

LPS Supplement

Ana Jimenez
Colgate University
Department of Biology

Sahil Lalwani
Colgate University
Department of Mathematics

William Cipolli III*
Colgate University
Department of Mathematics
will@cipolli.com

1 Introduction

The models are fit in R (R Core Team, 2019) and the mixed effects models are fit using the `lmerTest` package (Kuznetsova et al., 2017) for R. Best-subset model selection according to the Bayesian information criterion (BIC) (Schwarz et al., 1978) was completed via complete enumeration (Morgan and Tatar, 1972) for each model. BIC penalizes false positives more than false negatives when there are eight or more observations.

We adjusted the p-values in the MANOVA analyses and within each model reported using the approach in Benjamini and Hochberg (1995) instead of the overly conservative Bonferonni adjustment (Dunn, 1961). This approach allows for the control the expected proportion of false discoveries instead of the probability of making at least one false discovery, thus preserving power.

1.1 Overall MANOVA

The multivariate analysis of variance (MANOVA) results in Table 1 show significance for the multivariate analysis in sample type, size class, treatment, and the interaction of sample type $\times$ treatment so we probe each dependent variable separately using ANOVA below.

Table 1: Overall MANOVA.

	DF	Pillai	λ F	Num DF	Den DF	p-value	Adjusted
Sample Type	1.0000	0.2700	3.4030	10.0000	92.0000	0.0008	0.0019
Treatment	1.0000	0.2747	3.4842	10.0000	92.0000	0.0006	0.0019
Size Class	1.0000	0.3426	4.7953	10.0000	92.0000	<0.0001	0.0001
Sample Type : Treatment	1.0000	0.2261	2.6885	10.0000	92.0000	0.0062	0.0109
Sample Type : Size Class	1.0000	0.1352	1.4388	10.0000	92.0000	0.1759	0.2463
Treatment : Size Class	1.0000	0.0895	0.9041	10.0000	92.0000	0.5329	0.5329
Sample Type : Treatment : Size Class	1.0000	0.1173	1.2227	10.0000	92.0000	0.2871	0.3350

*All R Code and data can be provided by request to will@cipolli.com

Remark: We added 1 to Proton Leak /20K, Spare Respiratory Capacity/20K, and IL6/20K to avoid issues when performing the log-transform where measurements were zero.

1.2 ANOVA Results

The repeated measures ANOVA results below suggest significant differences in Non-Glycolytic Acidification/20K across sample type; Total Glycolytic Capacity/20K across sample type; Basal OCR/20K across sample type; Proton Leak across sample type; Maximal Respiration/20K across sample type; Spare Respiratory Capacity/20K across sample type; Non-Mito Respiration/20K across treatment, and sample type; and IL6/20K across treatment.

Table 2: ANOVA analysis for log-transformed Non-Glycolytic Acidification/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	16.6640	1.0000	<0.0001	0.0002
Treatment	5.2136	1.0000	0.0224	0.0598
Size Class	1.1631	1.0000	0.2808	0.4493
Sample Type : Treatment	0.2226	1.0000	0.6371	0.6371
Sample Type : Size Class	0.7730	1.0000	0.3793	0.5057
Treatment : Size Class	2.3270	1.0000	0.1271	0.2543
Sample Type : Treatment : Size Class	0.3023	1.0000	0.5825	0.6371

Table 3: ANOVA analysis for log-transformed Total Glycolysis/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	3.0555	1.0000	0.0805	0.3219
Treatment	0.7842	1.0000	0.3759	0.5011
Size Class	0.2390	1.0000	0.6249	0.7142
Sample Type : Treatment	1.1561	1.0000	0.2823	0.4552
Sample Type : Size Class	0.0298	1.0000	0.8629	0.8629
Treatment : Size Class	1.1456	1.0000	0.2845	0.4552
Sample Type : Treatment : Size Class	1.3932	1.0000	0.2379	0.4552

Table 4: ANOVA analysis for log-transformed Total Glycolytic Capacity/20K

	Chisq	DF	p-value	Adjusted
Sample Type	8.2595	1.0000	0.0041	0.0162
Treatment	0.4178	1.0000	0.5180	0.5640
Size Class	0.3329	1.0000	0.5640	0.5640
Sample Type : Treatment	1.2345	1.0000	0.2665	0.4265
Sample Type : Size Class	0.8186	1.0000	0.3656	0.4874
Treatment : Size Class	2.7680	1.0000	0.0962	0.2564
Sample Type : Treatment : Size Class	1.3505	1.0000	0.2452	0.4265

Table 5: ANOVA analysis for log-transformed Basal OCR/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	8.7711	1.0000	0.0031	0.0122
Treatment	0.0281	1.0000	0.8669	0.9263
Size Class	0.5168	1.0000	0.4722	0.8399
Sample Type : Treatment	0.3788	1.0000	0.5383	0.8399
Sample Type : Size Class	1.7109	1.0000	0.1909	0.5090
Treatment : Size Class	0.2322	1.0000	0.6299	0.8399
Sample Type : Treatment : Size Class	0.0085	1.0000	0.9263	0.9263

Table 6: ANOVA analysis for log-transformed Proton Leak/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	7.4823	1.0000	0.0062	0.0249
Treatment	0.1478	1.0000	0.7007	0.7442
Size Class	2.0142	1.0000	0.1558	0.2493
Sample Type : Treatment	2.2465	1.0000	0.1339	0.2493
Sample Type : Size Class	2.5069	1.0000	0.1133	0.2493
Treatment : Size Class	0.1557	1.0000	0.6931	0.7442
Sample Type : Treatment : Size Class	0.1064	1.0000	0.7442	0.7442

Table 7: ANOVA analysis for log-transformed Maximal Respiration/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	13.6533	1.0000	0.0002	0.0009
Treatment	0.0417	1.0000	0.8382	0.9626
Size Class	0.0022	1.0000	0.9626	0.9626
Sample Type : Treatment	0.0502	1.0000	0.8227	0.9626
Sample Type : Size Class	3.5546	1.0000	0.0594	0.1584
Treatment : Size Class	0.0232	1.0000	0.8791	0.9626
Sample Type : Treatment : Size Class	0.0741	1.0000	0.7855	0.9626

Table 8: ANOVA analysis for log-transformed Spare Respiratory Capacity/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	13.0005	1.0000	0.0003	0.0012
Treatment	1.1352	1.0000	0.2867	0.4587
Size Class	0.7584	1.0000	0.3838	0.5118
Sample Type : Treatment	0.2670	1.0000	0.6054	0.6919
Sample Type : Size Class	5.1709	1.0000	0.0230	0.0612
Treatment : Size Class	1.4011	1.0000	0.2365	0.4587
Sample Type : Treatment : Size Class	0.0911	1.0000	0.7628	0.7628

Table 9: ANOVA analysis for log-transformed Non-Mito Respiration/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	15.8392	1.0000	0.0001	0.0003
Treatment	6.0486	1.0000	0.0139	0.0371
Size Class	3.4725	1.0000	0.0624	0.1248
Sample Type : Treatment	0.0022	1.0000	0.9626	0.9626
Sample Type : Size Class	1.5444	1.0000	0.2140	0.3423
Treatment : Size Class	0.0329	1.0000	0.8561	0.9626
Sample Type : Treatment : Size Class	0.3929	1.0000	0.5308	0.7077

Table 10: ANOVA analysis for inverse squared IL6/20K.

