

Multivariate Regression with 20 top taxa

Proportion of overall mean abundance represented: 0.899084979434395

# Analysis of Variance Table

	Df	Pillai	approx F	num Df	den Df	Pr(>F)
(Intercept)	1	0.9942	634.86	20	74	< 2.2e-16 ***
Patient	20	6.7295	2.36	400	1860	< 2.2e-16 ***
daynumber_for_collection	1	0.2216	1.05	20	74	0.41518
Host_Age	1	0.7012	8.68	20	74	1.953e-12 ***
Host_Gender	1	0.4918	3.58	20	74	3.219e-05 ***
Medical_complications	1	0.6103	5.79	20	74	1.096e-08 ***
Patient_diagnosis	1	0.3307	1.83	20	74	0.03270 *
Post_visit_treatment	1	0.7053	8.85	20	74	1.232e-12 ***
Type	1	0.6623	7.25	20	74	1.107e-10 ***
Vacc_status	1	0.3335	1.85	20	74	0.02997 *
Fever	1	0.3354	1.87	20	74	0.02819 *
SYMPTOM_COUGH	1	0.5778	5.06	20	74	1.329e-07 ***
Residuals	93					

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

		Taxonomic Correlations																			
order:Actinomycetales	Rhodococcus	.17	-.03	.01	.14	.17	.15	-.33	.12	.04	-.39	.26	.13	.07	-.29	-.19	.67	.11	.21	.32	1.00
	Prevotella	-.13	.18	.72	.04	-.13	.23	-.35	-.04	.21	-.28	.04	-.05	.50	-.26	.19	.15	.46	.24	1.00	.32
family:Xanthomonadaceae	Moraxella	-.12	.07	.21	.00	-.08	.15	-.21	-.18	.31	-.22	-.01	.01	.07	-.16	-.11	.15	.13	1.00	.24	.21
	Rhizobium	-.08	.15	.47	-.11	-.06	.24	-.18	.06	.16	-.10	.01	-.13	.57	-.10	-.03	.01	1.00	.13	.46	.11
family:Pseudomonadaceae	Rhizobium	.07	-.05	-.05	-.02	.09	.10	-.12	.12	-.10	-.20	.25	.21	-.08	-.05	-.19	1.00	.01	.15	.15	.67
	Propionibacterium	.23	.28	.17	.12	.24	-.14	.21	-.12	.02	.24	-.15	.09	-.03	.26	1.00	-.19	-.03	-.11	.19	-.19
family:Xanthomonadaceae	Achromobacter	.38	.13	-.17	-.02	.32	-.31	.76	-.09	-.07	.71	.00	.11	-.21	1.00	.26	-.05	-.10	-.16	-.26	-.29
	Dolosigranulum	-.12	.19	.57	.03	-.11	.21	-.19	-.02	.22	-.09	-.03	-.15	1.00	-.21	-.03	-.08	.57	.07	.50	.07
family:Pseudomonadaceae	order:Rhizobiales	.35	-.06	-.10	.80	.42	.02	.00	.01	-.23	-.12	-.03	1.00	-.15	.11	.09	.21	-.13	.01	-.05	.13
	Stenotrophomonas	-.06	-.20	-.09	-.14	-.07	-.01	.03	.59	-.04	-.02	1.00	-.03	-.03	.00	-.15	.25	.01	-.01	.04	.26
family:Pseudomonadaceae	Dyella	.29	.17	-.15	-.19	.21	-.39	.81	-.08	-.02	1.00	-.02	-.12	-.09	.71	.24	-.20	-.10	-.22	-.28	-.39
	Streptococcus	-.16	.17	.26	-.05	-.21	.19	-.07	-.15	1.00	-.02	-.04	-.23	.22	-.07	.02	-.10	.16	.31	.21	.04
family:Pseudomonadaceae	Delftia	-.06	-.19	-.13	-.17	-.11	.08	-.00	1.00	-.15	-.08	.59	.01	-.02	-.09	-.12	.12	.06	-.18	-.04	.12
	family:Xanthomonadaceae	.49	.16	-.30	-.10	.41	-.48	1.00	-.00	-.07	.81	.03	.00	-.19	.76	.21	-.12	-.18	-.21	-.35	-.33
family:Pseudomonadaceae	Haemophilus	-.25	-.12	.24	.06	-.13	1.00	-.48	.08	.19	-.39	-.01	.02	.21	-.31	-.14	.10	.24	.15	.23	.15
	family:Pseudomonadaceae	.92	-.05	-.19	.39	1.00	-.13	.41	-.11	-.21	.21	-.07	.42	-.11	.32	.24	.09	-.06	-.08	-.13	.17
family:Pseudomonadaceae	Ochrobactrum	.34	.07	.05	1.00	.39	.06	-.10	-.17	-.05	-.19	-.14	.80	.03	-.02	.12	-.02	-.11	.00	.04	.14
	Corynebacterium	-.19	.35	1.00	.05	-.19	.24	-.30	-.13	.26	-.15	-.09	-.10	.57	-.17	.17	-.05	.47	.21	.72	.01
family:Pseudomonadaceae	Staphylococcus	.01	1.00	.35	.07	-.05	-.12	.16	-.19	.17	.17	-.20	-.06	.19	.13	.28	-.05	.15	.07	.18	-.03
	Pseudomonas	1.00	.01	-.19	.34	.92	-.25	.49	-.06	-.16	.29	-.06	.35	-.12	.38	.23	.07	-.08	-.12	-.13	.17
	Pseudomonas	Pseudomonas	Staphylococcus	Corynebacterium	Ochrobactrum	family:Pseudomonadaceae	Haemophilus	family:Xanthomonadaceae	Delftia	Streptococcus	Dyella	Stenotrophomonas	order:Rhizobiales	Dolosigranulum	Achromobacter	Propionibacterium	Rhizobium	Moraxella	Prevotella	order:Actinomycetales	Rhodococcus

Univariate Pr(>F)											
Rhodococcus	.00	.52	.07	.06	.76	.72	.05	.80	.04	.94	.69
order:Actinomycetales	.00	.55	.20	.52	.17	.39	.10	.08	.58	.05	.86
Prevotella	.00	.44	.01	.06	.30	.14	.01	.02	.27	.35	.92
Moraxella	.00	.20	.00	.96	.20	.15	.98	.49	.01	.82	.98
Rhizobium	.02	.06	.00	.00	.55	.91	.03	.31	.36	.90	.75
Propionibacterium	.01	.53	.00	.24	.97	.88	.08	.07	.64	.03	.63
Achromobacter	.00	.66	.34	.07	.67	.32	.73	.84	.01	.61	.07
Dolosigranulum	.00	.46	.67	.83	.40	.98	.52	.85	.16	.88	.70
order:Rhizobiales	.00	.09	.00	.19	.74	.05	.55	.00	.91	.58	.22
Stenotrophomonas	.00	.76	.00	.26	.18	.47	.00	.03	.21	.09	.00
Dyella	.01	.28	.37	.14	.93	.24	.77	.04	.00	.15	.17
Streptococcus	.01	.33	.08	.64	.12	.07	.46	.95	.79	.91	.56
Delftia	.00	.66	.00	.00	.00	.48	.00	.00	.12	.03	.00
family:Xanthomonadaceae	.00	.86	.44	.23	.33	.05	.77	.04	.01	.39	.28
Haemophilus	.00	.73	.04	.31	.01	.00	.05	.00	.24	.67	.69
family:Pseudomonadaceae	.03	.35	.00	.79	.45	.27	.43	.54	.56	.55	.19
Ochrobactrum	.01	.26	.00	.02	.10	.02	.06	.00	.34	.23	.33
Corynebacterium	.00	.35	.70	.14	.28	.01	.03	.70	.86	.24	.80
Staphylococcus	.00	.15	.78	.90	.85	.01	.53	.57	.92	.00	.61
Pseudomonas	.04	.96	.02	.46	.37	.20	.50	.97	.71	.82	.13
	Patient	daynumber_for_collection	Host_Age	Host_Gender	Medical_complications	Patient_diagnosis	Post_visit_treatment	Type	Vacc_status	Fever	SYMPTOM_COUGH

Univariate R Squared		
Rhodococcus	.50	.33
order:Actinomycetales	.55	.40
Prevotella	.50	.34
Moraxella	.65	.54
Rhizobium	.46	.28
Propionibacterium	.41	.22
Achromobacter	.53	.38
Dolosigranulum	.63	.51
order:Rhizobiales	.55	.40
Stenotrophomonas	.58	.45
Dyella	.41	.23
Streptococcus	.38	.17
Delftia	.89	.85
family:Xanthomonadaceae	.51	.35
Haemophilus	.61	.49
family:Pseudomonadaceae	.37	.17
Ochrobactrum	.58	.44
Corynebacterium	.60	.47
Staphylococcus	.52	.36
Pseudomonas	.34	.12
	R <sup>2</sup>	Adjusted R <sup>2</sup>

