

Statistical Analyses for Split-Plot Design

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Split-plot experimental design

Factorial experimental design is commonly used but sometimes it is not workable in some specific cases. For example, if a number of rice varieties are grown at different levels of fertilizer. It is more reasonable that different varieties are grown in a field block with the same level of fertilizer. That means each fertilizer treatment can be considered as a main plot and each variety considered as subplot. Such an experimental design is called split-plot experimental design, which is another design related to treatment design and local variation control.

The data used for our demonstrations come from the package `agridat`. There are three genotype groups. We only use the first group named "S1". Please look at the following R codes to get the sub data set.

```
require(agridat)

## Loading required package: agridat

data(gomez.groupsplot)
dat <- gomez.groupsplot
str(dat)

## 'data.frame': 270 obs. of 7 variables:
## $ x : int 1 3 5 6 7 8 1 3 5 6 ...
## $ y : int 27 9 4 20 18 3 26 1 14 21 ...
## $ rep : Factor w/ 3 levels "R1","R2","R3": 1 1 2 2 3 3 1 1 2 2 ...
## $ fert : Factor w/ 2 levels "F1","F2": 1 2 1 2 1 2 1 2 1 2 ...
## $ gen : Factor w/ 45 levels "G01","G02","G03",...: 1 1 1 1 1 1 2 2 2 2
## $ group: Factor w/ 3 levels "S1","S2","S3": 1 1 1 1 1 1 1 1 1 1 ...
## $ yield: num 4.25 4.33 3.55 5.27 3.11 ...

dat1=dat[which(dat$group=="S1"),]
```

ANOVA based analysis

First we will run this sub-data set and will consider different assumptions for this sub data set. Again, we will convert the variable `rep`, which is a block variable, into a factor variable, as we did before. The following data analysis is to treat `fert` and `gen` as factorial arrangement with RCB design.

Factorial design analysis

```
dat1=transform(dat1,rep=factor(rep))
mod1=aov(yield~fert*gen+rep,data=dat1)
a=summary(mod1)
data.frame(a[[1]])
```

	Df	Sum.Sq	Mean.Sq	F.value	Pr..F.
fert	1	39.636828	39.6368281	273.327918	0.0000000
gen	14	5.730485	0.4093204	2.822594	0.0028305
rep	2	3.833836	1.9169182	13.218698	0.0000186
fert:gen	14	2.143651	0.1531179	1.055872	0.4149113
Residuals	58	8.410908	0.1450157	NA	NA

Split-plot design analysis

As mentioned in this class, for split-plot design, the model should include main plot and block interaction effects too. In this demonstration, it is rep by fert interaction.

```
dat1=transform(dat1,rep=factor(rep))
mod2=aov(yield~fert*gen+rep+rep:fert,data=dat1)
a=summary(mod2)
data.frame(a[[1]])
```

	Df	Sum.Sq	Mean.Sq	F.value	Pr..F.
fert	1	39.636828	39.6368281	344.036660	0.0000000
gen	14	5.730485	0.4093204	3.552787	0.0003488
rep	2	3.833836	1.9169182	16.638318	0.0000021
fert:gen	14	2.143651	0.1531179	1.329021	0.2204093
fert:rep	2	1.959089	0.9795444	8.502174	0.0005963
Residuals	56	6.451819	0.1152111	NA	NA

You may compare two models through anova function or relative efficiency.

```
anova(mod1,mod2)
```

Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
58	8.410908	NA	NA	NA	NA
56	6.451819	2	1.959089	8.502174	0.0005963

The above results indicate that rep by fert interaction is significant either by mod2 or by comparing two models with a F-test. In addition, the above F-tests for mod1 and mod2 are right if all effects including block and block-main plot interaction effects (mod2). Since EMS for these mean squares could be different based on which types of these effects, appropriate F-tests could be different too. However, again, it is easy to employ linear mixed

model approaches to estimate variance components and fixed effects and to predict random effects. .

Linear mixed model approaches

Case 1: Both fertilizer and genotype are fixed

Factorial design analysis

The first case considers both fertilizer and genotype effects are fixed while block is random.

```
require(minque)
## Loading required package: minque
## Loading required package: klaR
## Loading required package: MASS
## Loading required package: Matrix
res=lmm.jack(yield~fert*gen|rep,data=dat1)[[1]]
data.frame(res$Var[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(rep)	0.0594385	0.0096398	0.0006618	0.0253881	0.0934890
V(e)	0.1458115	0.0103308	0.0000008	0.1093202	0.1823027