	Chisq	DF	p-value	Adjusted
Sample Type	0.1691	1.0000	0.6809	0.6809
Treatment	71.0564	1.0000	<0.0001	<0.0001
Size Class	3.3242	1.0000	0.0683	0.1365
Sample Type : Treatment	0.8265	1.0000	0.3633	0.4232
Sample Type : Size Class	2.7144	1.0000	0.0994	0.1591
Treatment : Size Class	0.8026	1.0000	0.3703	0.4232
Sample Type : Treatment : Size Class	5.0390	1.0000	0.0248	0.0661

In the sections below, we fit models to quantify the effect of treatment on Non-Mito Respiration/20K and IL6/20K.

2 Non-mito Respiration/20k

2.1 Full Model

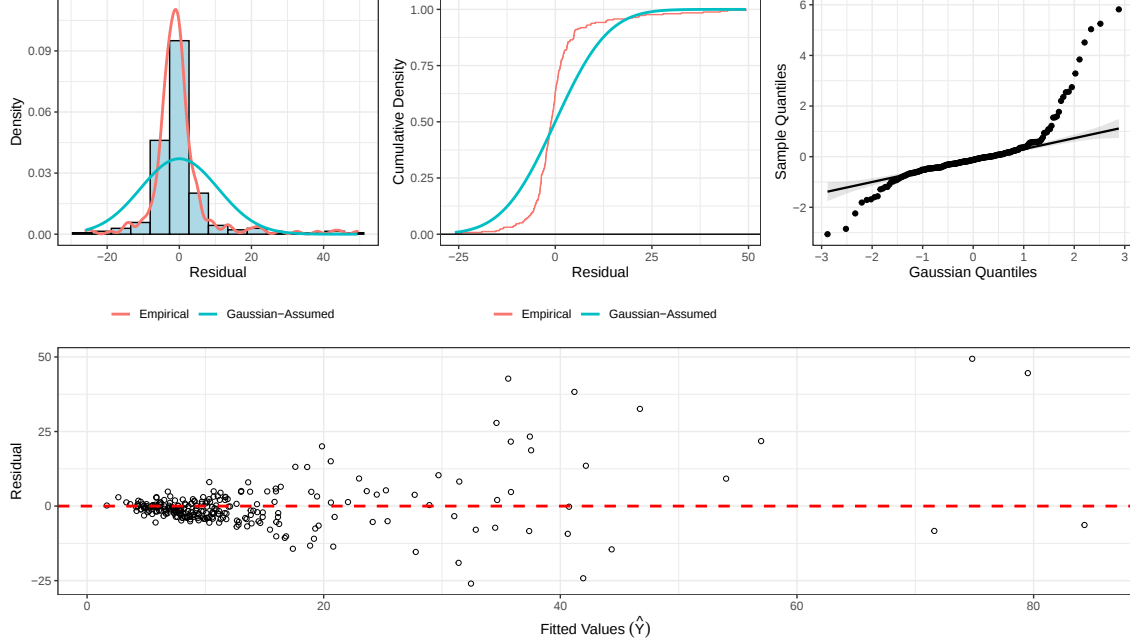


Figure 1: Residual analysis for the Non-mito Respiration/20k model.

Table 11: Summary of the full model for Non-Mito Respiration/20K.

	Estimate	SE	DF	t	p-value	Adjusted
Intercept	9.6923	8.9468	127.2830	1.0833	0.2807	0.4679
Sample Type = Deceased	11.8217	5.7146	179.8700	2.0687	0.0400	0.3342
Sex = Male	-4.6453	2.6962	121.7650	-1.7229	0.0874	0.3342
Size = Large	-5.8487	3.5402	180.0353	-1.6521	0.1003	0.3342
Breed Lifespan	0.6769	0.7465	121.9786	0.9067	0.3663	0.5233
Treatment = LPS	3.2033	2.6118	125.6679	1.2265	0.2223	0.4679
(Sample Type = Deceased):(Treatment = LPS)	1.5867	5.1136	125.6679	0.3103	0.7569	0.9461
(Size = Large):(Treatment = LPS)	-0.0568	3.1762	125.6679	-0.0179	0.9858	0.9858
(Sample Type = Deceased):(Size = Large)	-0.4885	7.5986	183.2861	-0.0643	0.9488	0.9858
(Sample Type = Deceased):(Size = Large):(Treatment = LPS)	-7.6915	6.9816	125.6679	-1.1017	0.2727	0.4679

2.2 Transformed Model

Remark: We added 1 to all measurements in order to complete the log transform.

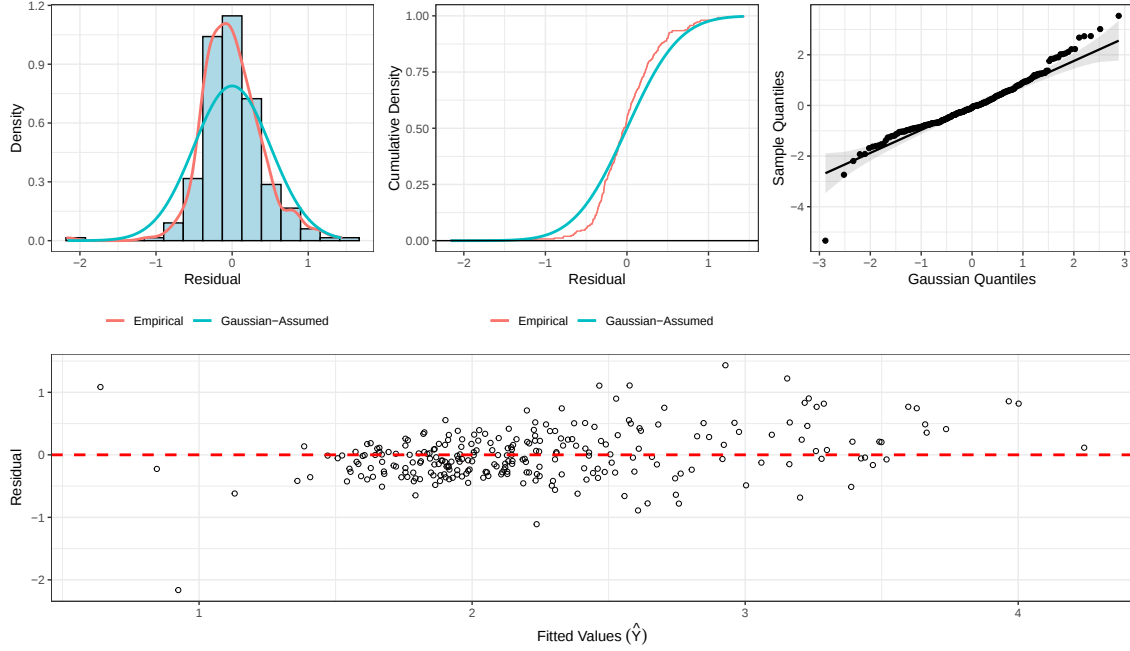


Figure 2: Residual analysis for the log-transformed Non-mito Respiration/20k model.