# Univariate Regression:

1.) Pseudomonas

Mean abundance: 29.5%

R^2: 0.3364

Adjusted R^2: 0.1223

## Analysis of Variance Table

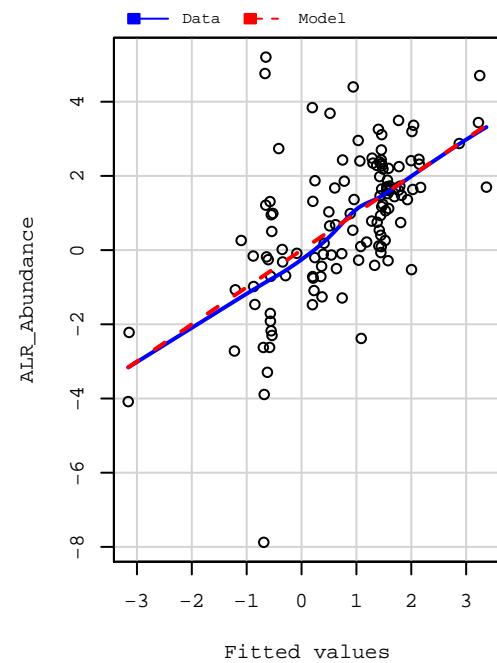
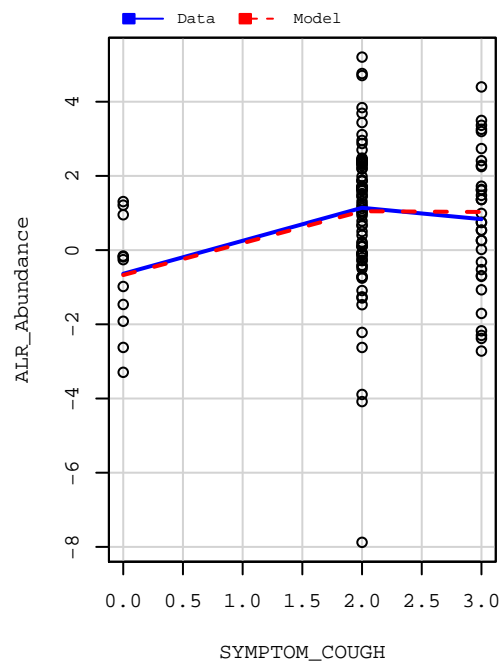
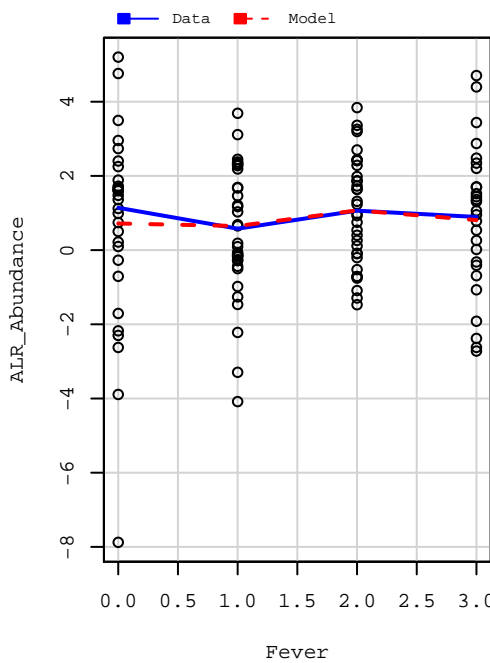
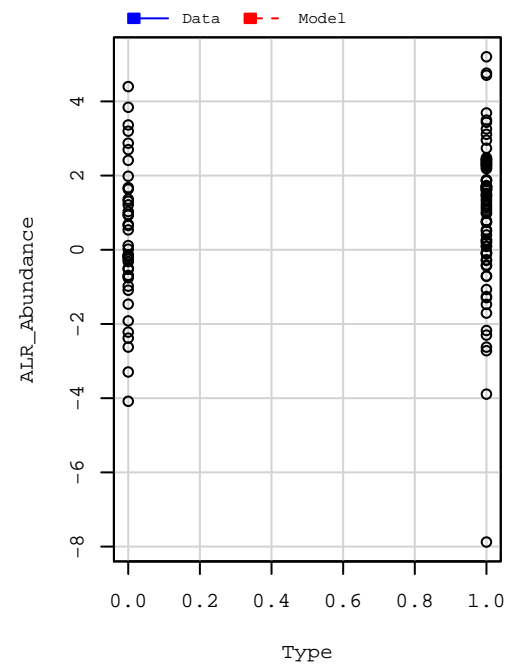
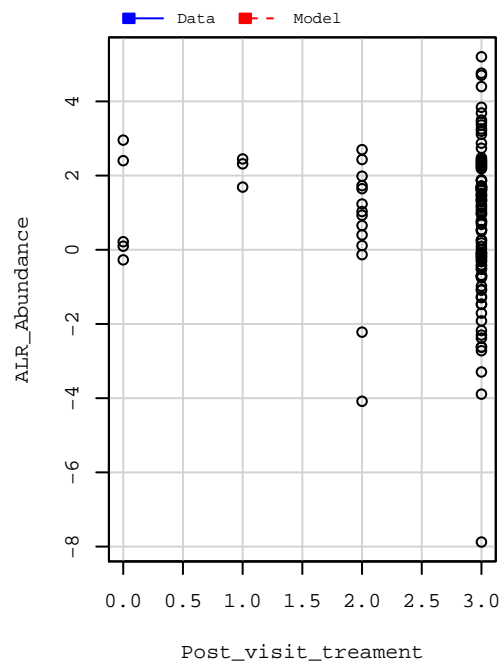
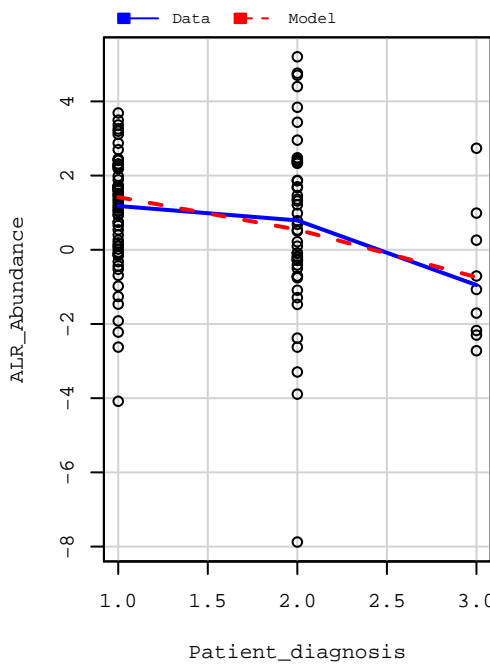
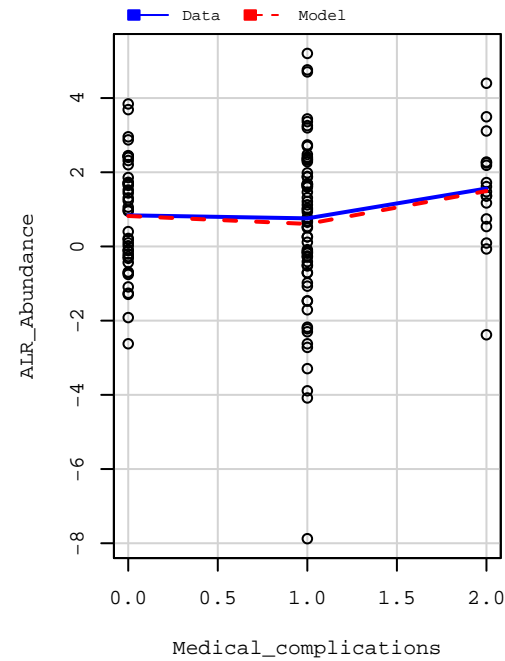
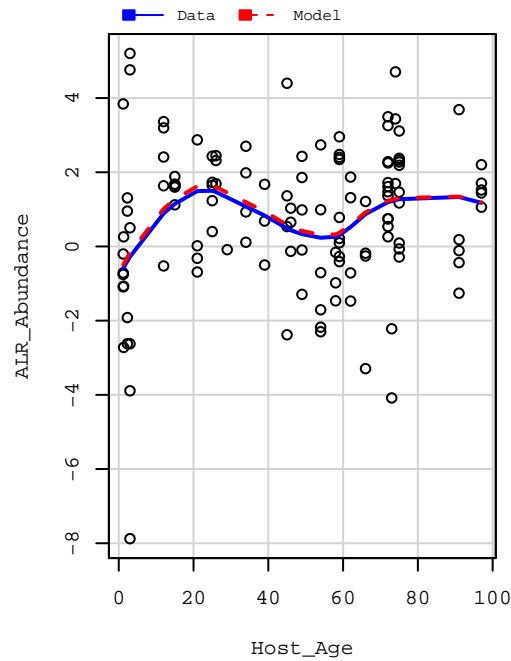
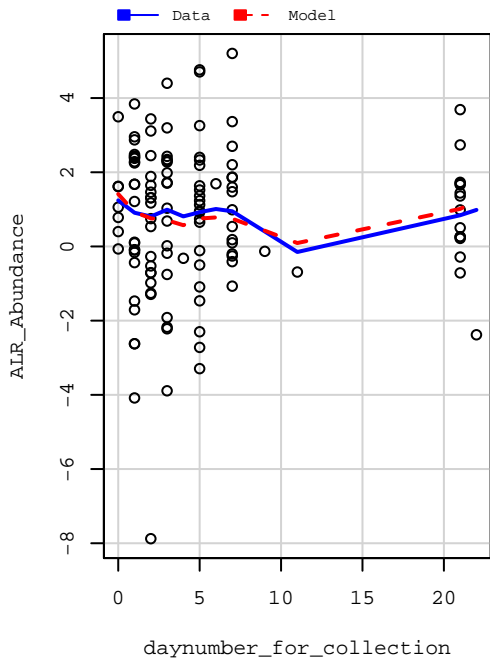
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	119.47	5.9734	1.7553	0.03790	*
daynumber_for_collection	1	0.01	0.0067	0.0020	0.96469	
Host_Age	1	19.74	19.7425	5.8013	0.01799	*
Host_Gender	1	1.89	1.8874	0.5546	0.45831	
Medical_complications	1	3.52	3.5175	1.0336	0.31195	
Patient_diagnosis	1	5.78	5.7821	1.6991	0.19563	
Post_visit_treatment	1	1.53	1.5293	0.4494	0.50428	
Type	1	0.01	0.0051	0.0015	0.96921	
Vacc_status	1	0.47	0.4738	0.1392	0.70989	
Fever	1	0.17	0.1702	0.0500	0.82352	
SYMPTOM_COUGH	1	7.85	7.8468	2.3058	0.13229	
Residuals	93	316.49	3.4031			

---

Signif. codes: 0 '\*\*\*\*' 0.001 '\*\*\*' 0.01 '\*\*' 0.05 '.' 0.1 ' ' 1

# 1.) Pseudomonas [29.5%]



Univariate Regression:

2.) Staphylococcus

Mean abundance: 12.1%

R<sup>2</sup>: 0.5189

Adjusted R<sup>2</sup>: 0.3637

Analysis of Variance Table

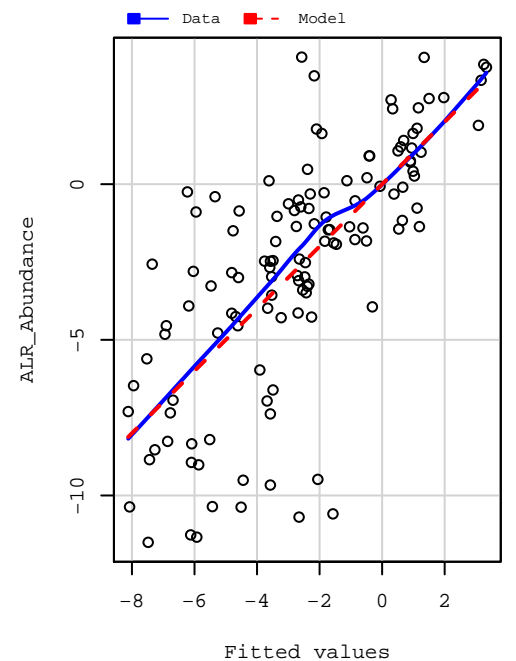
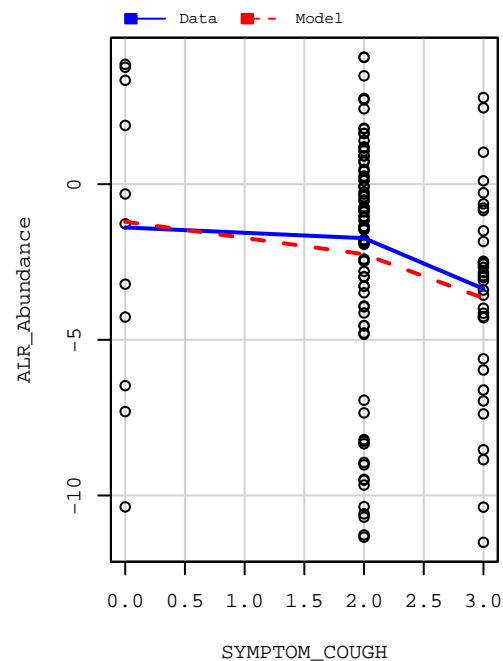
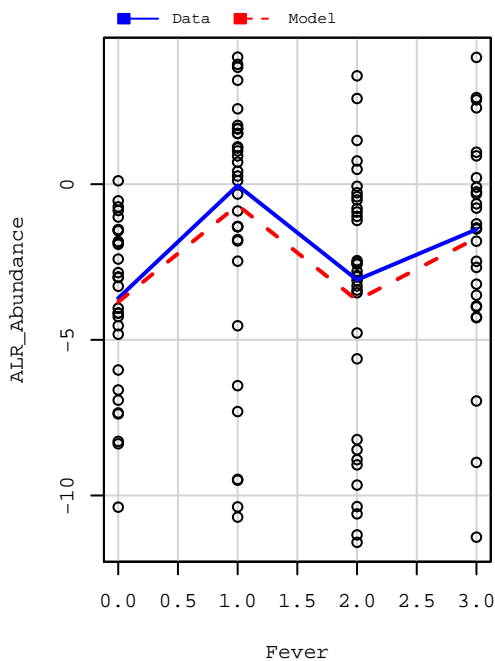
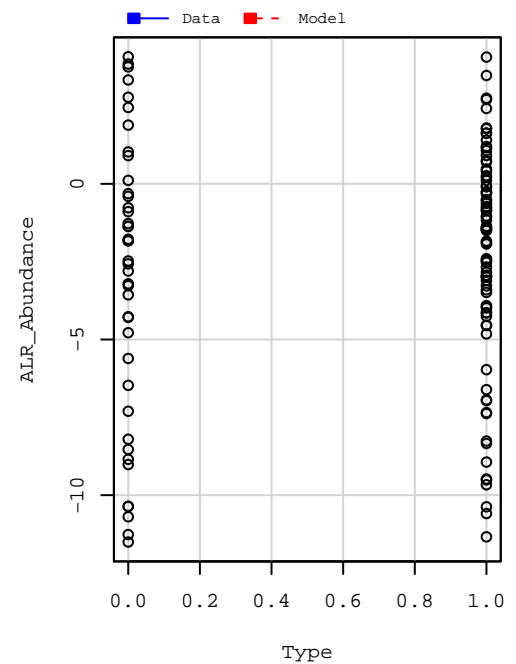
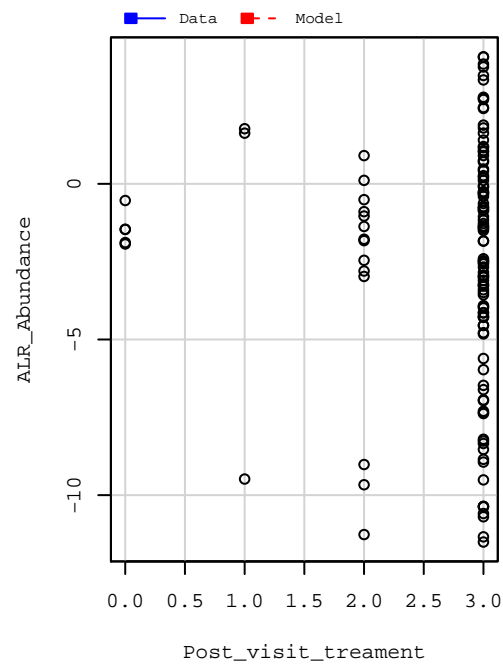
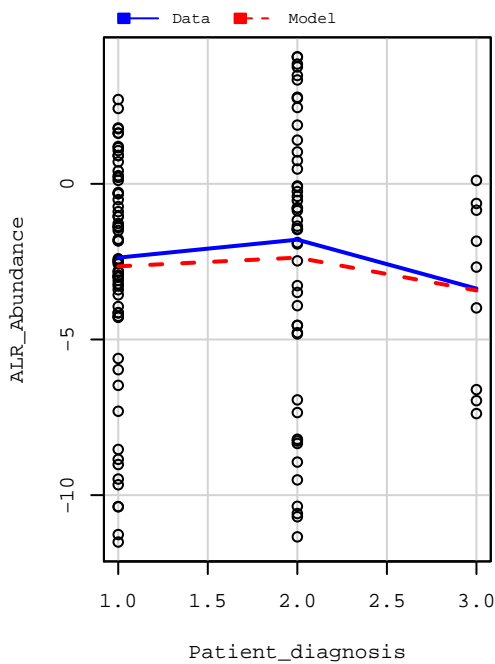
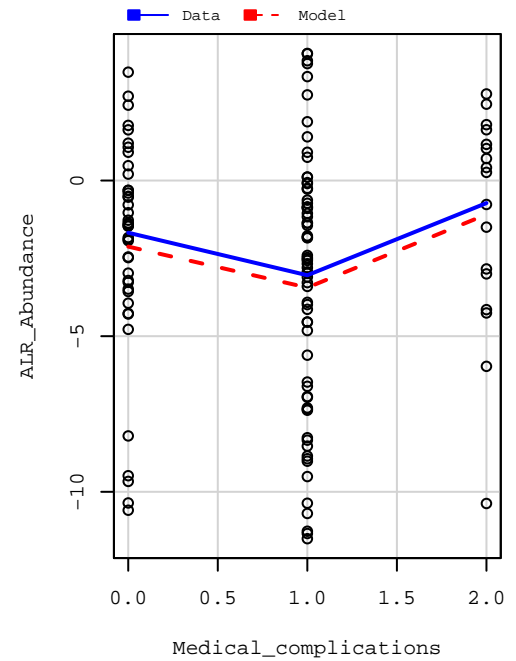
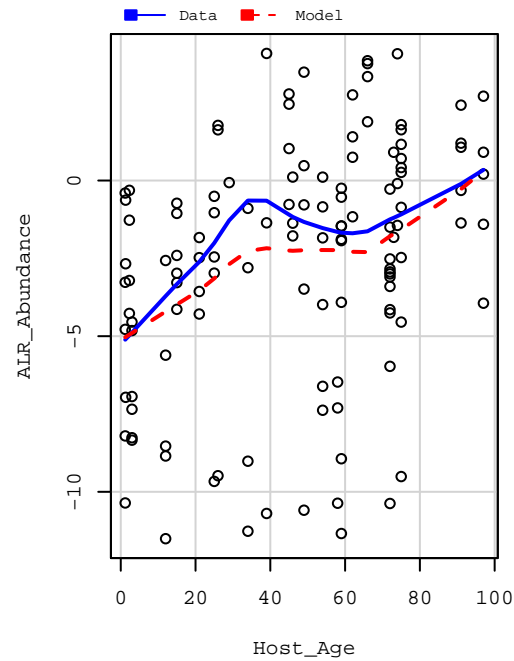
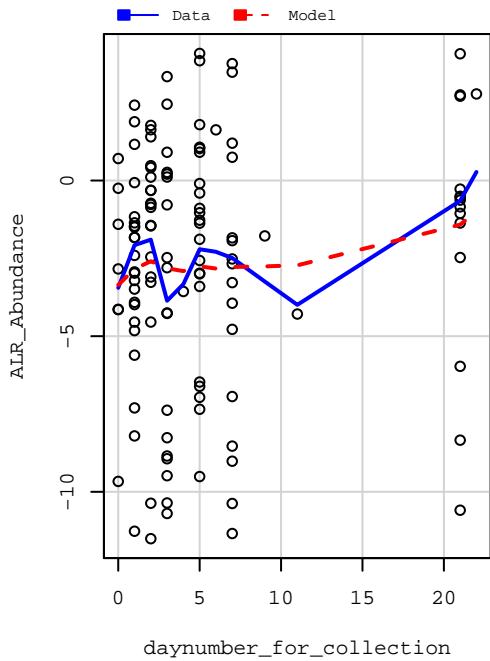
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	772.52	38.626	3.9911	2.586e-06	***
daynumber_for_collection	1	20.61	20.613	2.1299	0.147818	
Host_Age	1	0.79	0.789	0.0816	0.775820	
Host_Gender	1	0.16	0.162	0.0168	0.897225	
Medical_complications	1	0.36	0.360	0.0372	0.847511	
Patient_diagnosis	1	63.49	63.488	6.5600	0.012038	*
Post_visit_treatment	1	3.80	3.801	0.3928	0.532385	
Type	1	3.14	3.144	0.3248	0.570085	
Vacc_status	1	0.11	0.106	0.0110	0.916800	
Fever	1	103.20	103.196	10.6629	0.001531	**
SYMPTOM_COUGH	1	2.49	2.487	0.2570	0.613416	
Residuals	93	900.06	9.678			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

## 2.) Staphylococcus [12.1%]





Univariate Regression:

3.) Corynebacterium

Mean abundance: 10.0%

R<sup>2</sup>: 0.5983

Adjusted R<sup>2</sup>: 0.4687

Analysis of Variance Table

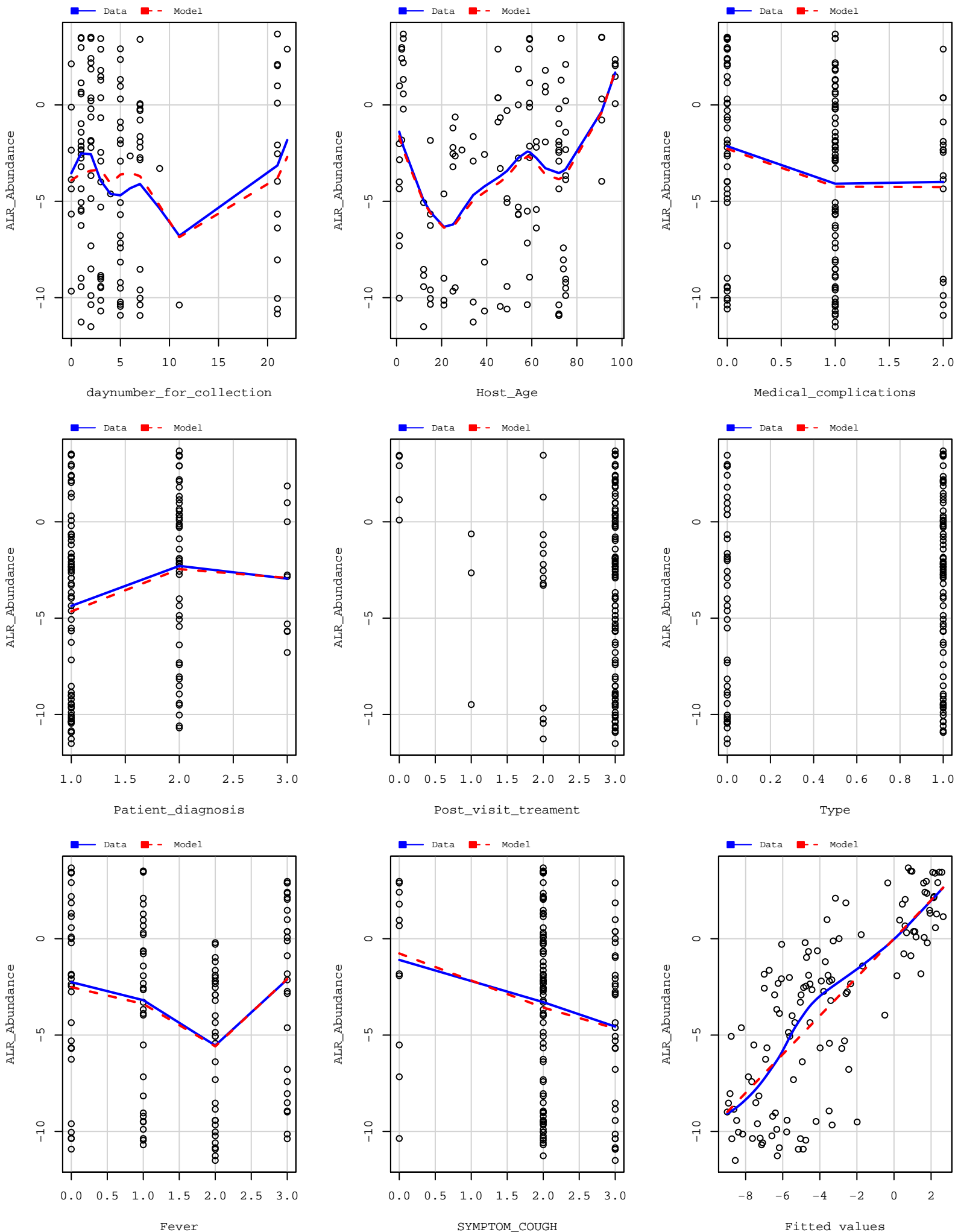
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	1336.08	66.804	6.0459	7.189e-10	***
daynumber_for_collection	1	9.66	9.658	0.8741	0.35225	
Host_Age	1	1.66	1.659	0.1501	0.69931	
Host_Gender	1	24.86	24.864	2.2503	0.13698	
Medical_complications	1	13.02	13.023	1.1786	0.28046	
Patient_diagnosis	1	71.72	71.715	6.4903	0.01249	*
Post_visit_treatment	1	55.43	55.432	5.0167	0.02749	*
Type	1	1.63	1.628	0.1474	0.70195	
Vacc_status	1	0.33	0.327	0.0296	0.86376	
Fever	1	15.46	15.463	1.3994	0.23984	
SYMPTOM_COUGH	1	0.72	0.717	0.0649	0.79955	
Residuals	93	1027.61	11.050			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