```
data.frame(res$PVar[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(rep)/VP	0.2886951	0.0315772	3e-05	0.1771560	0.4002341
V(e)/VP	0.7113049	0.0315772	0e+00	0.5997659	0.8228440

```
data.frame(res$FixedEffect[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
mu	3.9443802	0.0074829	0.0000000	3.9179487	3.9708116
fert(F1)	-0.4318462	0.0312474	0.0000009	-0.5422204	-0.3214719
fert(F2)	0.4318462	0.0312474	0.0000009	0.3214719	0.5422204
gen(G01)	0.1325809	0.0416543	0.0436742	-0.0145533	0.2797151
gen(G02)	-0.2114309	0.0548103	0.0153431	-0.4050355	-0.0178263
gen(G03)	-0.2513337	0.0505952	0.0030858	-0.4300496	-0.0726179
gen(G04)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G05)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606

gen(G06)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G07)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G08)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G09)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G10)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G11)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G12)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G13)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G14)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
gen(G15)	0.0275153	0.0050238	0.0015656	0.0097700	0.0452606
fert:gen(F1:G01)	-0.0082541	0.0807418	0.9928135	-0.2934559	0.2769478
fert:gen(F2:G01)	0.1133196	0.0772817	0.5226941	-0.1596599	0.3862992
fert:gen(F1:G02)	-0.3145958	0.0608253	0.0023396	-0.5294470	-0.0997446
fert:gen(F2:G02)	0.0756497	0.0833569	0.8216952	-0.2187895	0.3700888
fert:gen(F1:G03)	-0.3153611	0.0809964	0.0145281	-0.6014623	-0.0292599
fert:gen(F2:G03)	0.0365121	0.0792592	0.9584050	-0.2434527	0.3164768
fert:gen(F1:G04)	0.3104004	0.0635110	0.0034451	0.0860624	0.5347384
fert:gen(F2:G04)	0.6025789	0.0617282	0.0000175	0.3845384	0.8206194
fert:gen(F1:G05)	-0.4389099	0.1764346	0.1301416	-1.0621242	0.1843045
fert:gen(F2:G05)	0.3517217	0.1535994	0.1758986	-0.1908326	0.8942760
fert:gen(F1:G06)	-0.5132211	0.0869069	0.0009098	-0.8201995	-0.2062427
fert:gen(F2:G06)	0.3347228	0.1984620	0.4057200	-0.3662984	1.0357440
fert:gen(F1:G07)	-0.2754170	0.1522886	0.3476111	-0.8133411	0.2625071
fert:gen(F2:G07)	0.5709318	0.1747097	0.0382075	-0.0461899	1.1880534
fert:gen(F1:G08)	-0.4435127	0.0350986	0.0000020	-0.5674903	-0.3195351
fert:gen(F2:G08)	-0.3879456	0.0536692	0.0001972	-0.5775197	-0.1983715
fert:gen(F1:G09)	-0.5228541	0.0289707	0.0000001	-0.6251864	-0.4205217
fert:gen(F2:G09)	0.1754309	0.1137295	0.4808118	-0.2262923	0.5771542
fert:gen(F1:G10)	0.1232984	0.0309238	0.0126150	0.0140671	0.2325297
fert:gen(F2:G10)	0.0601966	0.0325152	0.3285586	-0.0546557	0.1750490
fert:gen(F1:G11)	0.1540651	0.0440641	0.0267295	-0.0015811	0.3097113
fert:gen(F2:G11)	0.5523724	0.0630105	0.0000423	0.3298022	0.7749425
fert:gen(F1:G12)	-0.2559428	0.0712485	0.0230374	-0.5076117	-0.0042740
fert:gen(F2:G12)	0.4641937	0.0305228	0.0000004	0.3563788	0.5720086
fert:gen(F1:G13)	-0.6684354	0.0533143	0.0000021	-0.8567560	-0.4801148
fert:gen(F2:G13)	0.2126568	0.1102573	0.2959987	-0.1768017	0.6021154

```
fert:gen(F1:G14) -0.0391260 0.0907357 0.9632165 -0.3596289 0.2813769
fert:gen(F2:G14) 0.1857381 0.0476127 0.0143640 0.0175574 0.3539188
fert:gen(F1:G15) -0.2227580 0.0510440 0.0072281 -0.4030589 -0.0424570
fert:gen(F2:G15) 0.0825445 0.0847630 0.7911443 -0.2168611 0.3819502
data.frame(res$RandomEffect[[1]])
```

	Pre	SE	PValue	X2.5.LL	X97.5.UL
rep(R1)	0.1208506	0.0256745	0.0044280	0.0301613	0.2115398
rep(R2)	0.1582166	0.0178247	0.0000382	0.0952549	0.2211783
rep(R3)	-0.2790671	0.0231431	0.0000030	-0.3608147	-0.1973196

Both fertilizer and genotype effects are fixed while block and block and main factor interaction effects are random.

```
require(minque)
res=lmm.jack(yield~fert*gen|rep+rep:fert,data=dat1)[[1]]
data.frame(res$Var[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(rep)	0.0312351	0.0100066	0.0481145	-0.0041108	0.0665810
V(fert:rep)	0.0578626	0.0132221	0.0071017	0.0111584	0.1045667
V(e)	0.1149846	0.0093836	0.0000026	0.0818393	0.1481298

```
data.frame(res$PVar[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(rep)/VP	0.1535817	0.0491057	0.0476527	-0.0198729	0.3270363
V(fert:rep)/VP	0.2820379	0.0510959	0.0014814	0.1015536	0.4625223
V(e)/VP	0.5643803	0.0400662	0.0000008	0.4228558	0.7059049