Table 12: Summary of the log-transformed full model for Non-Mito Respiration/20K.

	Estimate	SE	DF	t	p-value	Adjusted
Intercept	1.5889	0.3912	128.1664	4.0621	0.0001	0.0008
Sample Type = Deceased	0.6432	0.2533	187.7880	2.5389	0.0119	0.0596
Sex = Male	-0.1666	0.1177	121.7684	-1.4161	0.1593	0.2655
Size = Large	-0.2914	0.1569	187.9586	-1.8570	0.0649	0.1298
Breed Lifespan	0.0650	0.0326	122.0284	1.9957	0.0482	0.1298
Treatment = LPS	0.2297	0.1226	125.6599	1.8731	0.0634	0.1298
(Sample Type = Deceased):(Treatment = LPS)	0.0104	0.2401	125.6599	0.0431	0.9657	0.9657
(Size = Large):(Treatment = LPS)	0.0553	0.1491	125.6599	0.3709	0.7114	0.8892
(Sample Type = Deceased):(Size = Large)	-0.0852	0.3371	191.4937	-0.2528	0.8007	0.8897
(Sample Type = Deceased):(Size = Large):(Treatment = LPS)	-0.2335	0.3278	125.6599	-0.7123	0.4776	0.6822

2.3 Best Subsets Model

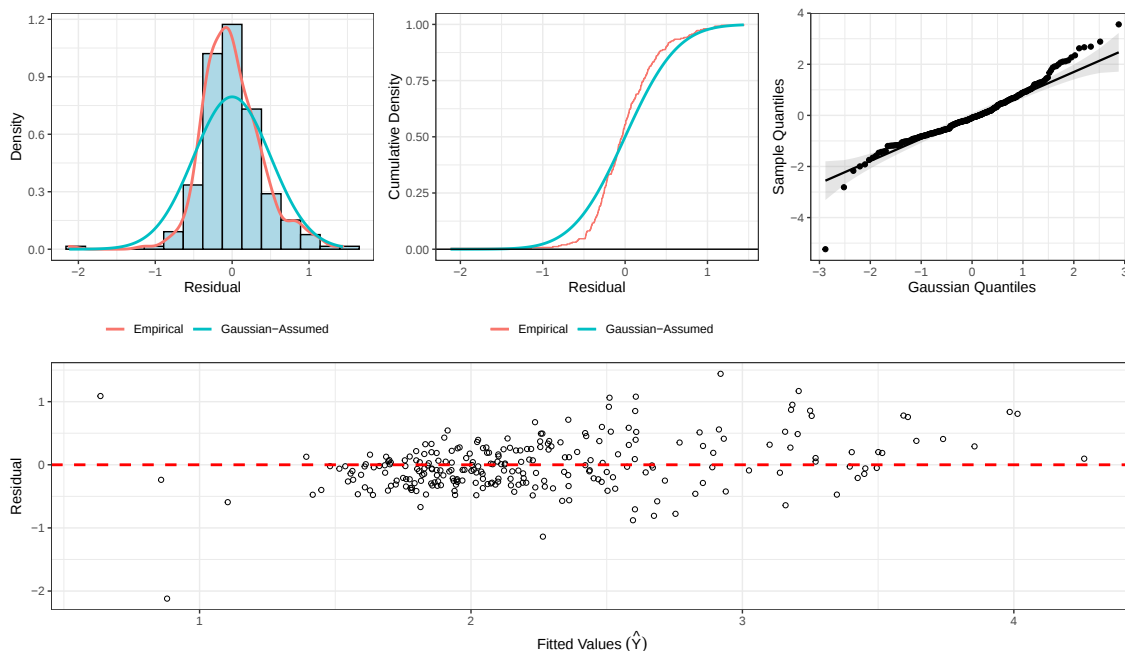


Figure 3: Residual analysis for the log-transformed Non-mito Respiration/20k best subsets model.

Table 13: Summary of the log-transformed best subsets model for Non-Mito Respiration/20K.

	Estimate	SE	DF	t	p-value	Adjusted
Intercept	2.3496	0.1178	142.7149	19.9506	<0.0001	<0.0001
Sample Type = Deceased	0.6551	0.1459	123.9553	4.4912	<0.0001	<0.0001
Sex = Male	-0.1829	0.1169	123.8057	-1.5643	0.1203	0.1203
Size = Large	-0.3817	0.1215	123.9009	-3.1424	0.0021	0.0026
Treatment = LPS	0.2455	0.0625	128.6554	3.9295	0.0001	0.0002

2.4 Analysis

A log transform of Non-Mito Respiration/20K was completed to correct issues with the diagnostic plots in the full model. Figure 1 shows the diagnostic plots for the pre-log-transform model and Figure 2 shows the diagnostic plots for the transformed model. Note that the residuals vs fitted plot is more closely fit by a horizontal line at zero, without the megaphone pattern in the original, and the Normal Q-Q plot fits well except for the tails.

After completing model building from the full set of explanatory variables using best subsets, the reduced model that minimizes BIC suggests that body mass, sex, size class and treatment are

significantly associated with Non-Mito Respiration/20K.

This yields a regression equation of,

$$\log(Y_i) = \alpha_i + 2.3496 + 0.6551X_{1i} - 0.1829X_{2i} - 0.3817X_{3i} + 0.2455X_{4i} + \epsilon_i.$$

Where

Y_i = Non-Mito Respiration/20K

α_i = The random intercept for dog i

X_{1i} = Sample Type (1=Deceased, 0=Recently born)

X_{2i} = Sex (1=Male, 0=Female)

X_{3i} = Size class (1=Large, 0=Small)

X_{4i} = Treatment (1=LPS, 0=Control)

for each observation $i = 1, 2, \dots, n$.

To be interpretable, in terms of the response variable, we solve the regression equation for Y_i .

$$\begin{aligned} Y_i &= e^{\alpha_i} e^{2.3496} e^{0.6551X_{1i}} e^{-0.1829X_{2i}} e^{-0.3817X_{3i}} e^{0.2455X_{4i}} e^{\epsilon_i} \\ &= e^{\alpha_i} (10.4814) (1.9253)^{X_{1i}} (0.8329)^{X_{2i}} (0.6827)^{X_{3i}} (1.2783)^{X_{4i}} e^{\epsilon_i} \end{aligned}$$

- We expect a 92.53% increase in Non-Mito Respiration/20K for deceased dogs compared to recently born dogs
- We expect a 16.71% decrease in Non-Mito Respiration/20K for male dogs compared to female dogs
- We expect a 31.73% decrease in Non-Mito Respiration/20K for large breed dogs compared to small breed dogs
- We expect a 27.83% increase in Non-Mito Respiration/20K for dogs in LPS treatment group compared to those in control treatment group

