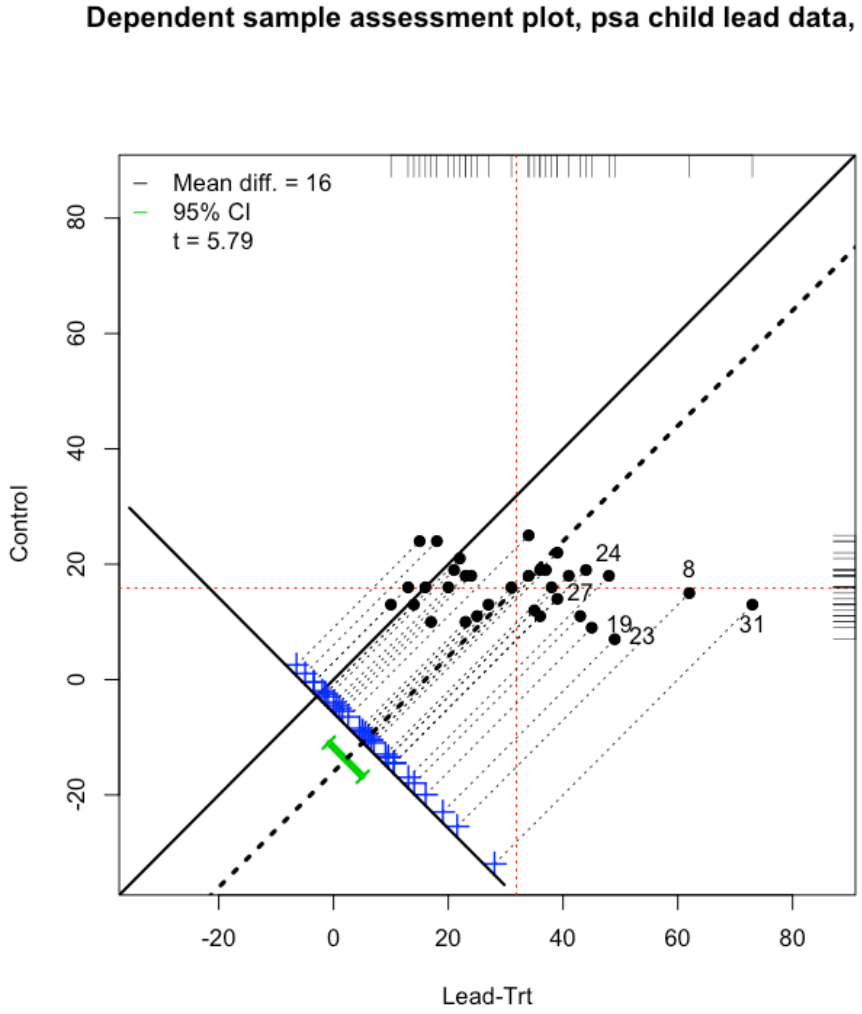
Here is an example using matched pairs. The data show lead in children's blood, the same data you saw in the Enhancing DepSample... document. Read that description carefully. Note that more extensive use is made of **granova.ds** features here than in previous pdf; on the second page, the Two Way ANOVA, w/ granova.2w entails a 'quadratic' fit (which you should study).

I: Dependent sample analysis (paired data) Using data lead.x2.rosnbm (below), and the command

- **granova.ds(lead.x2.rosnbm,colors=c(1,2,1,4,1,'green3'),ptcex=c(.9,1.5),ident=T,main=""), I obtained*:**
- ***If you want to replicate, but not put the 'ident' values in, just run granova.ds(lead.x2.rosnbm).**

Summary Stats	
n	33.000
mean(x)	31.879
mean(y)	15.879
mean(D=x-y)	16.000
SD(D)	15.865
ES(D)	1.009
r(x,y)	-0.178
r(x+y,d)	0.824
LL 95%CI	10.375
UL 95%CI	21.625
t(D-bar)	5.794
df.t	32.000
pval.t	0.000

Note that six points have been identified, as child pairs <24,27,…,31> for which the child of a battery factory worker had 'notably' more lead in his/her blood than did the matched child whose parent did not work in a lead-based battery factory. This result is not captured from a standard (numerical) analysis, but it seems central to our interpretation of the results in the matched pairs observational study. Interestingly, the parents of these six children had been found often to have used relatively poor hygiene, compared to their counterparts, i.e. for points to the left of these in the plot.