```
data.frame(res$FixedEffect[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
mu	3.9476916	0.0203617	0.0000000	3.8757687	4.0196144
fert(F1)	-0.4276610	0.0341491	0.0000021	-0.5482850	-0.3070370
fert(F2)	0.4276610	0.0341491	0.0000021	0.3070370	0.5482850
gen(G01)	0.1378937	0.0430995	0.0425510	-0.0143452	0.2901325
gen(G02)	-0.2201409	0.0853995	0.1131839	-0.5217949	0.0815131
gen(G03)	-0.2498342	0.0363318	0.0002902	-0.3781679	-0.1215004
gen(G04)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G05)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910

gen(G06)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G07)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G08)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G09)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G10)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G11)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G12)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G13)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G14)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
gen(G15)	0.0276735	0.0063465	0.0072662	0.0052559	0.0500910
fert:gen(F1:G01)	0.0011635	0.0780580	0.9957173	-0.2745582	0.2768852
fert:gen(F2:G01)	0.1090567	0.0555933	0.2828769	-0.0873137	0.3054270
fert:gen(F1:G02)	-0.3219766	0.0468976	0.0002937	-0.4876316	-0.1563216
fert:gen(F2:G02)	0.0741622	0.0866680	0.8439030	-0.2319723	0.3802967
fert:gen(F1:G03)	-0.3143988	0.0237847	0.0000013	-0.3984127	-0.2303849
fert:gen(F2:G03)	0.0368912	0.0296935	0.6492352	-0.0679942	0.1417767
fert:gen(F1:G04)	0.3106885	0.0388270	0.0000884	0.1735411	0.4478359
fert:gen(F2:G04)	0.6015871	0.0511291	0.0000036	0.4209853	0.7821889
fert:gen(F1:G05)	-0.4670517	0.0842720	0.0014392	-0.7647229	-0.1693805
fert:gen(F2:G05)	0.3511031	0.0947173	0.0193094	0.0165362	0.6856700
fert:gen(F1:G06)	-0.5225224	0.0584453	0.0000361	-0.7289669	-0.3160778
fert:gen(F2:G06)	0.3633063	0.1643924	0.1981247	-0.2173719	0.9439846
fert:gen(F1:G07)	-0.2385266	0.1794523	0.6000924	-0.8724002	0.3953470
fert:gen(F2:G07)	0.5977904	0.1414919	0.0088585	0.0980030	1.0975777
fert:gen(F1:G08)	-0.4493028	0.0594134	0.0001384	-0.6591667	-0.2394388
fert:gen(F2:G08)	-0.3838942	0.1195379	0.0417511	-0.8061341	0.0383458
fert:gen(F1:G09)	-0.5283384	0.0585363	0.0000334	-0.7351042	-0.3215726
fert:gen(F2:G09)	0.1725362	0.0696937	0.1325771	-0.0736407	0.4187132
fert:gen(F1:G10)	0.1114754	0.0581451	0.3006985	-0.0939089	0.3168597
fert:gen(F2:G10)	0.0586836	0.0555575	0.7501975	-0.1375603	0.2549275
fert:gen(F1:G11)	0.1480279	0.0542344	0.0892916	-0.0435426	0.3395984
fert:gen(F2:G11)	0.5553736	0.0781542	0.0002251	0.2793121	0.8314351
fert:gen(F1:G12)	-0.2599854	0.1018006	0.1174679	-0.6195723	0.0996016
fert:gen(F2:G12)	0.4626236	0.0340605	0.0000011	0.3423128	0.5829345
fert:gen(F1:G13)	-0.6750332	0.0567374	0.0000033	-0.8754448	-0.4746215
fert:gen(F2:G13)	0.1979043	0.1290407	0.4856227	-0.2579021	0.6537106

```
fert:gen(F1:G14) -0.0574378 0.0860391 0.9106387 -0.3613511 0.2464755
fert:gen(F2:G14) 0.1995056 0.1177391 0.4017966 -0.2163804 0.6153917
fert:gen(F1:G15) -0.2182243 0.0703714 0.0496896 -0.4667948 0.0303463
fert:gen(F2:G15) 0.0848128 0.0846682 0.7776360 -0.2142579 0.3838835
data.frame(res$RandomEffect[[1]])
```

	Pre	SE	PValue	X2.5.LL	X97.5.UL
rep(R1)	0.0864756	0.0153250	0.0012653	0.0323436	0.1406077
rep(R2)	0.1139885	0.0264115	0.0077533	0.0206959	0.2072811
rep(R3)	-0.2004641	0.0328923	0.0007215	-0.3166487	-0.0842795
fert:rep(F1:R1)	0.2667137	0.0416790	0.0005014	0.1194924	0.4139349
fert:rep(F2:R1)	-0.1498447	0.0349824	0.0081295	-0.2734119	-0.0262775
fert:rep(F1:R2)	-0.1843649	0.0339609	0.0016670	-0.3043241	-0.0644057
fert:rep(F2:R2)	0.3363749	0.0365948	0.0000287	0.2071122	0.4656377
fert:rep(F1:R3)	-0.0823488	0.0263592	0.0479141	-0.1754564	0.0107589
fert:rep(F2:R3)	-0.1865302	0.0405031	0.0051116	-0.3295980	-0.0434625

Case 2: Fertilizer fixed but genotype random

Factorial design analysis

```
require(minique)
res=lmm.jack(yield~fert|gen*fert+rep,data=dat1)[[1]]
data.frame(res$Var[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(gen)	0.0427802	0.0112268	0.0164791	0.0031239	0.0824364
V(rep)	0.0599734	0.0059927	0.0000142	0.0388057	0.0811412
V(fert:gen)	0.0073609	0.0093635	0.8711894	-0.0257133	0.0404352
V(e)	0.1442927	0.0148187	0.0000179	0.0919490	0.1966363