### 3.) *Corynebacterium* [10.0%]



# Univariate Regression:

## 4.) Ochrobactrum

Mean abundance: 9.2%

R<sup>2</sup>: 0.5783

Adjusted R<sup>2</sup>: 0.4422

## Analysis of Variance Table

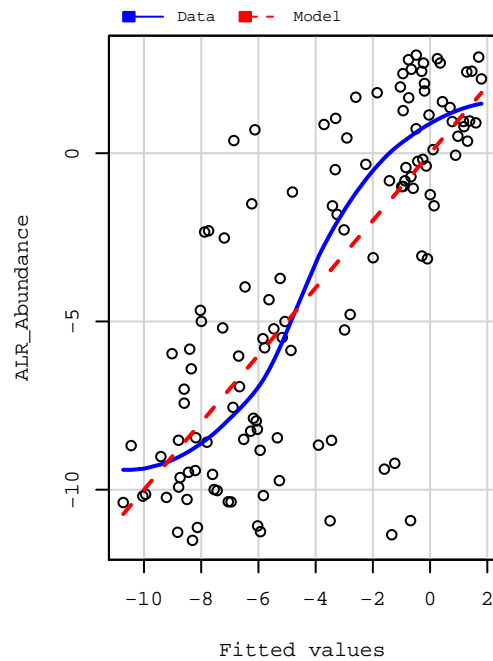
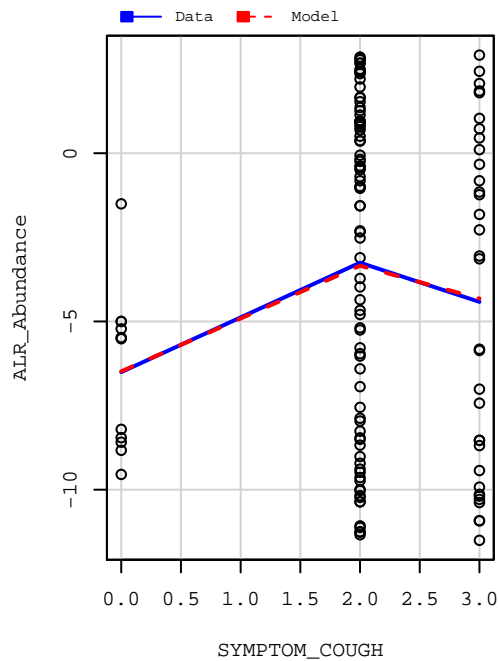
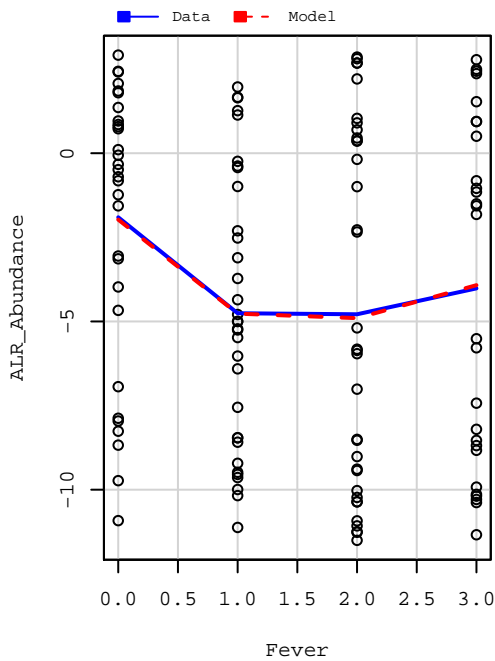
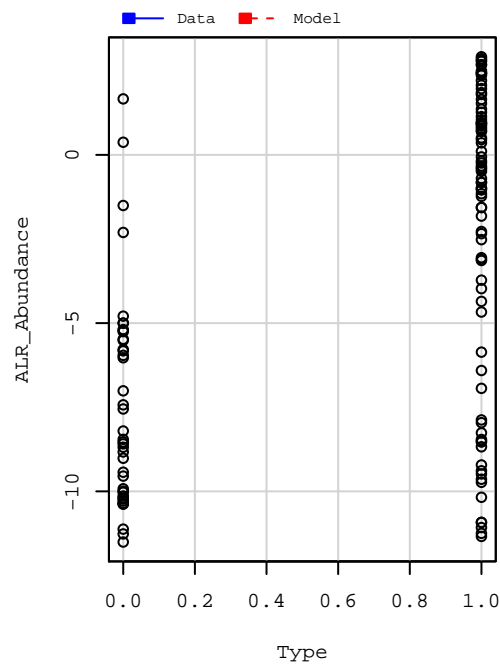
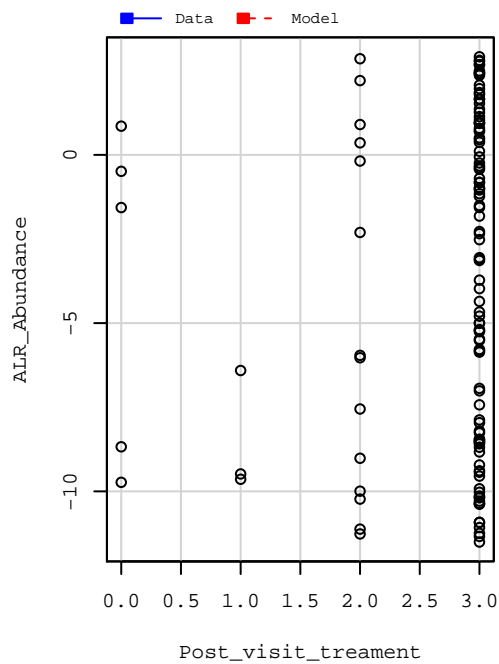
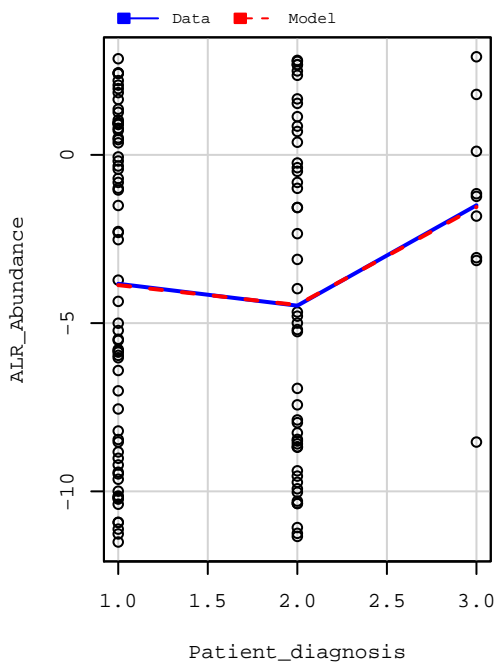
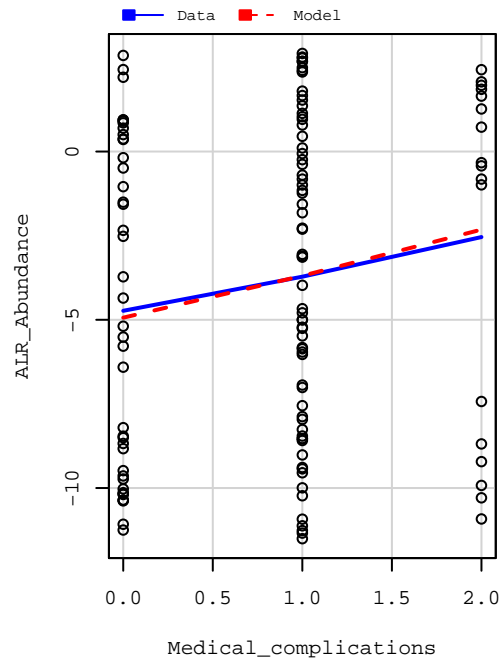
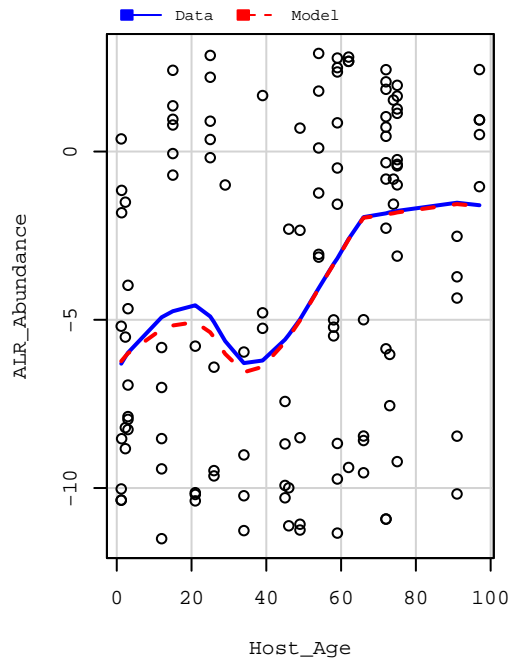
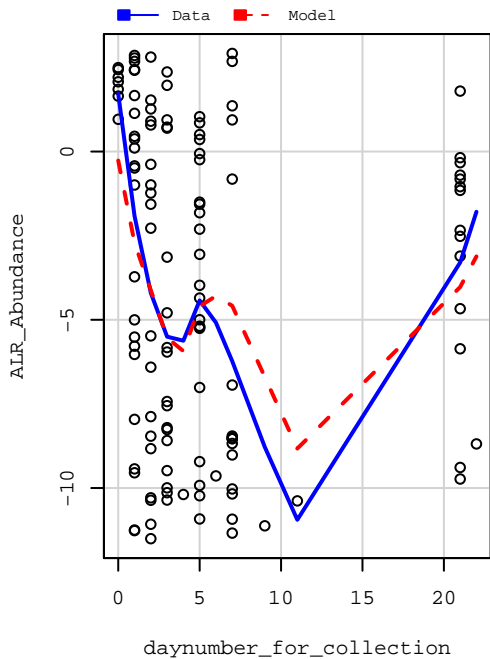
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	516.14	25.81	2.0641	0.01075	*
daynumber_for_collection	1	16.27	16.27	1.3014	0.25689	
Host_Age	1	268.45	268.45	21.4706	1.167e-05	***
Host_Gender	1	72.50	72.50	5.7990	0.01801	*
Medical_complications	1	35.51	35.51	2.8400	0.09530	.
Patient_diagnosis	1	65.87	65.87	5.2682	0.02397	*
Post_visit_treatment	1	46.98	46.98	3.7575	0.05560	.
Type	1	530.78	530.78	42.4520	3.676e-09	***
Vacc_status	1	11.63	11.63	0.9301	0.33734	
Fever	1	18.57	18.57	1.4854	0.22602	
SYMPTOM_COUGH	1	11.74	11.74	0.9393	0.33497	
Residuals	93	1162.77	12.50			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 4.) Ochromabtrum [9.2%]