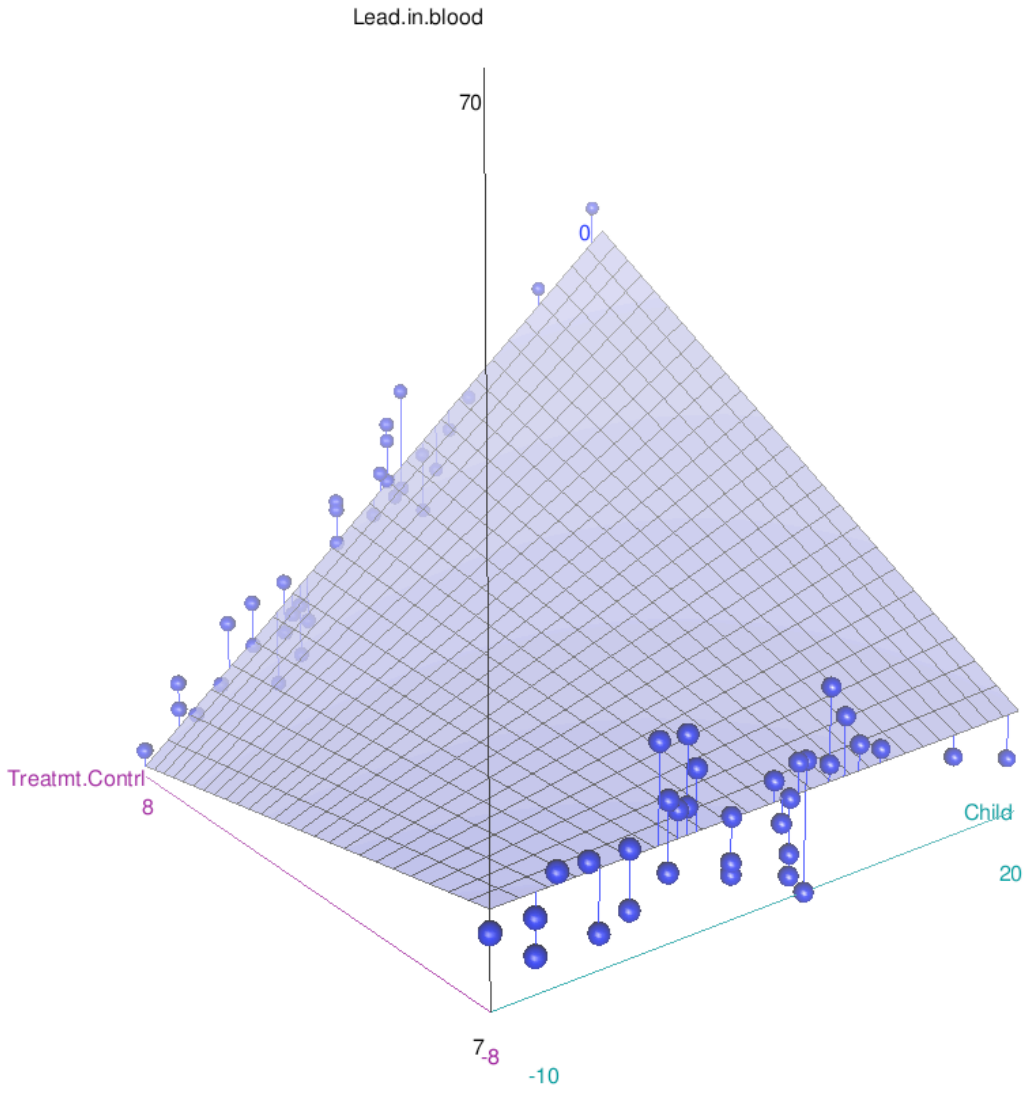
The foregoing graphic shows my results of running granova.ds; data are given below.
The same data can be examined using a two-way ANOVA, here using: ***granova.2w***

Exercise: ***EXAMINE FOLLOWING IN DETAIL, AND, if you can, SHOW THAT YOU CAN DO ALL OF THIS, including granova.1w and .2w using BOTH the lead data (below) AND A NEW DATA SET OF your own choosing. A function 'twoCol2.3' has been included below to facilitate getting data in the format you see below on the right side (for entry into granova.2w).***