```
data.frame(res$PVar[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(gen)/VP	0.1683283	0.0455030	0.0195352	0.0075995	0.3290571
V(rep)/VP	0.2356440	0.0177059	0.0000013	0.1731020	0.2981860
V(fert:gen)/VP	0.0292470	0.0372346	0.8714319	-0.1022756	0.1607696
V(e)/VP	0.5667807	0.0420287	0.0000011	0.4183240	0.7152374

```
data.frame(res$FixedEffect[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
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```
mu      3.9480396  0.011905      0  3.9059881  3.9900911
fert(F1) -0.6642067  0.016169      0 -0.7213200 -0.6070934
fert(F2)  0.6642067  0.016169      0  0.6070934  0.7213200
```

```
data.frame(res$RandomEffect[[1]])
```

	Pre	SE	PValue	X2.5.LL	X97.5.UL
gen(G01)	0.1465340	0.0729759	0.2651996	-0.1112365	0.4043044
gen(G02)	-0.2398702	0.0796000	0.0570585	-0.5210389	0.0412985
gen(G03)	-0.3002578	0.0650895	0.0050563	-0.5301715	-0.0703441
gen(G04)	0.3677629	0.0560287	0.0004139	0.1698546	0.5656711
gen(G05)	-0.0172755	0.0420355	0.9662666	-0.1657560	0.1312051
gen(G06)	-0.0517731	0.0788844	0.9139160	-0.3304139	0.2268678
gen(G07)	0.1475406	0.0557998	0.1020621	-0.0495594	0.3446406
gen(G08)	-0.2984051	0.0406282	0.0001740	-0.4419149	-0.1548954
gen(G09)	-0.1148411	0.0330284	0.0275459	-0.2315062	0.0018239
gen(G10)	0.0856885	0.0163935	0.0021744	0.0277821	0.1435949
gen(G11)	0.2878893	0.0346932	0.0000660	0.1653437	0.4104350
gen(G12)	0.0988792	0.0228896	0.0077086	0.0180269	0.1797315
gen(G13)	-0.1533010	0.0334868	0.0053144	-0.2715854	-0.0350166
gen(G14)	0.0734202	0.0614342	0.6756733	-0.1435820	0.2904223
gen(G15)	-0.0319908	0.0449066	0.8967914	-0.1906130	0.1266314
rep(R1)	0.1209871	0.0201075	0.0007930	0.0499621	0.1920120
rep(R2)	0.1591791	0.0320962	0.0031202	0.0458068	0.2725514
rep(R3)	-0.2801661	0.0144108	0.0000000	-0.3310690	-0.2292633
fert:gen(F1:G01)	0.0764388	0.0860057	0.8299169	-0.2273565	0.3802342
fert:gen(F2:G01)	-0.0401109	0.0573511	0.9009401	-0.2426903	0.1624685
fert:gen(F1:G02)	-0.0169388	0.0247827	0.9058678	-0.1044778	0.0706002
fert:gen(F2:G02)	-0.0553897	0.0742154	0.8854376	-0.3175383	0.2067590
fert:gen(F1:G03)	-0.0329549	0.0507817	0.9160149	-0.2123295	0.1464196
fert:gen(F2:G03)	-0.0600111	0.0649701	0.8144736	-0.2895030	0.1694808
fert:gen(F1:G04)	0.0807875	0.0840879	0.7973510	-0.2162336	0.3778087
fert:gen(F2:G04)	0.0340392	0.0366615	0.8122981	-0.0954592	0.1635376
fert:gen(F1:G05)	-0.0615883	0.0782173	0.8707196	-0.3378727	0.2146961
fert:gen(F2:G05)	0.0601507	0.0909883	0.9125389	-0.2612443	0.3815457
fert:gen(F1:G06)	-0.0687881	0.0763761	0.8247351	-0.3385691	0.2009928
fert:gen(F2:G06)	0.0475792	0.0866540	0.9411264	-0.2585059	0.3536643
fert:gen(F1:G07)	-0.0420245	0.0539425	0.8737957	-0.2325640	0.1485150

fert:gen(F2:G07)	0.0898316	0.0983920	0.8192678	-0.2577153	0.4373785
fert:gen(F1:G08)	0.0169504	0.0209658	0.8627519	-0.0571066	0.0910074
fert:gen(F2:G08)	-0.1112890	0.1159322	0.7977285	-0.5207925	0.2982146
fert:gen(F1:G09)	-0.0480754	0.0481100	0.7788255	-0.2180128	0.1218619
fert:gen(F2:G09)	0.0108575	0.0450571	0.9848095	-0.1482964	0.1700114
fert:gen(F1:G10)	0.0921539	0.0939166	0.7875933	-0.2395847	0.4238925
fert:gen(F2:G10)	-0.0629855	0.0647480	0.7916452	-0.2916929	0.1657219
fert:gen(F1:G11)	0.0554999	0.0563296	0.7856442	-0.1434713	0.2544712
fert:gen(F2:G11)	0.0361846	0.0413146	0.8354638	-0.1097496	0.1821188
fert:gen(F1:G12)	-0.0260692	0.0275946	0.8048418	-0.1235408	0.0714025
fert:gen(F2:G12)	0.0557771	0.0579897	0.7968351	-0.1490582	0.2606123
fert:gen(F1:G13)	-0.0888101	0.0919457	0.7949183	-0.4135872	0.2359669
fert:gen(F2:G13)	0.0450685	0.0531867	0.8473299	-0.1428012	0.2329383
fert:gen(F1:G14)	0.0495363	0.0520750	0.8018067	-0.1344065	0.2334791
fert:gen(F2:G14)	-0.0261707	0.0344080	0.8804473	-0.1477092	0.0953677
fert:gen(F1:G15)	0.0138826	0.0196838	0.8990730	-0.0556459	0.0834112
fert:gen(F2:G15)	-0.0235316	0.0358389	0.9138359	-0.1501243	0.1030610