3 IL-6 (ng/mL/20K)

3.1 Full Model

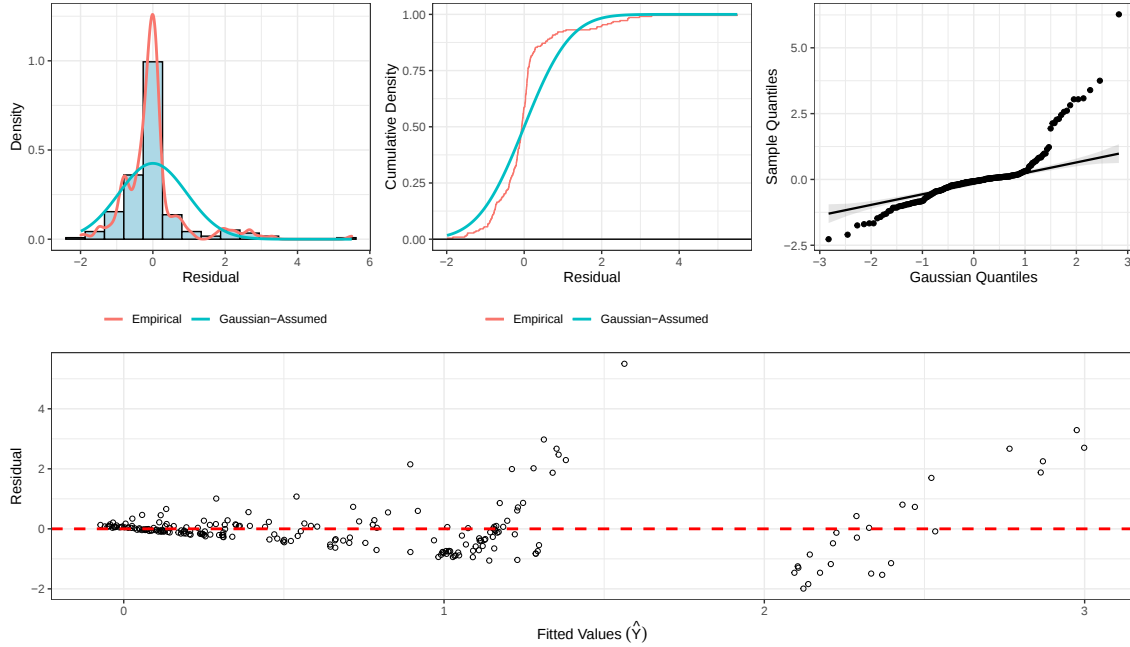


Figure 4: Residual analysis for the IL-6 (ng/mL/20K) model.

Table 14: Summary of the full model for IL6/20K.

	Estimate	SE	DF	t	p-value	Adjusted
Intercept	-0.4941	0.5550	116.0651	-0.8902	0.3752	0.6253
Sample Type = Deceased	-0.2571	0.3666	200.0986	-0.7013	0.4839	0.6548
Sex = Male	0.0124	0.1512	105.9473	0.0818	0.9350	0.9350
Size = Large	-0.1310	0.2423	202.4966	-0.5407	0.5893	0.6548
Breed Lifespan	0.0743	0.0477	103.6516	1.5581	0.1222	0.3056
Treatment = LPS	2.0804	0.2655	105.3759	7.8364	<0.0001	<0.0001
(Sample Type = Deceased):(Treatment = LPS)	-1.6144	0.4740	108.4960	-3.4056	0.0009	0.0044
(Size = Large):(Treatment = LPS)	-1.0390	0.3149	105.6197	-3.2997	0.0013	0.0044
(Sample Type = Deceased):(Size = Large)	0.6150	0.4787	204.9545	1.2848	0.2003	0.4006
(Sample Type = Deceased):(Size = Large):(Treatment = LPS)	0.3826	0.6431	107.1213	0.5950	0.5531	0.6548

3.2 Transformed Model

Remark: We added 1 to all measurements in order to complete the inverse-squared transform.

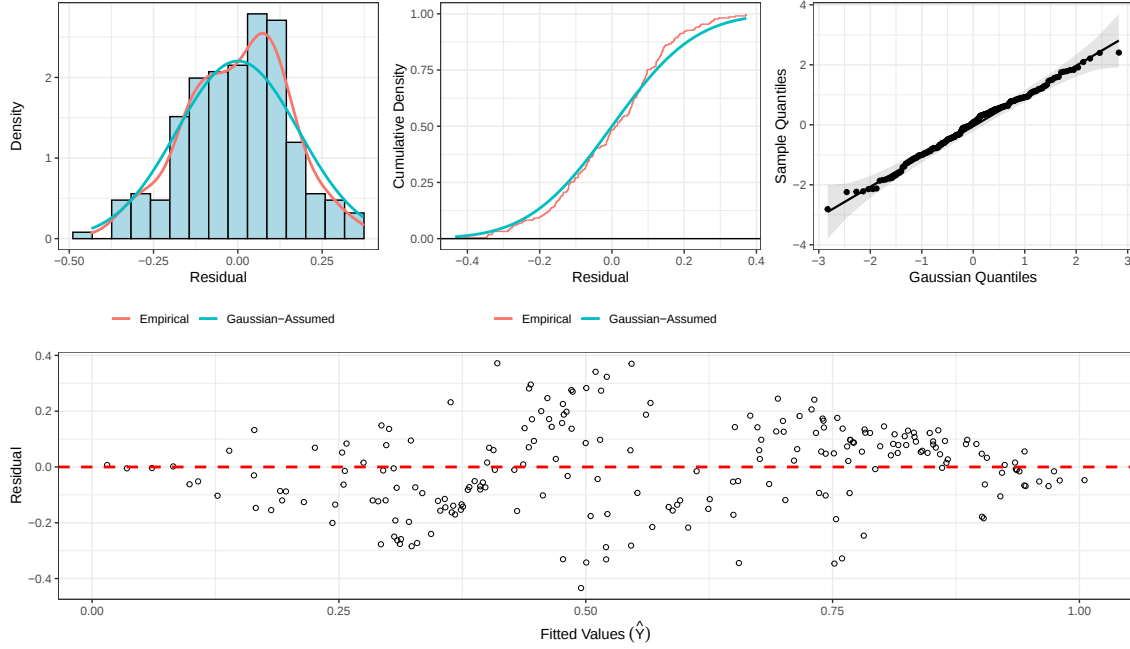


Figure 5: Residual analysis for the inverse squared full model for IL6/20K.

Table 15: Summary of the inverse squared full model for IL6/20K.