II: TWO WAY ANOVA, using second form of data, as shown below:

```
To generate* the three column matrix needed, use blood.leadx3 = twoCol2.3(twocols of ds data) #function below

>granova.2w  (Initial results, effects for the two factors) are row and col contrasts (will discuss) (means are zero)
$Treatmt.Contrl.effects
 2  1
-8  8     #NOTE: these are TREATMENT EFFECTS for Lead vs. Control (compare w/ granova.ds result);< interpret

$Child.effects
     18      12      14      30      15       7      16      32      17      13      33       2       4      11      21
-12.400 -10.400 -10.400  -9.380  -7.880  -7.380  -5.880  -5.880  -4.380  -3.880  -3.880  -3.380  -2.880  -2.880  -2.380
      6       9      26      10      20       1      19      27      22       5
 -0.379  -0.379  -0.379   2.120   2.620   3.120   3.120   3.120   3.620   4.120
     23       3      29      28      25      24       8      31
  4.120   5.620   5.620   6.620   7.620   9.120  14.600  19.100

$CellCounts.Reordered   # Focus on the reordering; compare w/ result of apply(lead.x2.rosnbm, 1, mean)
              Child
Treatmt.Contrl 18 12 14 30 15 7 16 32 17 13 33 2 4 11 21 6 9 26 10 20 1 19 27 22 5 23 3 29 28 25 24 8 31
             2  1  1  1  1  1 1  1  1  1  1  1 1 1  1  1 1 1  1  1  1 1  1  1  1 1  1 1  1  1  1  1 1  1
             1  1  1  1  1  1 1  1  1  1  1  1 1 1  1  1 1 1  1  1  1 1  1  1  1 1  1 1  1  1  1  1 1  1

$CellMeans.Reordered  # When n=1 for each cell, naturally the 'means' are just the data values in 'cells'
              Child (col. values (18, 12, etc. are the position in the ordered set of pair means for 'child'
Treatmt.Contrl 18 12 14 30 15  7 16 32 17 13 33  2  4 11 21  6  9 26 10 20  1 19 27 22  5 23  3 29 28 25 24  8 31
             2 13 13 10 16 16 10 16 11 24 19 13 18 24 18 21 11 16 12 18 14 16  9 11 19 19  7 18 25 22 19 18 15 13
             1 10 14 17 13 16 23 20 25 15 21 27 23 18 24 22 36 31 35 34 39 38 45 43 36 37 49 41 34 39 44 48 62 73
$aov.summary
                    Df Sum Sq Mean Sq
factor(A)            1   4224    4224
factor(B)           32   3282     103
factor(A):factor(B) 32   4027     126     # See granova.2w function at end…copy/load to R.
```

See snapshot of the dynamic graphic next page for granova.2w output. You should be able to run the dynamic version in R by yourself. The key is to be able to see the similarities and differences in the two analyses, but to do this most effectively, you will want to run granova.2w with arg 'fit' set at 'linear' (its default). We shall discuss the linear and 'quadradic' analyses in class.



---See granova.2w dynamic graphic for the 2w analysis.

Input data for grannova.ds	Input data for granova.2w [obtained w/ func: twoCols2.3]

lead.x2.rosnbm

	Lead-Trt	Control
[1,]	38	16
[2,]	23	18
[3,]	41	18
[4,]	18	24
[5,]	37	19
[6,]	36	11
[7,]	23	10
[8,]	62	15
[9,]	31	16
[10,]	34	18
[11,]	24	18
[12,]	14	13
[13,]	21	19
[14,]	17	10
[15,]	16	16
[16,]	20	16
[17,]	15	24
[18,]	10	13
[19,]	45	9
[20,]	39	14
[21,]	22	21
[22,]	36	19
[23,]	49	7
[24,]	48	18
[25,]	44	19
[26,]	35	12
[27,]	43	11
[28,]	39	22
[29,]	34	25
[30,]	13	16
[31,]	73	13
[32,]	25	11
[33,]	27	13

lead.psa.A.B.df

	Lead.in.blood	Treatmt.Contrl	Child
1	38	1	1
2	16	2	1
3	23	1	2
4	18	2	2
5	41	1	3
6	18	2	3
7	18	1	4
8	24	2	4
9	37	1	5
10	19	2	5
11	36	1	6
12	11	2	6
13	23	1	7
14	10	2	7
15	62	1	8
16	15	2	8
17	31	1	9
18	16	2	9
19	34	1	10
20	18	2	10
21	24	1	11
22	18	2	11
23	14	1	12
24	13	2	12
25	21	1	13
26	19	2	13
27	17	1	14
28	10	2	14
29	16	1	15
30	16	2	15
31	20	1	16
32	16	2	16
33	15	1	17
34	24	2	17
35	10	1	18
36	13	2	18
37	45	1	19
38	9	2	19
39	39	1	20
40	14	2	20
41	22	1	21
42	21	2	21
43	36	1	22
44	19	2	22
45	49	1	23
46	7	2	23

	47	48	1	24
	48	18	2	24
	49	44	1	25
	50	19	2	25
	51	35	1	26
	52	12	2	26
	53	43	1	27
	54	11	2	27
	55	39	1	28
	56	22	2	28
	57	34	1	29
	58	25	2	29
	59	13	1	30
	60	16	2	30
	61	73	1	31
	62	13	2	31
	63	25	1	32
	64	11	2	32
	65	27	1	33
	66	13	2	33

```
#The following function takes data from a two dependent sample set-up, and converts it to be able to use granova.2w

twoCols2.3 <- function (xx)
{
  # xx is assumed to be a matrix w/ two columns of (quantitative) data (e.g., data for dep. Sample analysis
    xv = c(xx[, 1], xx[, 2])  #same as xv = as.vector(xx)
    ncx = nrow(xx)
    xx3 = data.frame(xv, rep(1:ncx, 2), rep(1:2, ea = ncx))
    dimnames(xx3)[2]=list(c("Response","FactorA","FactorB"))
    xx3 = round(xx3,2)
}
```