Split-plot design analysis

```
require(minqu)
res=lmm.jack(yield~fert|gen*fert+rep+rep:fert,data=dat1)[[1]]
data.frame(res$Var[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(gen)	0.0429392	0.0102794	0.0095038	0.0066297	0.0792486
V(rep)	0.0299993	0.0067143	0.0062201	0.0062825	0.0537162
V(fert:gen)	0.0123174	0.0083692	0.5196732	-0.0172450	0.0418798
V(fert:rep)	0.0581854	0.0129683	0.0060544	0.0123778	0.1039930
V(e)	0.1149937	0.0072988	0.0000003	0.0892123	0.1407752

```
data.frame(res$PVar[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(gen)/VP	0.1660638	0.0375681	0.0066619	0.0333634	0.2987643
V(rep)/VP	0.1164344	0.0270412	0.0078678	0.0209176	0.2119511
V(fert:gen)/VP	0.0472924	0.0303100	0.4712355	-0.0597708	0.1543555
V(fert:rep)/VP	0.2236038	0.0397591	0.0012960	0.0831640	0.3640436
V(e)/VP	0.4466056	0.0348513	0.0000018	0.3235016	0.5697096

```
data.frame(res$FixedEffect[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
mu	3.949086	0.0158159	0	3.8932201	4.0049524
fert(F1)	-0.663238	0.0172214	0	-0.7240686	-0.6024074
fert(F2)	0.663238	0.0172214	0	0.6024074	0.7240686

```
data.frame(res$RandomEffect[[1]])
```

	Pre	SE	PValue	X2.5.LL	X97.5.UL
gen(G01)	0.1394352	0.0310984	0.0060811	0.0295871	0.2492832
gen(G02)	-0.2392546	0.0343173	0.0002610	-0.3604724	-0.1180367
gen(G03)	-0.2999031	0.0361100	0.0000656	-0.4274535	-0.1723527
gen(G04)	0.3704987	0.0408779	0.0000322	0.2261068	0.5148905
gen(G05)	-0.0259140	0.0471774	0.9410784	-0.1925574	0.1407294
gen(G06)	-0.0411825	0.0703656	0.9327393	-0.2897327	0.2073677
gen(G07)	0.1512280	0.0838451	0.3498205	-0.1449356	0.4473916
gen(G08)	-0.2987515	0.0807102	0.0194677	-0.5838416	-0.0136615
gen(G09)	-0.1170646	0.0332346	0.0256717	-0.2344581	0.0003288
gen(G10)	0.0908668	0.0395007	0.1731397	-0.0486601	0.2303937
gen(G11)	0.2858069	0.0608528	0.0044927	0.0708586	0.5007553
gen(G12)	0.0980034	0.0463317	0.2275780	-0.0656526	0.2616594
gen(G13)	-0.1613616	0.0379360	0.0084937	-0.2953617	-0.0273616
gen(G14)	0.0821908	0.0539382	0.4909945	-0.1083336	0.2727151
gen(G15)	-0.0345977	0.0276473	0.6441698	-0.1322554	0.0630600
rep(R1)	0.0867264	0.0124098	0.0002562	0.0428917	0.1305610
rep(R2)	0.1112372	0.0175308	0.0005344	0.0493137	0.1731607
rep(R3)	-0.1979636	0.0235396	0.0000593	-0.2811118	-0.1148153
fert:gen(F1:G01)	0.1268628	0.0702167	0.3484221	-0.1211614	0.3748870
fert:gen(F2:G01)	-0.0507639	0.0457417	0.7221537	-0.2123359	0.1108081
fert:gen(F1:G02)	-0.0577349	0.0434734	0.6007411	-0.2112946	0.0958248
fert:gen(F2:G02)	-0.0707683	0.0544773	0.6172143	-0.2631967	0.1216602
fert:gen(F1:G03)	-0.0473398	0.0268179	0.3676048	-0.1420680	0.0473884
fert:gen(F2:G03)	-0.1158751	0.0663883	0.3769944	-0.3503763	0.1186261
fert:gen(F1:G04)	0.1408311	0.0596802	0.1582853	-0.0699754	0.3516376
fert:gen(F2:G04)	0.0569887	0.0303814	0.3180148	-0.0503266	0.1643040
fert:gen(F1:G05)	-0.0970192	0.0587029	0.4228030	-0.3043736	0.1103352
fert:gen(F2:G05)	0.0861517	0.0642025	0.5928869	-0.1406287	0.3129321
fert:gen(F1:G06)	-0.1156209	0.0693857	0.4158789	-0.3607099	0.1294680

fert:gen(F2:G06)	0.0996137	0.0759074	0.6096854	-0.1685117	0.3677390
fert:gen(F1:G07)	-0.0624059	0.0542840	0.7006880	-0.2541515	0.1293397
fert:gen(F2:G07)	0.1470174	0.0837872	0.3725986	-0.1489415	0.4429764
fert:gen(F1:G08)	0.0190141	0.0235970	0.8637839	-0.0643366	0.1023649
fert:gen(F2:G08)	-0.1777826	0.1085015	0.4300714	-0.5610389	0.2054738
fert:gen(F1:G09)	-0.0946956	0.0446705	0.2260638	-0.2524840	0.0630928
fert:gen(F2:G09)	0.0277760	0.0368264	0.8826885	-0.1023048	0.1578567
fert:gen(F1:G10)	0.1599717	0.0748760	0.2206755	-0.1045104	0.4244538
fert:gen(F2:G10)	-0.1166412	0.0576222	0.2591979	-0.3201784	0.0868961
fert:gen(F1:G11)	0.0990958	0.0515889	0.2991922	-0.0831299	0.2813215
fert:gen(F2:G11)	0.0548125	0.0467121	0.6876615	-0.1101872	0.2198123
fert:gen(F1:G12)	-0.0348621	0.0380390	0.8177089	-0.1692261	0.0995019
fert:gen(F2:G12)	0.0896065	0.0384985	0.1662000	-0.0463804	0.2255934
fert:gen(F1:G13)	-0.1483990	0.0676200	0.2026767	-0.3872509	0.0904529
fert:gen(F2:G13)	0.0652937	0.0363614	0.3534620	-0.0631444	0.1937317
fert:gen(F1:G14)	0.0830316	0.0468304	0.3639504	-0.0823861	0.2484492
fert:gen(F2:G14)	-0.0467834	0.0440937	0.7477609	-0.2025343	0.1089675
fert:gen(F1:G15)	0.0292703	0.0171636	0.3964133	-0.0313562	0.0898969
fert:gen(F2:G15)	-0.0486458	0.0359991	0.5875293	-0.1758043	0.0785127
fert:rep(F1:R1)	0.2688873	0.0340519	0.0000982	0.1486069	0.3891678
fert:rep(F2:R1)	-0.1515937	0.0292611	0.0023128	-0.2549517	-0.0482356
fert:rep(F1:R2)	-0.1868715	0.0294534	0.0005347	-0.2909087	-0.0828343
fert:rep(F2:R2)	0.3373297	0.0428105	0.0000999	0.1861115	0.4885479
fert:rep(F1:R3)	-0.0820158	0.0232953	0.0257387	-0.1643012	0.0002696
fert:rep(F2:R3)	-0.1857360	0.0329417	0.0012725	-0.3020948	-0.0693772

Other applications: Repeated measurement analysis

Sometimes, a repeated measurements data set or a space-related or time-related data set can be analyzed by treating it as a split-plot experimental design. We will use a data set from the package minque. This is a space-based data set, which contains cotton boll rate at different positions for different genotypes. We may run several different ways of data analyses. The first way is to run data analysis for each position, which is similar to an RCB design with one factor. Please refer to Chapter 4 for detailed information. The second way is to treat genotypes as main plots while positions as split plots. Therefore, block(Rep here) and genotype interaction effects should be included in the data analysis. Please focus on how to develop a model frame and interpret the results generated.