	Estimate	SE	DF	t	p-value	Adjusted
Intercept	0.7371	0.1338	111.3988	5.5068	<0.0001	<0.0001
Sample Type = Deceased	0.0502	0.0823	178.2511	0.6096	0.5429	0.7374
Sex = Male	0.0004	0.0368	105.6745	0.0103	0.9918	0.9918
Size = Large	0.1654	0.0542	181.9016	3.0512	0.0026	0.0087
Breed Lifespan	-0.0056	0.0116	103.6032	-0.4826	0.6304	0.7374
Treatment = LPS	-0.4853	0.0512	104.8905	-9.4736	<0.0001	<0.0001
(Sample Type = Deceased):(Treatment = LPS)	0.1870	0.0918	107.6726	2.0378	0.0440	0.0880
(Size = Large):(Treatment = LPS)	0.0265	0.0608	105.1098	0.4361	0.6636	0.7374
(Sample Type = Deceased):(Size = Large)	-0.2744	0.1066	186.3956	-2.5738	0.0108	0.0271
(Sample Type = Deceased):(Size = Large):(Treatment = LPS)	0.2314	0.1243	106.4552	1.8619	0.0654	0.1090

3.2.1 Post-hoc Analysis of the Transformed Model

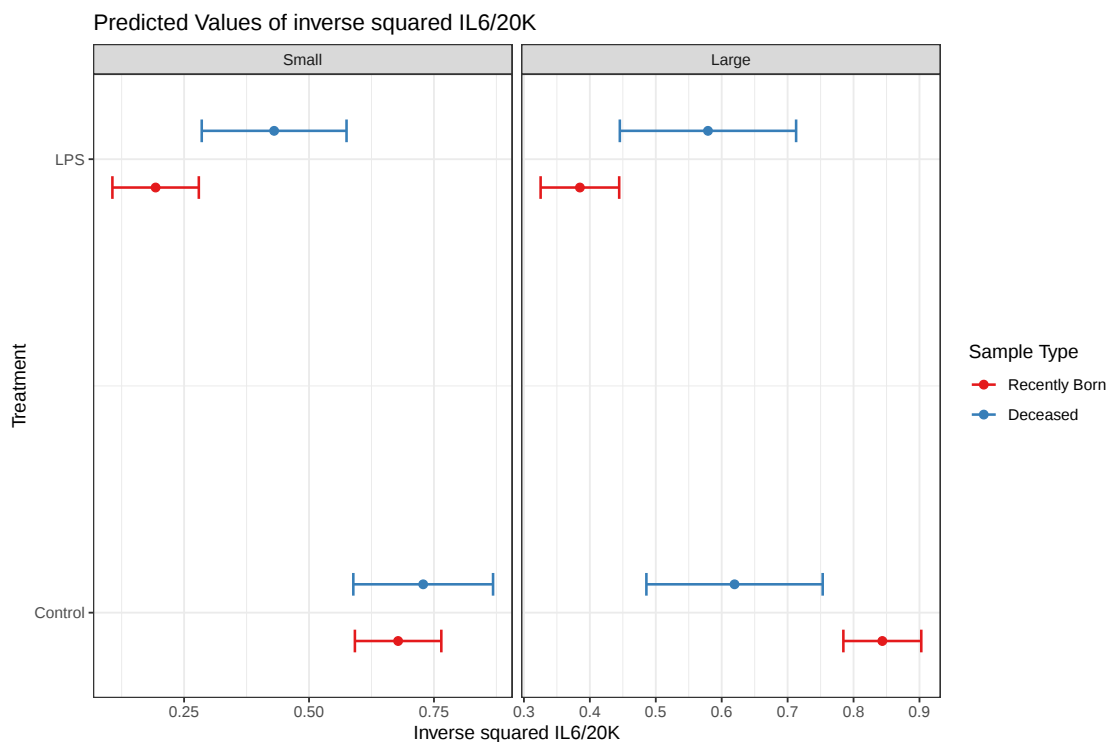


Figure 6: Marginal means for the inverse squared full model for IL6/20K.

Table 16: Summary of the marginal means for the inverse squared full model for IL6/20K.

Treatment	Sample.type	Size	emmean	SE	df	lower.CL	upper.CL
Control	Recently Born	Small	0.6782	0.0441	187.1389	0.5912	0.7653
LPS	Recently Born	Small	0.1930	0.0441	187.1389	0.1059	0.2800
Control	Deceased	Small	0.7284	0.0713	170.2869	0.5876	0.8692
LPS	Deceased	Small	0.4302	0.0740	177.3517	0.2842	0.5761
Control	Recently Born	Large	0.8436	0.0301	176.1786	0.7842	0.9031
LPS	Recently Born	Large	0.3849	0.0304	177.7950	0.3249	0.4449
Control	Deceased	Large	0.6195	0.0682	183.3142	0.4849	0.7541
LPS	Deceased	Large	0.5792	0.0682	183.3142	0.4446	0.7138

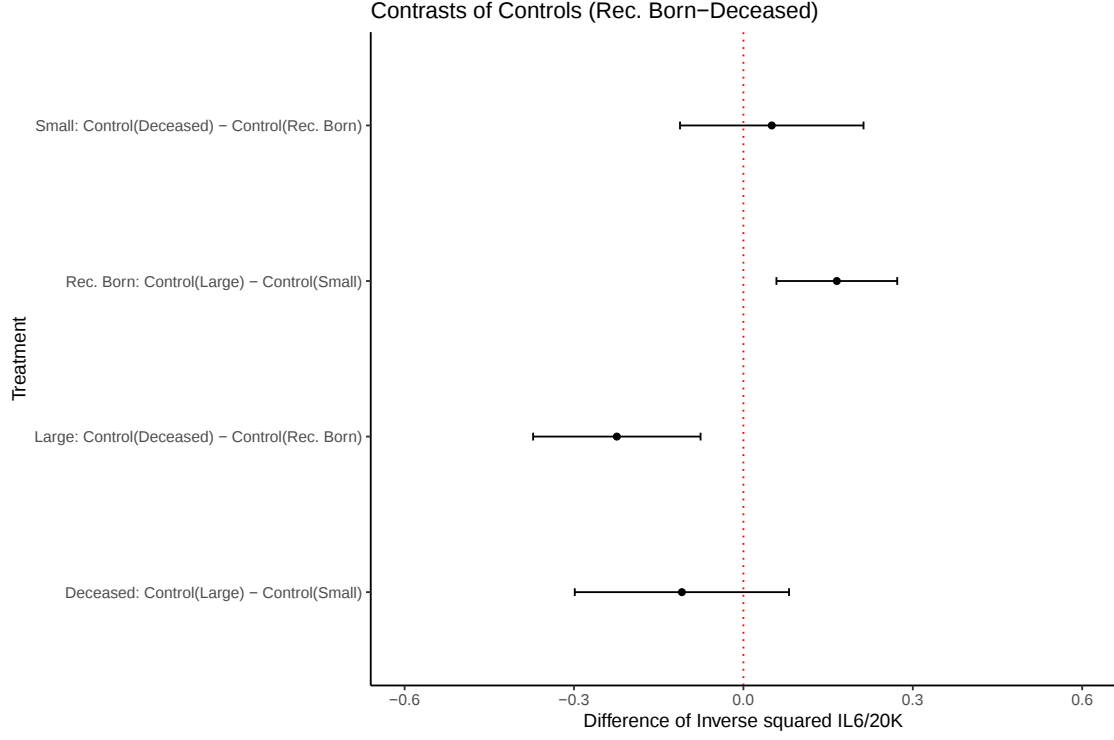


Figure 7: Pairwise control contrasts for the inverse squared full model for IL6/20K.

Table 17: Summary of the pairwise control contrast for the inverse squared full model for IL6/20K.