Univariate Regression:

5.) family:Pseudomonadaceae

Mean abundance: 4.4%

R<sup>2</sup>: 0.3721

Adjusted R<sup>2</sup>: 0.1696

Analysis of Variance Table

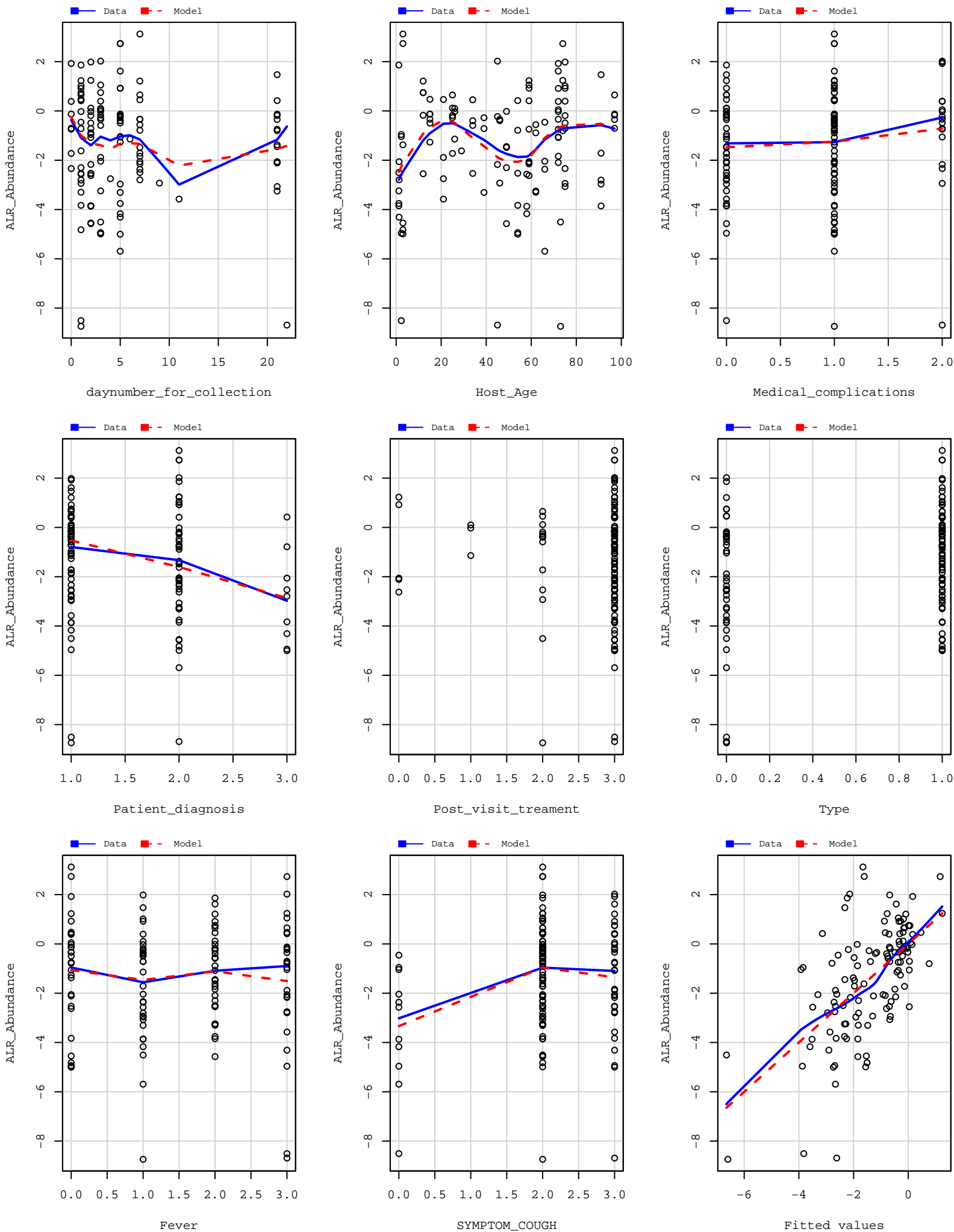
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	146.85	7.343	1.7801	0.0343423	*
daynumber_for_collection	1	3.59	3.587	0.8696	0.3534671	
Host_Age	1	55.02	55.019	13.3390	0.0004296	***
Host_Gender	1	0.29	0.290	0.0703	0.7914747	
Medical_complications	1	2.34	2.338	0.5668	0.4534251	
Patient_diagnosis	1	5.16	5.157	1.2502	0.2663922	
Post_visit_treatment	1	2.58	2.575	0.6244	0.4314284	
Type	1	1.58	1.580	0.3832	0.5374194	
Vacc_status	1	1.43	1.433	0.3474	0.5570109	
Fever	1	1.46	1.458	0.3534	0.5536414	
SYMPTOM_COUGH	1	7.07	7.070	1.7141	0.1936822	
Residuals	93	383.60	4.125			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 5.) family:Pseudomonadaceae [4.4%]