```
require(minique)
data(brate)
names(brate)

## [1] "Year" "Geno" "Pos" "Rep" "Brate"

brate=transform(brate, Geno=factor(Geno),Pos=factor(Pos),Rep=factor(Rep))
res=lmm.jack(Brate~Pos|Geno*Pos+Rep+Rep:Geno,data=brate)[[1]]
data.frame(res$Var[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(Geno)	0.0000063	0.0000198	0.9780305	-0.0000636	0.0000761
V(Rep)	0.0005113	0.0001727	0.0620819	-0.0000988	0.0011214
V(Pos:Geno)	0.0036431	0.0009651	0.0173988	0.0002342	0.0070519
V(Geno:Rep)	0.0008975	0.0005082	0.3672575	-0.0008976	0.0026926
V(e)	0.0250745	0.0009644	0.0000000	0.0216679	0.0284811

```
data.frame(res$PVar[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
V(Geno)/VP	0.0002192	0.0006933	0.9780305	-0.0022296	0.0026680
V(Rep)/VP	0.0169521	0.0056830	0.0598710	-0.0031216	0.0370258
V(Pos:Geno)/VP	0.1203859	0.0285983	0.0090612	0.0193690	0.2214027
V(Geno:Rep)/VP	0.0297033	0.0167234	0.3624916	-0.0293682	0.0887747
V(e)/VP	0.8327395	0.0322943	0.0000000	0.7186674	0.9468117