Control Difference	Estimate	SE	DF	t ratio	Lower	Upper	p-value	Adjusted
Large: Control(Deceased) - Control(Rec. Born)	-0.2242	0.0751	180.9908	-2.9835	-0.3724	-0.0759	0.0032	0.0065
Small: Control(Deceased) - Control(Rec. Born)	0.0502	0.0823	177.9219	0.6096	-0.1123	0.2127	0.5429	0.5429
Rec. Born: Control(Large) - Control(Small)	0.1654	0.0542	181.6068	3.0512	0.0584	0.2724	0.0026	0.0065
Deceased: Control(Large) - Control(Small)	-0.1090	0.0962	180.6854	-1.1331	-0.2987	0.0808	0.2587	0.3449

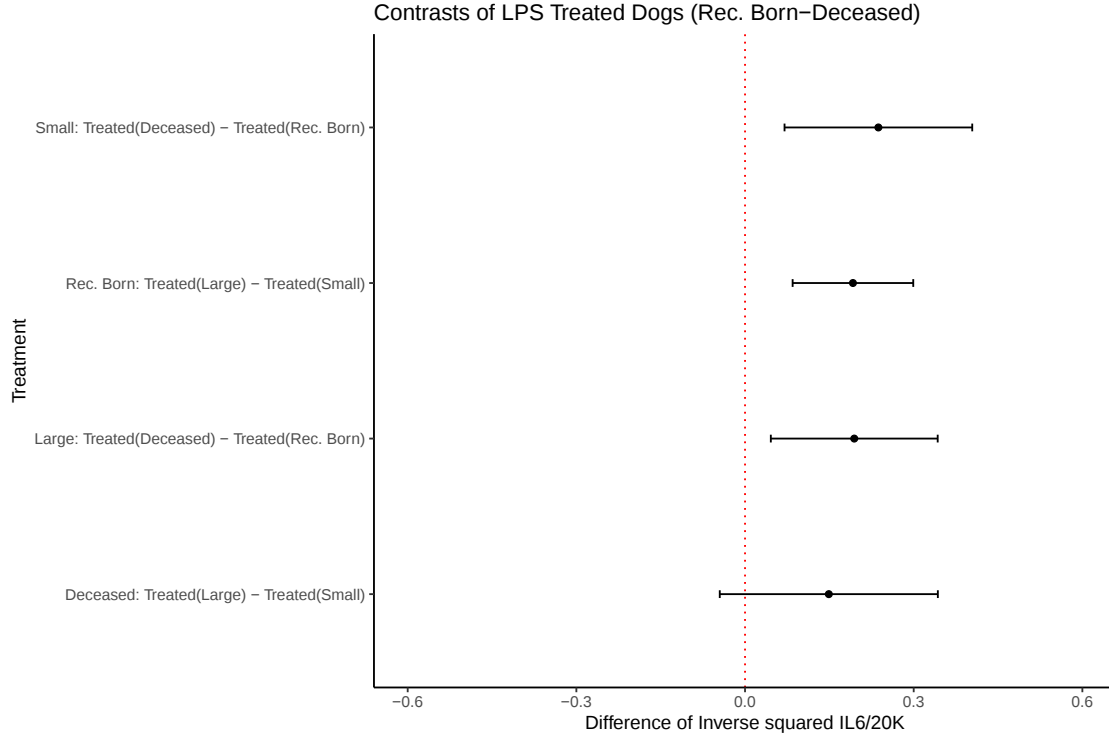


Figure 8: Pairwise treatment contrasts for the inverse squared full model for IL6/20K.

Table 18: Summary of the pairwise treated contrast for the inverse squared full model for IL6/20K.

Control Difference	Estimate	SE	DF	t ratio	Lower	Upper	p-value	Adjusted
Large: Treated(Deceased) - Treated(Rec. Born)	0.1943	0.0752	181.1528	2.5830	0.0459	0.3427	0.0106	0.0141
Small: Treated(Deceased) - Treated(Rec. Born)	0.2372	0.0846	182.6239	2.8035	0.0703	0.4041	0.0056	0.0112
Rec. Born: Treated(Large) - Treated(Small)	0.1919	0.0544	182.0856	3.5300	0.0846	0.2992	0.0005	0.0021
Deceased: Treated(Large) - Treated(Small)	0.1490	0.0983	184.3355	1.5158	-0.0449	0.3429	0.1313	0.1313

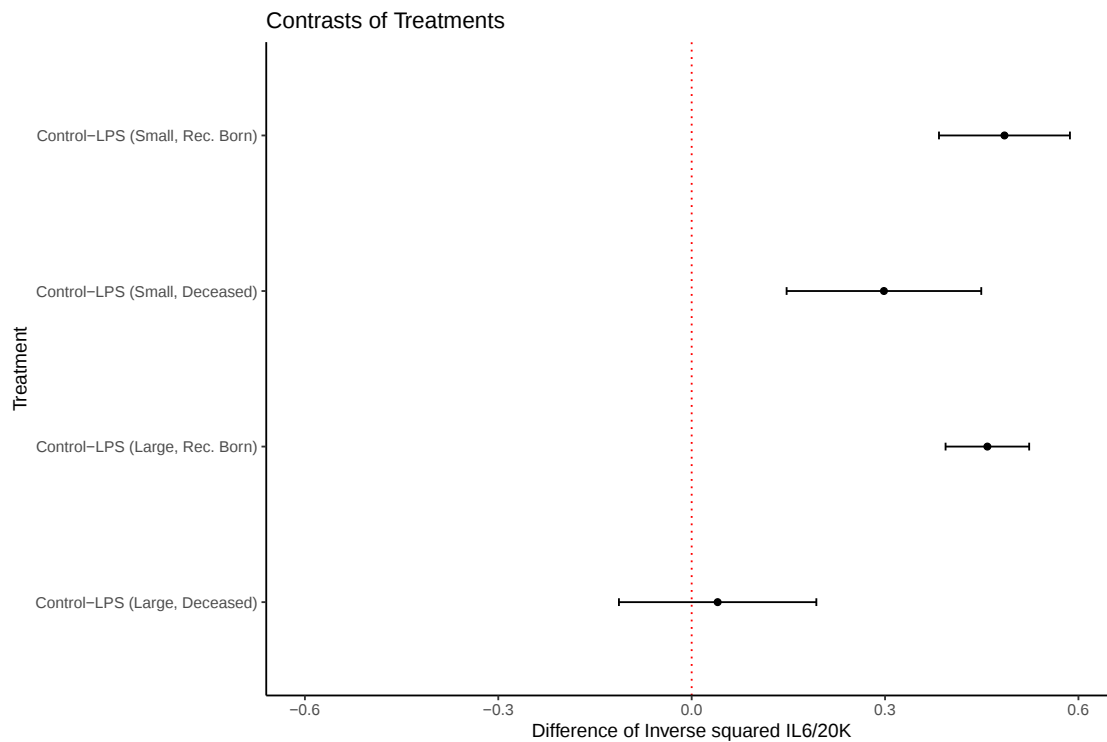


Figure 9: Pairwise treatment contrasts for the inverse squared full model for IL6/20K.

Table 19: Summary of the pairwise treatment contrasts for the inverse squared full model for IL6/20K.