# Univariate Regression:

6.) Haemophilus

Mean abundance: 3.3%

R^2: 0.6131

Adjusted R^2: 0.4883

## Analysis of Variance Table

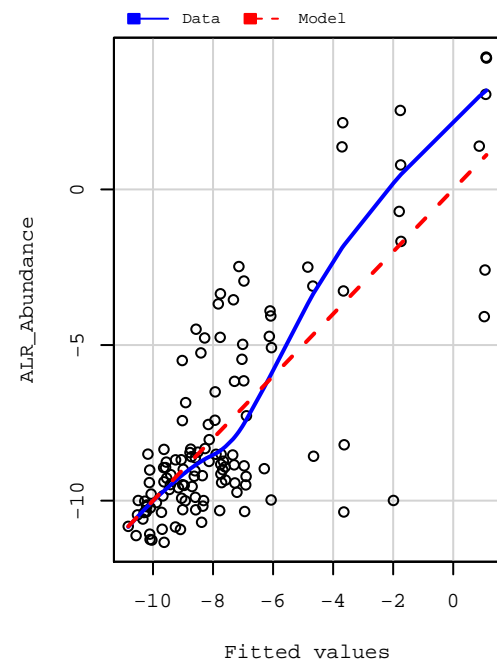
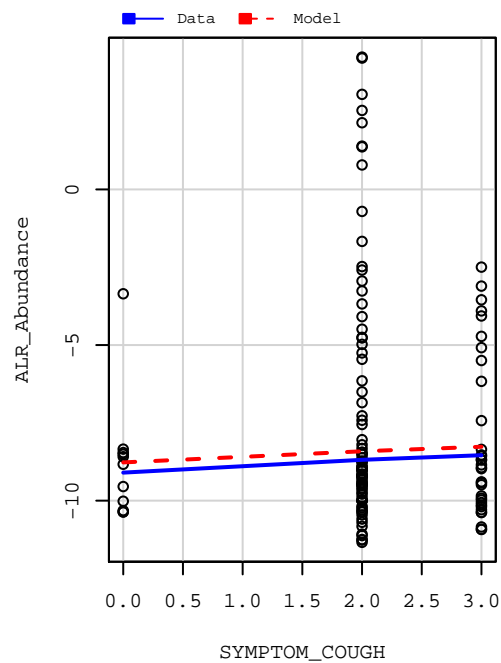
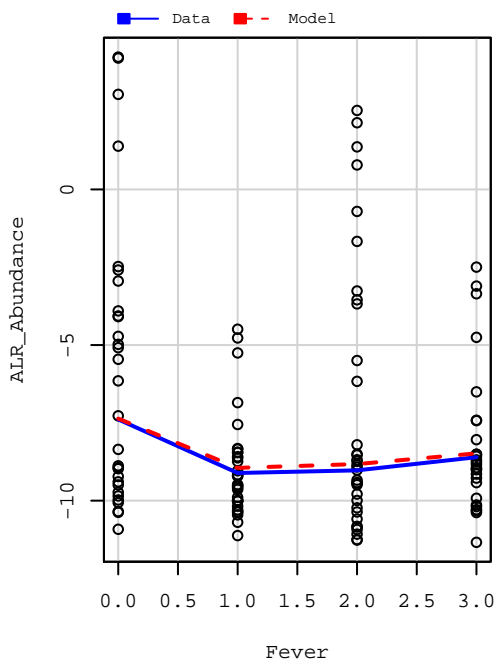
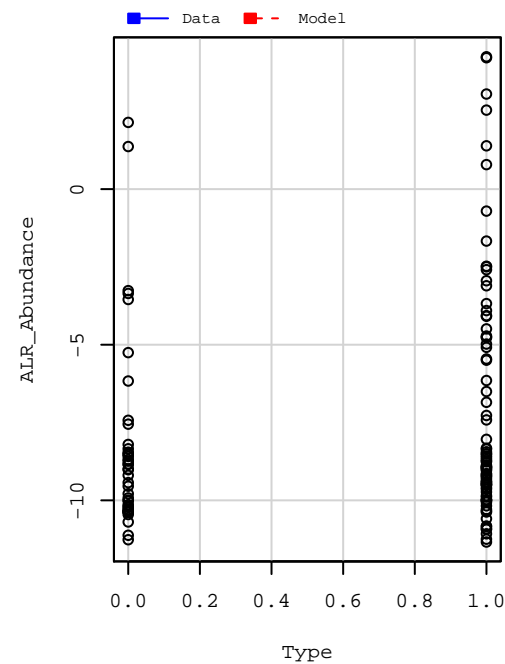
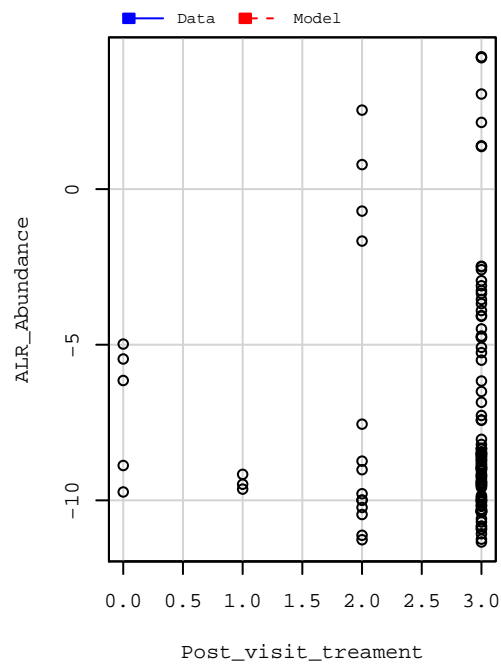
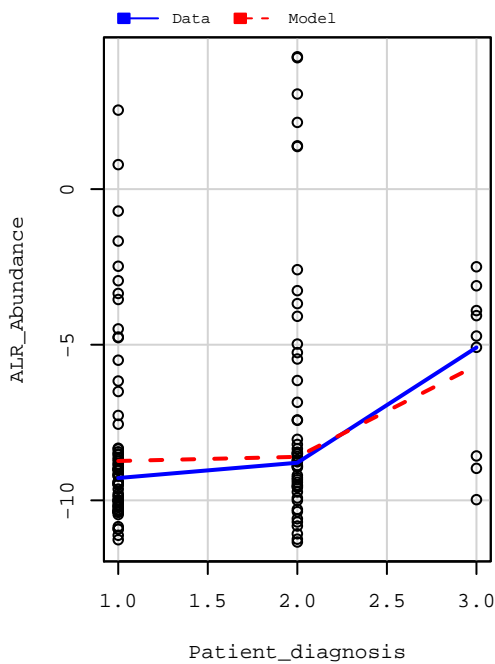
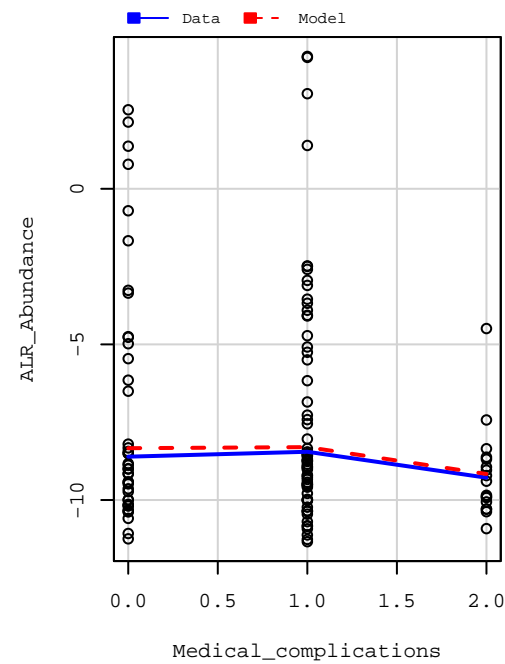
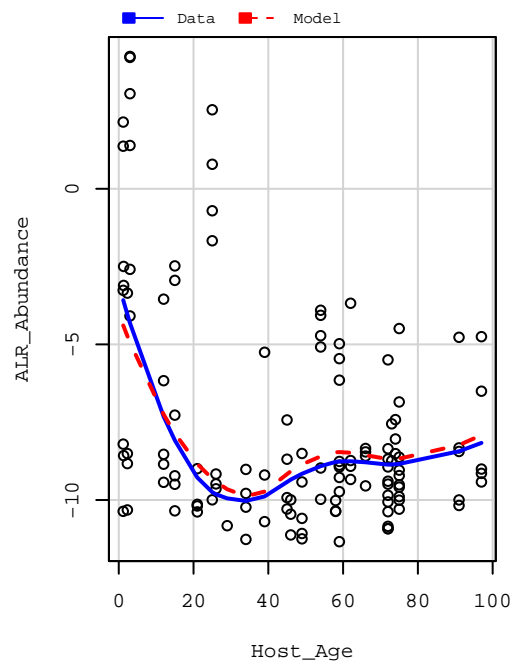
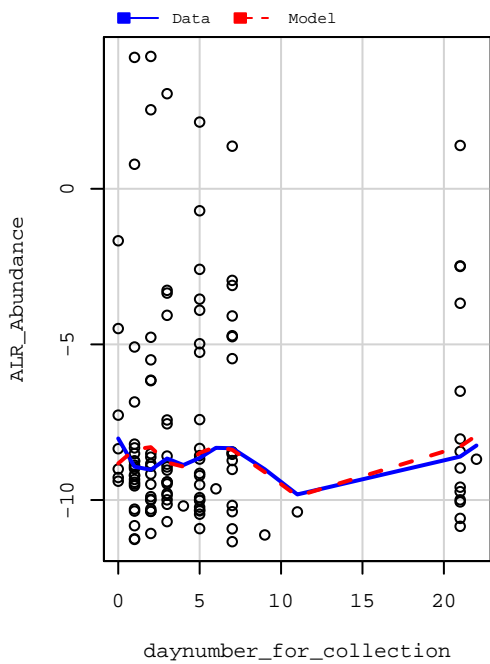
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	682.41	34.120	5.1626	2.133e-08	***
daynumber_for_collection	1	0.80	0.798	0.1208	0.7289477	
Host_Age	1	29.17	29.168	4.4133	0.0383663	*
Host_Gender	1	6.99	6.989	1.0575	0.3064520	
Medical_complications	1	49.40	49.398	7.4743	0.0074931	**
Patient_diagnosis	1	63.60	63.599	9.6229	0.0025446	**
Post_visit_treatment	1	26.80	26.805	4.0557	0.0469118	*
Type	1	103.48	103.480	15.6570	0.0001483	***
Vacc_status	1	9.24	9.243	1.3985	0.2399972	
Fever	1	1.23	1.233	0.1865	0.6668324	
SYMPTOM_COUGH	1	1.05	1.048	0.1585	0.6914291	
Residuals	93	614.65	6.609			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 6.) Haemophilus [3.3%]