```
data.frame(res$FixedEffect[[1]])
```

	Estimate	SE	PValue	X2.5.LL	X97.5.UL
mu	0.2984838	0.0035932	0.0000000	0.2857918	0.3111759
Pos(5)	-0.0822500	0.0102534	0.0000866	-0.1184679	-0.0460321
Pos(6)	0.0369239	0.0124968	0.0626076	-0.0072181	0.0810658
Pos(7)	0.0727221	0.0095621	0.0001323	0.0389461	0.1064981
Pos(8)	0.1043943	0.0122973	0.0000549	0.0609568	0.1478319
Pos(9)	0.1424064	0.0097178	0.0000006	0.1080806	0.1767323
Pos(10)	0.0444745	0.0105407	0.0089317	0.0072420	0.0817070
Pos(11)	0.0832169	0.0109846	0.0001365	0.0444164	0.1220174
Pos(12)	0.0162389	0.0160313	0.7720897	-0.0403882	0.0728659
Pos(13)	-0.0104393	0.0125222	0.8528697	-0.0546712	0.0337926
Pos(14)	-0.0414534	0.0086826	0.0040300	-0.0721227	-0.0107841
Pos(15)	-0.0973529	0.0121112	0.0000852	-0.1401330	-0.0545728
Pos(16)	-0.0957614	0.0072241	0.0000013	-0.1212788	-0.0702440

Pos(17) -0.1731201 0.0175130 0.0000158 -0.2349806 -0.1112596

`data.frame(res$RandomEffect[[1]])`

	Pre	SE	PValue	X2.5.LL	X97.5.UL
Geno(1)	0.0005703	0.0018034	0.9780305	-0.0057999	0.0069405
Geno(2)	-0.0001319	0.0004172	0.9780305	-0.0016054	0.0013416
Geno(3)	0.0009635	0.0030468	0.9780305	-0.0097986	0.0117256
Geno(4)	-0.0003482	0.0011012	0.9780305	-0.0042381	0.0035417
Geno(5)	-0.0010536	0.0033318	0.9780305	-0.0128225	0.0107152
Rep(1)	-0.0284500	0.0059175	0.0038463	-0.0493521	-0.0075479
Rep(2)	0.0131177	0.0082005	0.4503287	-0.0158489	0.0420842
Rep(3)	0.0191187	0.0077237	0.1326381	-0.0081634	0.0464008
Rep(4)	-0.0037864	0.0054474	0.9022957	-0.0230282	0.0154555
Pos:Geno(5:1)	-0.1208037	0.0132072	0.0000299	-0.1674549	-0.0741525
Pos:Geno(5:2)	0.0912032	0.0193658	0.0044126	0.0227980	0.1596084
Pos:Geno(5:3)	0.0084166	0.0112919	0.8857713	-0.0314693	0.0483025
Pos:Geno(5:4)	0.0460848	0.0139375	0.0359577	-0.0031460	0.0953157
Pos:Geno(5:5)	-0.0249009	0.0173938	0.5421186	-0.0863405	0.0365386
Pos:Geno(6:1)	-0.1288387	0.0265832	0.0036445	-0.2227376	-0.0349398
Pos:Geno(6:2)	0.0125729	0.0178835	0.8997847	-0.0505964	0.0757422
Pos:Geno(6:3)	0.1642097	0.0460717	0.0240587	0.0014722	0.3269472
Pos:Geno(6:4)	0.0108158	0.0195997	0.9405133	-0.0584155	0.0800472
Pos:Geno(6:5)	-0.0587597	0.0157705	0.0187526	-0.1144653	-0.0030542
Pos:Geno(7:1)	-0.0616263	0.0186753	0.0363353	-0.1275924	0.0043398
Pos:Geno(7:2)	0.0887578	0.0202829	0.0071038	0.0171130	0.1604026
Pos:Geno(7:3)	-0.0254874	0.0243067	0.7541412	-0.1113451	0.0603704
Pos:Geno(7:4)	0.0093343	0.0164105	0.9366532	-0.0486319	0.0673004
Pos:Geno(7:5)	-0.0109783	0.0153987	0.8966115	-0.0653705	0.0434139
Pos:Geno(8:1)	-0.0414265	0.0190559	0.2089284	-0.1087372	0.0258842
Pos:Geno(8:2)	0.0318966	0.0111151	0.0715982	-0.0073649	0.0711581
Pos:Geno(8:3)	-0.0469882	0.0254718	0.3314571	-0.1369613	0.0429849
Pos:Geno(8:4)	0.0363047	0.0299185	0.6654593	-0.0693756	0.1419851
Pos:Geno(8:5)	0.0202133	0.0210914	0.7984720	-0.0542871	0.0947138
Pos:Geno(9:1)	-0.0701112	0.0191284	0.0205826	-0.1376777	-0.0025447
Pos:Geno(9:2)	0.0010547	0.0199028	0.9946085	-0.0692474	0.0713568
Pos:Geno(9:3)	0.0035247	0.0329916	0.9926219	-0.1130104	0.1200597
Pos:Geno(9:4)	0.0070656	0.0137705	0.9486913	-0.0415755	0.0557068

Pos:Geno(9:5)	0.0584662	0.0124206	0.0044268	0.0145934	0.1023390
Pos:Geno(10:1)	-0.0471409	0.0173447	0.0909221	-0.1084070	0.0141252
Pos:Geno(10:2)	0.0094228	0.0115869	0.8609187	-0.0315053	0.0503508
Pos:Geno(10:3)	0.0906294	0.0180789	0.0029002	0.0267700	0.1544889
Pos:Geno(10:4)	-0.0421529	0.0147480	0.0729031	-0.0942467	0.0099409
Pos:Geno(10:5)	-0.0107584	0.0081633	0.6065028	-0.0395933	0.0180764
Pos:Geno(11:1)	0.0376287	0.0211819	0.3623522	-0.0371916	0.1124490
Pos:Geno(11:2)	-0.0288915	0.0192931	0.5054133	-0.0970397	0.0392568
Pos:Geno(11:3)	0.0287307	0.0163429	0.3710169	-0.0289968	0.0864581
Pos:Geno(11:4)	-0.0364654	0.0195226	0.3214033	-0.1054244	0.0324935