Treatment Difference	Estimate	SE	DF	t ratio	Lower	Upper	p-value	Adjusted
Control-LPS (Small, Rec. Born)	0.4853	0.0512	104.2220	9.4736	0.3837	0.5868	<0.0001	<0.0001
Control-LPS (Large, Rec. Born)	0.4587	0.0327	104.9812	14.0266	0.3939	0.5236	<0.0001	<0.0001
Control-LPS (Small, Deceased)	0.2983	0.0762	108.2879	3.9154	0.1473	0.4492	0.0002	0.0002
Control-LPS (Large, Deceased)	0.0403	0.0772	104.2220	0.5220	-0.1128	0.1934	0.6028	0.6028

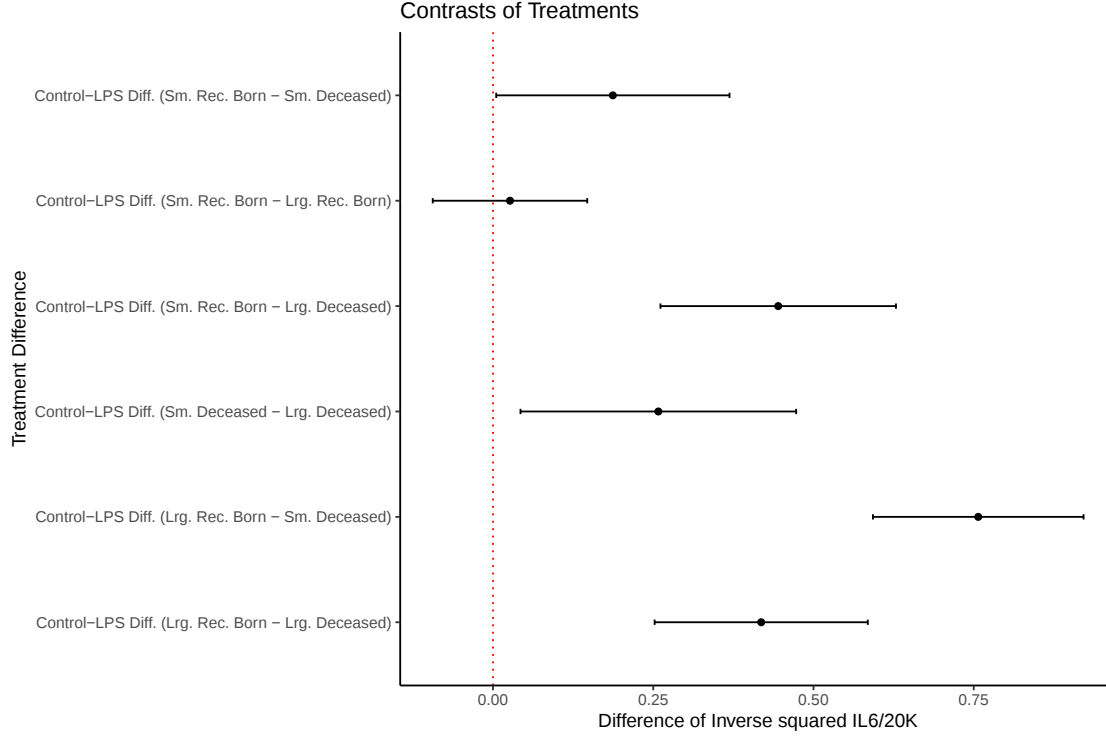


Figure 10: Pairwise treatment contrasts for the inverse squared full model for IL6/20K.

Table 20: Summary of the pairwise treatment contrasts for the inverse squared full model for IL6/20K.

Treatment Difference	Estimate	SE	DF	t ratio	Lower	Upper	p-value	Adjusted
Control-LPS Diff. (Sm. Rec. Born - Sm. Deceased)	0.1870	0.0918	107.0047	2.0371	0.0050	0.3690	0.0441	0.0529
Control-LPS Diff. (Lrg. Rec. Born - Lrg. Deceased)	0.4184	0.0839	104.3371	4.9898	0.2522	0.5847	<0.0001	<0.0001
Control-LPS Diff. (Sm. Rec. Born - Lrg. Rec. Born)	0.0265	0.0608	104.4413	0.4361	-0.0940	0.1470	0.6636	0.6636
Control-LPS Diff. (Sm. Deceased - Lrg. Deceased)	0.2580	0.1085	106.2072	2.3781	0.0429	0.4730	0.0192	0.0288
Control-LPS Diff. (Sm. Rec. Born - Lrg. Deceased)	0.4449	0.0927	104.2220	4.8018	0.2612	0.6287	<0.0001	<0.0001
Control-LPS Diff. (Lrg. Rec. Born - Sm. Deceased)	0.7570	0.0829	107.7766	9.1322	0.5927	0.9213	<0.0001	<0.0001

3.3 Best Subsets Model

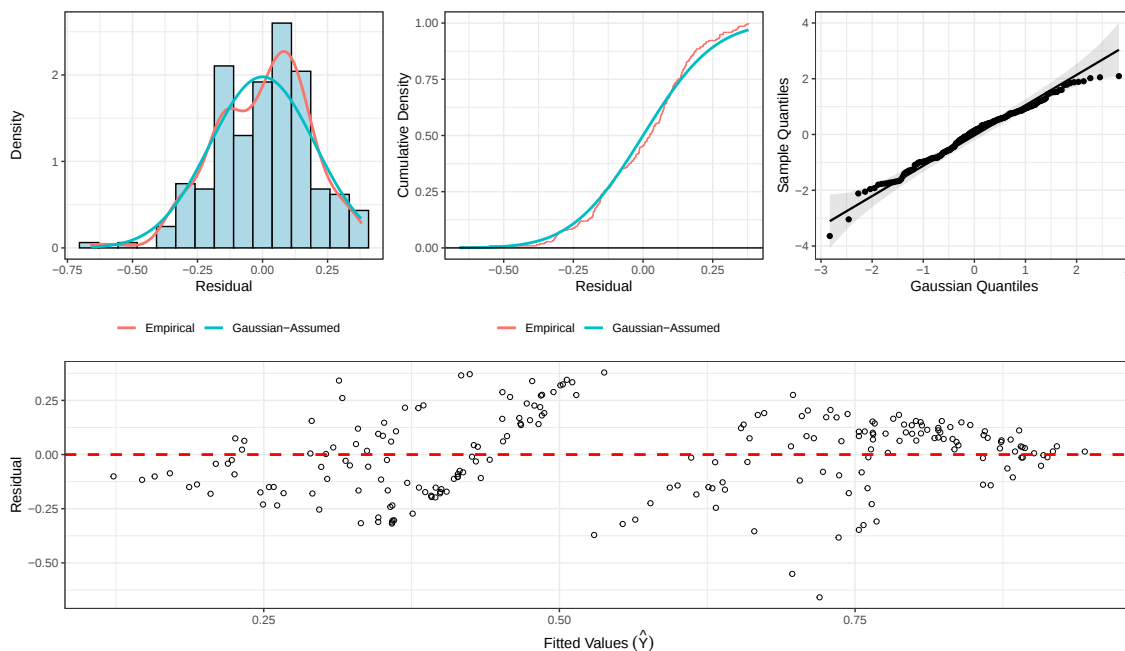


Figure 11: Residual analysis for the inverse squared best subsets model for IL6/20K.

Table 21: Summary of the inverse squared best subsets model for IL6/20K.

	Estimate	SE	DF	t	p-value	Adjusted
Intercept	0.6831	0.0357	141.6291	19.1092	<0.0001	<0.0001
Sex = Male	-0.0138	0.0365	108.2573	-0.3796	0.7050	0.7050
Size = Large	0.1449	0.0380	108.4211	3.8136	0.0002	0.0003
Treatment = LPS	-0.4064	0.0274	108.9707	-14.8554	<0.0001	<0.0001

3.4 Analysis

An inverse squared transform of IL6/20K was completed to correct issues with the diagnostic plots in the full model. Figure 4 shows the diagnostic plots for the pre-inverse-square-transform model and Figure 5 shows the diagnostic plots for the transformed model. Note that the residuals vs fitted plot is more closely fit by a horizontal line at zero, without the megaphone pattern in the original, and the Normal Q-Q plot fits well except for the tails.

After completing model building from the full set of explanatory variables using best subsets, the reduced model that minimizes BIC suggests that size class and treatment are significantly associated with IL6/20K.

This yields a regression equation of,

$$\frac{1}{(Y_i)^2} = \alpha_i + 0.6831 - 0.0138X_{1i} + 0.1449X_{2i} - 0.4064X_{3i} + \epsilon_i.$$

Where

$$Y_i = \text{IL6/20K}$$

$$\alpha_i = \text{The random intercept for dog } i$$

$$X_{1i} = \text{Sex (1=Male, 0=Female)}$$

$$X_{2i} = \text{Size (1=Large, 0=Small)}$$

$$X_{3i} = \text{Treatment (1=LPS, 0=Control)}$$

for each observation $i = 1, 2, \dots, n$.

Untangling the inverse-squared transformation is challenging, but we can make the following interpretations.

- We expect an increase in IL6/20K for male dogs compared to female dogs
- We expect a decrease in IL6/20K for large dogs compared to small dogs
- We expect an increase in IL6/20K for dogs treated with LPS compared to untreated dogs

Table 22: Averages $\pm$ standard error of the mean (SEM) per each cellular metabolic rate variable within each group.

Variable (units)	Size and Age	Treatment	Mean $\pm$ SEM	Treatment	Mean $\pm$ SEM
Basal OCR (pmole/min/20K cells)	Large deceased	Control	31.06 $\pm$ 12.91	LPS	27.55 $\pm$ 8.06
Basal OCR (pmole/min/20K cells)	Large rec. born	Control	15.17 $\pm$ 1.55	LPS	17.04 $\pm$ 1.64
Basal OCR (pmole/min/20K cells)	Small deceased	Control	57.58 $\pm$ 22.20	LPS	47.98 $\pm$ 11.36
Basal OCR (pmole/min/20K cells)	Small rec. born	Control	25.84 $\pm$ 5.72	LPS	22.92 $\pm$ 5.71
Proton leak (pmole/min/20K cells)	Large deceased	Control	10.77 $\pm$ 5.11	LPS	10.42 $\pm$ 2.55
Proton leak (pmole/min/20K cells)	Large rec. born	Control	6.75 $\pm$ 1.42	LPS	6.57 $\pm$ 0.71
Proton leak (pmole/min/20K cells)	Small deceased	Control	18.23 $\pm$ 4.94	LPS	23.71 $\pm$ 4.55
Proton leak (pmole/min/20K cells)	Small rec. born	Control	10.65 $\pm$ 3.13	LPS	9.10 $\pm$ 1.46
Maximal respiration (pmole/min/20K cells)	Large deceased	Control	43.15 $\pm$ 12.55	LPS	37.54 $\pm$ 6.75
Maximal respiration (pmole/min/20K cells)	Large rec. born	Control	27.48 $\pm$ 2.35	LPS	29.27 $\pm$ 2.72
Maximal respiration (pmole/min/20K cells)	Small deceased	Control	110.83 $\pm$ 42.25	LPS	84.57 $\pm$ 20.41
Maximal respiration (pmole/min/20K cells)	Small rec. born	Control	48.85 $\pm$ 11.15	LPS	38.72 $\pm$ 9.93
Spare respiratory capacity (pmole/min/20K cells)	Large deceased	Control	13.04 $\pm$ 1.99	LPS	14.48 $\pm$ 2.34
Spare respiratory capacity (pmole/min/20K cells)	Large rec. born	Control	12.52 $\pm$ 1.12	LPS	14.92 $\pm$ 1.88
Spare respiratory capacity (pmole/min/20K cells)	Small deceased	Control	53.24 $\pm$ 21.01	LPS	44.61 $\pm$ 10.45
Spare respiratory capacity (pmole/min/20K cells)	Small rec. born	Control	25.02 $\pm$ 5.85	LPS	16.73 $\pm$ 4.45
Non-mitochondrial respiration (pmole/min/20K cells)	Large deceased	Control	17.33 $\pm$ 5.57	LPS	15.02 $\pm$ 3.67
Non-mitochondrial respiration (pmole/min/20K cells)	Large rec. born	Control	7.77 $\pm$ 1.04	LPS	10.94 $\pm$ 1.21
Non-mitochondrial respiration (pmole/min/20K cells)	Small deceased	Control	29.26 $\pm$ 9.11	LPS	34.05 $\pm$ 7.12
Non-mitochondrial respiration (pmole/min/20K cells)	Small rec. born	Control	12.85 $\pm$ 2.26	LPS	15.87 $\pm$ 3.06
Glycolysis (mpH/min/20K cells)	Large deceased	Control	57.54 $\pm$ 11.31	LPS	50.07 $\pm$ 8.71
Glycolysis (mpH/min/20K cells)	Large rec. born	Control	46.66 $\pm$ 6.21	LPS	46.54 $\pm$ 6.59
Glycolysis (mpH/min/20K cells)	Small deceased	Control	59.98 $\pm$ 7.42	LPS	83.97 $\pm$ 13.30
Glycolysis (mpH/min/20K cells)	Small rec. born	Control	45.22 $\pm$ 4.12	LPS	53.38 $\pm$ 7.42
Glycolytic capacity (mpH/min/20K cells)	Large deceased	Control	69.72 $\pm$ 13.42	LPS	49.55 $\pm$ 5.59
Glycolytic capacity (mpH/min/20K cells)	Large rec. born	Control	41.37 $\pm$ 5.22	LPS	44.00 $\pm$ 4.30
Glycolytic capacity (mpH/min/20K cells)	Small deceased	Control	73.80 $\pm$ 9.22	LPS	103.44 $\pm$ 18.50
Glycolytic capacity (mpH/min/20K cells)	Small rec. born	Control	46.98 $\pm$ 4.61	LPS	54.85 $\pm$ 9.14
Non-glycolytic acidification (mpH/min/20K cells)	Large deceased	Control	20.27 $\pm$ 3.44	LPS	14.95 $\pm$ 1.90
Non-glycolytic acidification (mpH/min/20K cells)	Large rec. born	Control	10.86 $\pm$ 1.02	LPS	11.24 $\pm$ 1.01
Non-glycolytic acidification (mpH/min/20K cells)	Small deceased	Control	27.89 $\pm$ 4.51	LPS	35.23 $\pm$ 6.64
Non-glycolytic acidification (mpH/min/20K cells)	Small rec. born	Control	13.24 $\pm$ 1.54	LPS	18.24 $\pm$ 2.34

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