Pos:Geno(11:5)	-0.0010024	0.0153345	0.9941981	-0.0551679	0.0531630
Pos:Geno(12:1)	0.0462537	0.0081635	0.0012286	0.0174180	0.0750894
Pos:Geno(12:2)	-0.0644702	0.0145586	0.0065856	-0.1158950	-0.0130453
Pos:Geno(12:3)	-0.0984198	0.0187477	0.0021097	-0.1646417	-0.0321978
Pos:Geno(12:4)	0.0754441	0.0247008	0.0534916	-0.0118056	0.1626939
Pos:Geno(12:5)	0.0411921	0.0126854	0.0394695	-0.0036161	0.0860002
Pos:Geno(13:1)	0.0205297	0.0092863	0.1979026	-0.0122720	0.0533315
Pos:Geno(13:2)	-0.0035662	0.0135565	0.9830270	-0.0514513	0.0443190
Pos:Geno(13:3)	-0.0050584	0.0085178	0.9306302	-0.0351455	0.0250287
Pos:Geno(13:4)	0.0463270	0.0178136	0.1092243	-0.0165955	0.1092496
Pos:Geno(13:5)	-0.0582322	0.0130803	0.0063656	-0.1044355	-0.0120289
Pos:Geno(14:1)	0.0807984	0.0075280	0.0000079	0.0542076	0.1073892
Pos:Geno(14:2)	-0.0283801	0.0231768	0.6592804	-0.1102468	0.0534866
Pos:Geno(14:3)	-0.0187673	0.0230266	0.8602189	-0.1001036	0.0625689
Pos:Geno(14:4)	-0.0161156	0.0115885	0.5652153	-0.0570492	0.0248180
Pos:Geno(14:5)	-0.0175354	0.0096451	0.3433057	-0.0516046	0.0165338
Pos:Geno(15:1)	0.1109362	0.0121537	0.0000304	0.0680060	0.1538664
Pos:Geno(15:2)	-0.0218285	0.0148107	0.5185132	-0.0741439	0.0304868
Pos:Geno(15:3)	0.0189212	0.0350013	0.9429793	-0.1047128	0.1425552
Pos:Geno(15:4)	-0.0961888	0.0149214	0.0004745	-0.1488951	-0.0434824
Pos:Geno(15:5)	-0.0118401	0.0243708	0.9539322	-0.0979244	0.0742443
Pos:Geno(16:1)	0.0696160	0.0165619	0.0091440	0.0111148	0.1281173
Pos:Geno(16:2)	-0.0650657	0.0094760	0.0002935	-0.0985373	-0.0315941
Pos:Geno(16:3)	-0.0545141	0.0125668	0.0075076	-0.0989034	-0.0101249
Pos:Geno(16:4)	0.0001454	0.0156307	0.9958624	-0.0550666	0.0553574
Pos:Geno(16:5)	0.0498184	0.0182032	0.0882628	-0.0144803	0.1141171

Pos:Geno(17:1)	0.1190720	0.0407076	0.0656053	-0.0247182	0.2628622
Pos:Geno(17:2)	-0.0282872	0.0150408	0.3159190	-0.0814152	0.0248408
Pos:Geno(17:3)	-0.0496911	0.0174648	0.0744131	-0.1113815	0.0119992
Pos:Geno(17:4)	-0.0450599	0.0164347	0.0875776	-0.1031118	0.0129920
Pos:Geno(17:5)	0.0039662	0.0119883	0.9764677	-0.0383796	0.0463121
Geno:Rep(1:1)	-0.0087754	0.0063523	0.5704225	-0.0312132	0.0136625
Geno:Rep(1:2)	0.0453840	0.0190983	0.1543489	-0.0220764	0.1128445
Geno:Rep(1:3)	-0.0196310	0.0103532	0.3094202	-0.0562013	0.0169394
Geno:Rep(1:4)	-0.0048685	0.0074937	0.9158108	-0.0313383	0.0216014
Geno:Rep(2:1)	0.0240760	0.0102673	0.1618888	-0.0121910	0.0603430
Geno:Rep(2:2)	-0.0323144	0.0127613	0.1214786	-0.0773908	0.0127619
Geno:Rep(2:3)	-0.0287837	0.0111900	0.1141585	-0.0683100	0.0107425
Geno:Rep(2:4)	0.0323496	0.0142448	0.1809486	-0.0179670	0.0826662
Geno:Rep(3:1)	0.0266347	0.0121879	0.2054584	-0.0164162	0.0696855
Geno:Rep(3:2)	-0.0188493	0.0180362	0.7559237	-0.0825580	0.0448594
Geno:Rep(3:3)	0.0127551	0.0135154	0.8052927	-0.0349850	0.0604953
Geno:Rep(3:4)	-0.0082503	0.0271210	0.9792528	-0.1040491	0.0875485
Geno:Rep(4:1)	-0.0093386	0.0067356	0.5675913	-0.0331306	0.0144533
Geno:Rep(4:2)	0.0049836	0.0101543	0.9530098	-0.0308841	0.0408513
Geno:Rep(4:3)	0.0336752	0.0146805	0.1748404	-0.0181801	0.0855305
Geno:Rep(4:4)	-0.0331231	0.0152843	0.2110239	-0.0871114	0.0208652
Geno:Rep(5:1)	-0.0571045	0.0188451	0.0555678	-0.1236703	0.0094614
Geno:Rep(5:2)	0.0129901	0.0138012	0.8064564	-0.0357595	0.0617397
Geno:Rep(5:3)	0.0176917	0.0097243	0.3427294	-0.0166570	0.0520404
Geno:Rep(5:4)	0.0104987	0.0105761	0.7820505	-0.0268590	0.0478563

Conclusions

Split-plot design is a mixture of treatment design and experiment design (local control) When two factors or more factors are applied. Sometimes, repeated measurement data can be analyzed by split-block design/model. In other words, split-plot design is a specific model for repeated measurement data analysis.