# Univariate Regression:

7.) family:Xanthomonadaceae

Mean abundance: 3.2%

R^2: 0.5088

Adjusted R^2: 0.3503

## Analysis of Variance Table

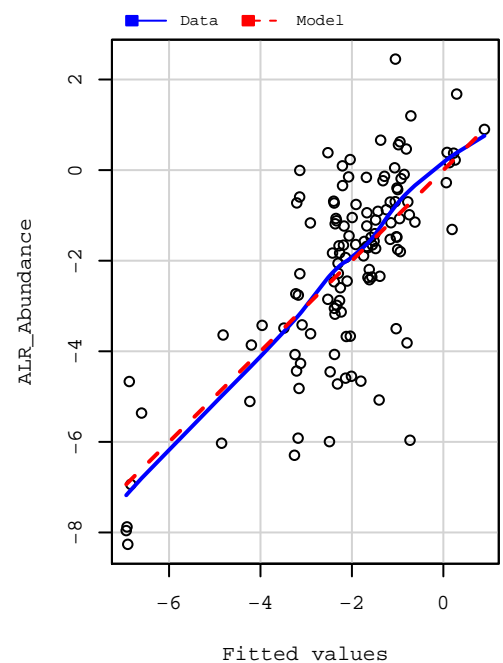
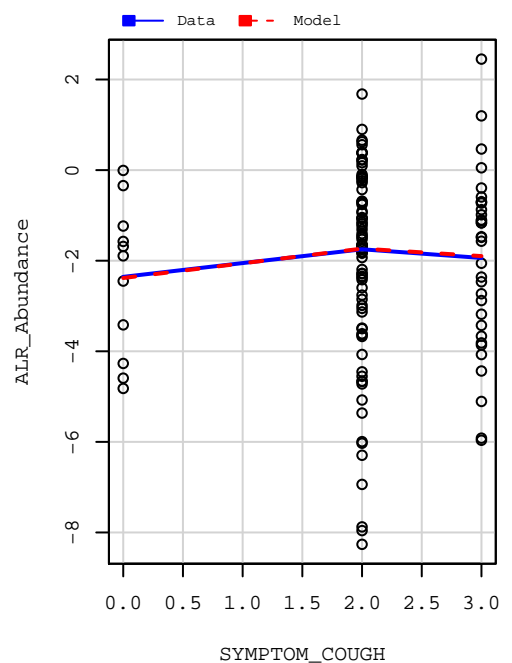
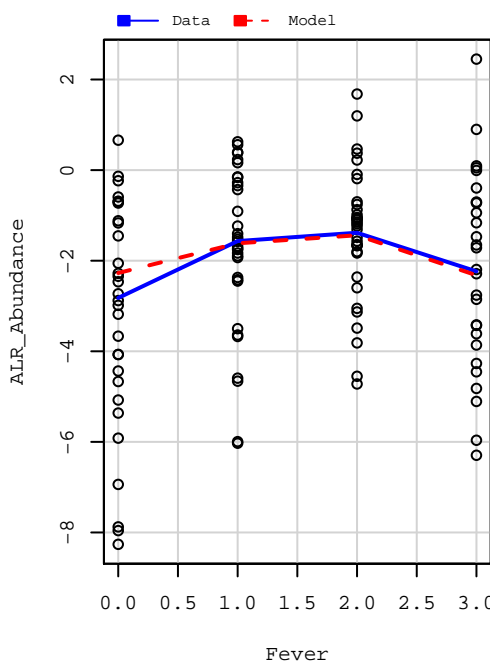
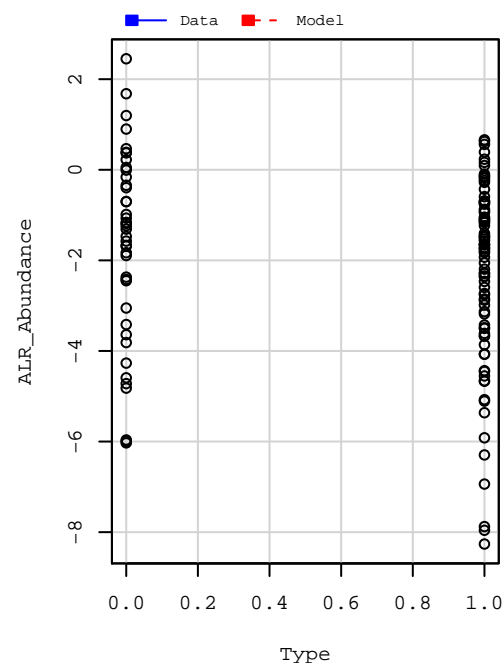
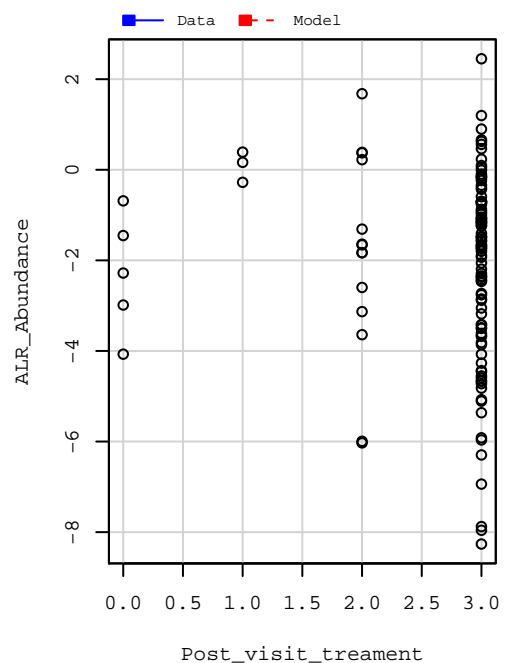
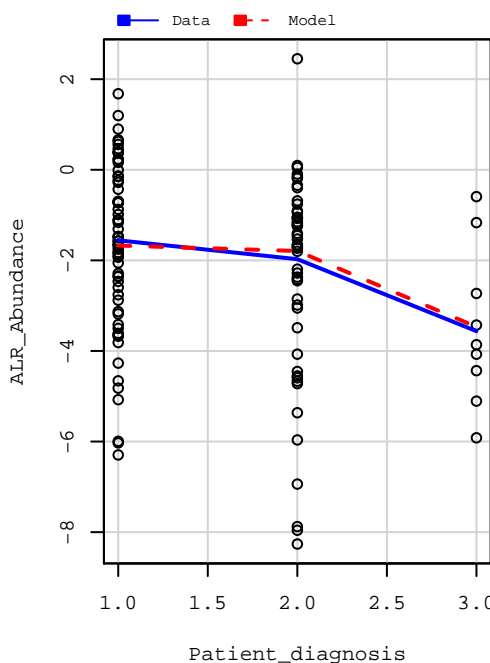
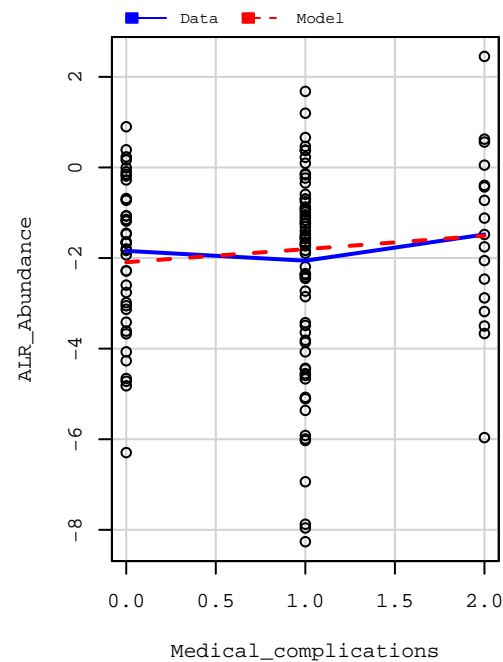
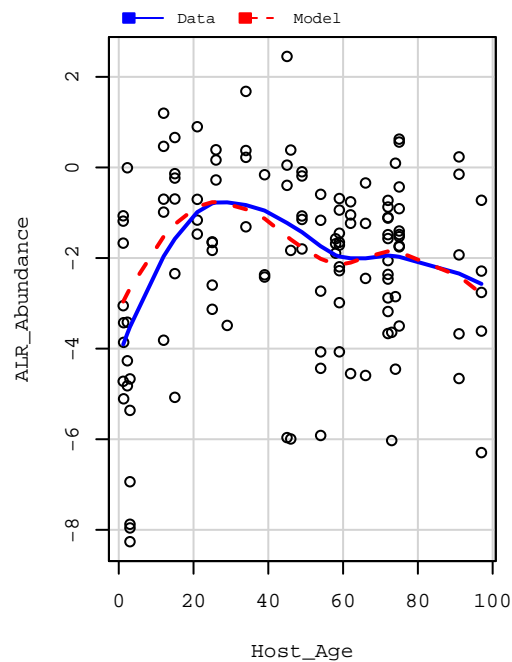
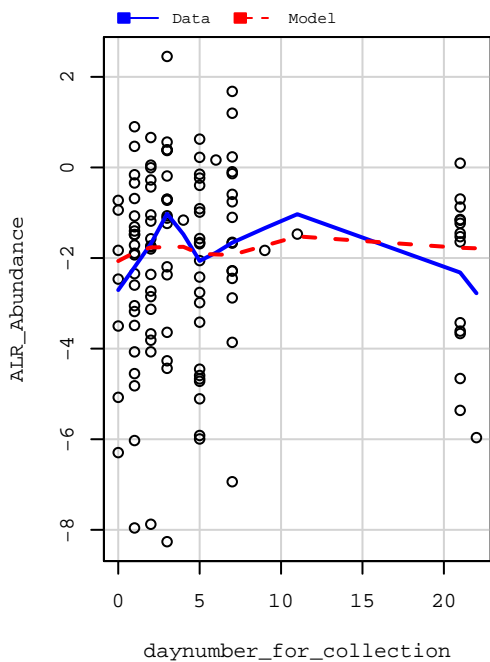
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	211.327	10.5663	3.7644	6.788e-06	***
daynumber_for_collection	1	0.090	0.0899	0.0320	0.858355	
Host_Age	1	1.701	1.7014	0.6061	0.438224	
Host_Gender	1	4.023	4.0225	1.4331	0.234307	
Medical_complications	1	2.727	2.7266	0.9714	0.326894	
Patient_diagnosis	1	11.457	11.4572	4.0818	0.046224	*
Post_visit_treatment	1	0.248	0.2485	0.0885	0.766731	
Type	1	11.931	11.9314	4.2507	0.042024	*
Vacc_status	1	21.535	21.5349	7.6721	0.006771	**
Fever	1	2.081	2.0811	0.7414	0.391424	
SYMPTOM_COUGH	1	3.278	3.2779	1.1678	0.282648	
Residuals	93	261.044	2.8069			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 7.) family:Xanthomonadaceae [3.2%]



Univariate Regression:

8.) Delftia

Mean abundance: 3.1%

R<sup>2</sup>: 0.8867

Adjusted R<sup>2</sup>: 0.8501

Analysis of Variance Table

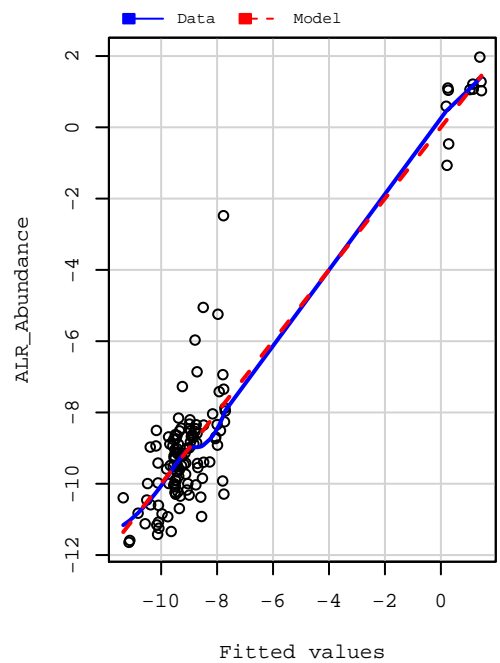
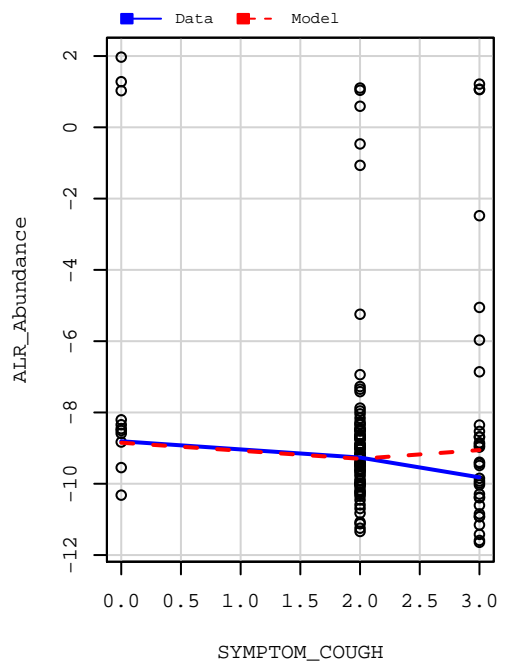
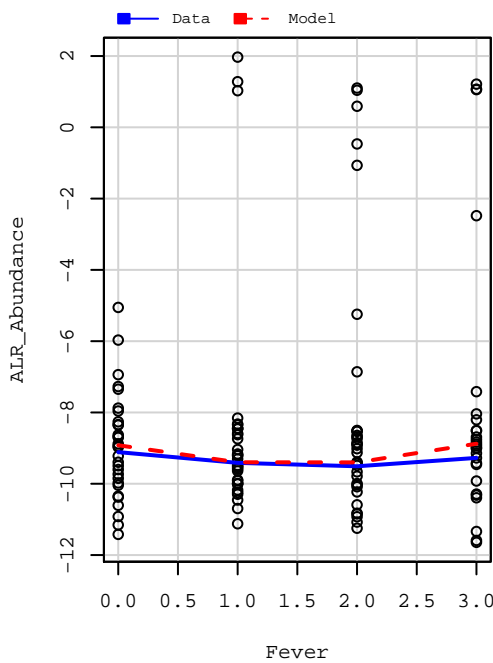
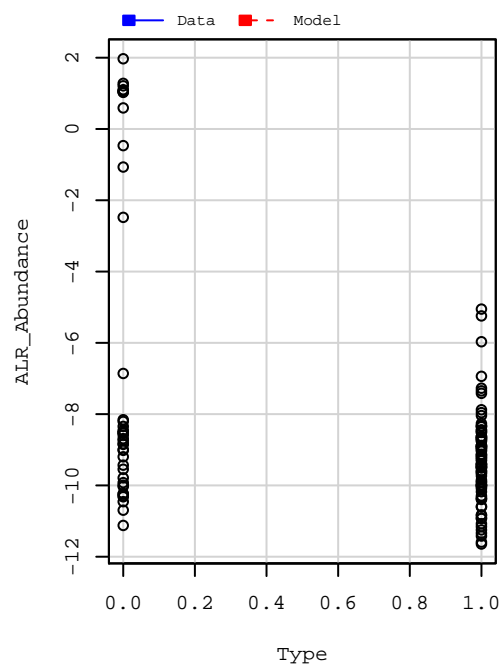
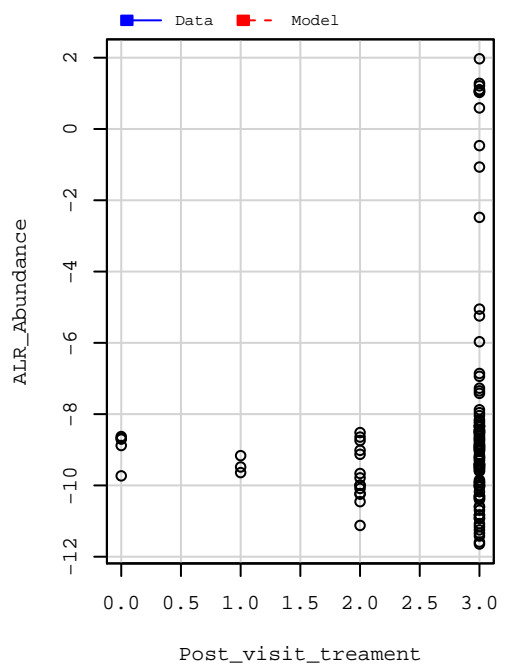
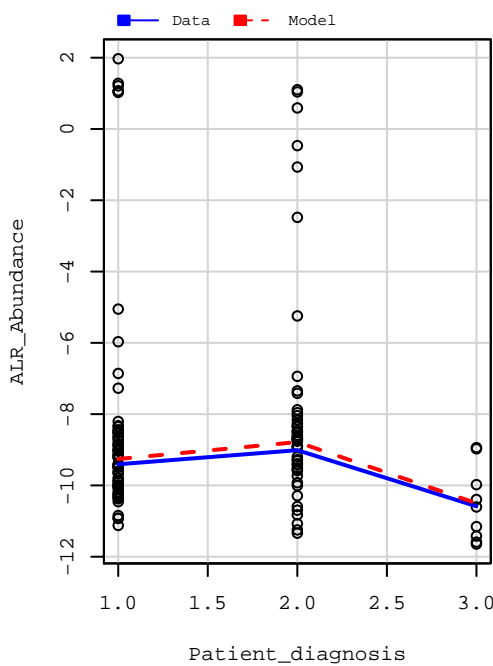
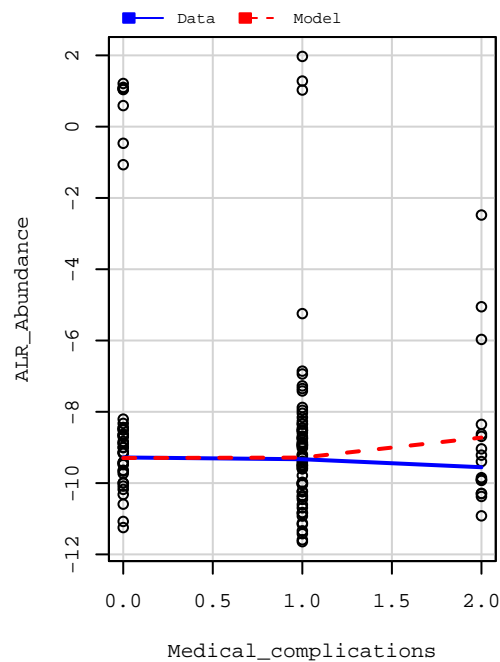
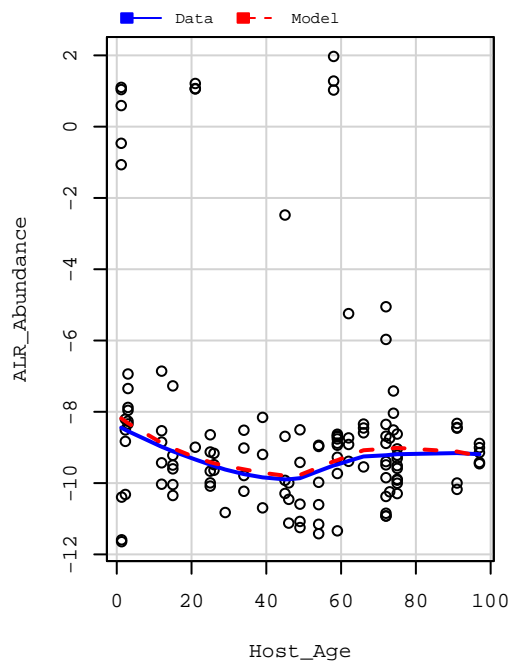
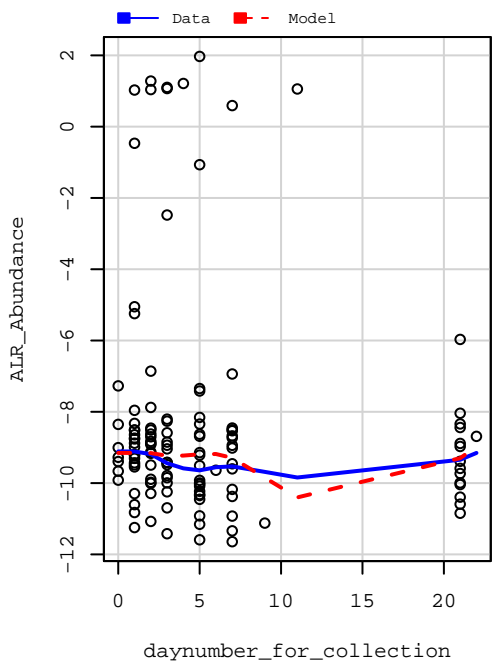
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	620.52	31.026	20.9534	< 2.2e-16	***
daynumber_for_collection	1	0.28	0.281	0.1895	0.664356	
Host_Age	1	50.66	50.662	34.2146	7.303e-08	***
Host_Gender	1	16.82	16.821	11.3602	0.001094	**
Medical_complications	1	117.06	117.065	79.0595	4.524e-14	***
Patient_diagnosis	1	0.75	0.748	0.5049	0.479153	
Post_visit_treatment	1	152.21	152.214	102.7977	< 2.2e-16	***
Type	1	31.06	31.059	20.9754	1.440e-05	***
Vacc_status	1	3.58	3.585	2.4211	0.123105	
Fever	1	7.15	7.155	4.8318	0.030421	*
SYMPTOM_COUGH	1	77.36	77.364	52.2479	1.340e-10	***
Residuals	93	137.71	1.481			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 8.) Delftia [3.1%]



# Univariate Regression:

9.) Streptococcus

Mean abundance: 2.4%

R^2: 0.3757

Adjusted R^2: 0.1743

## Analysis of Variance Table

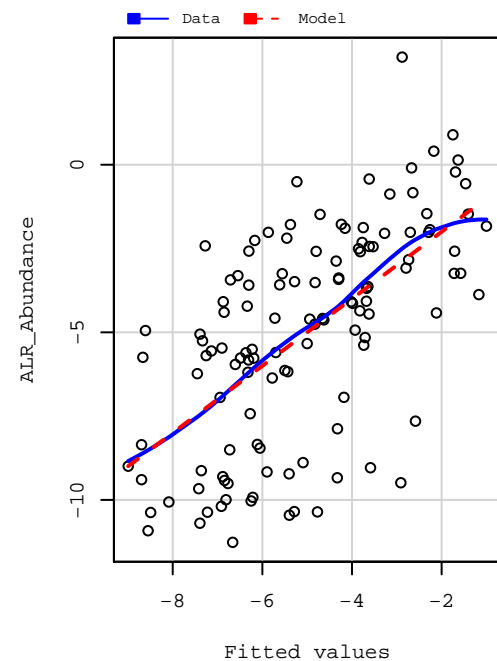
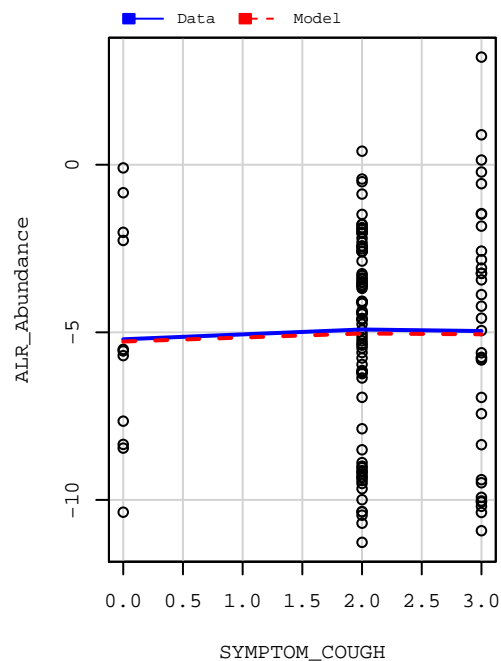
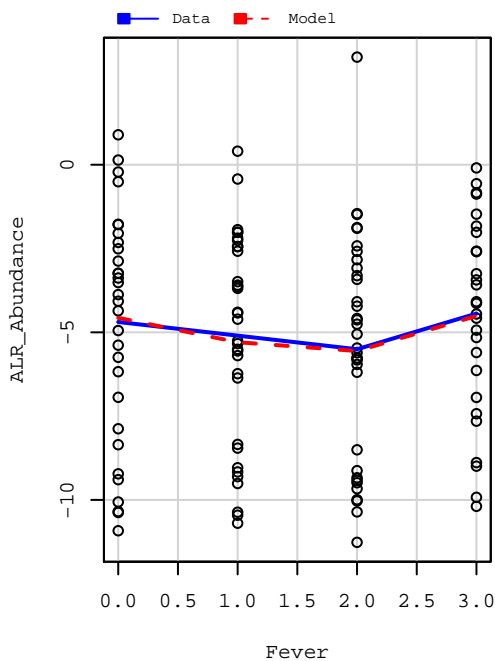
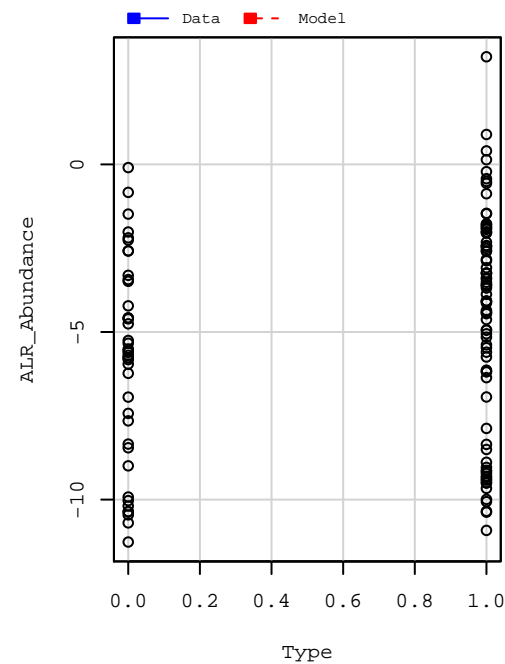
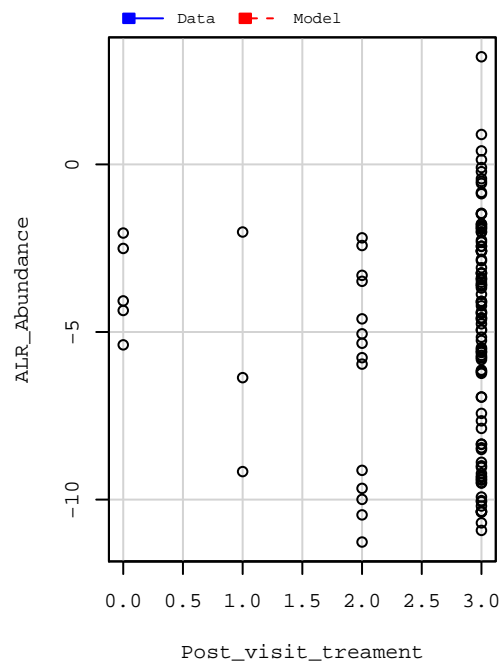
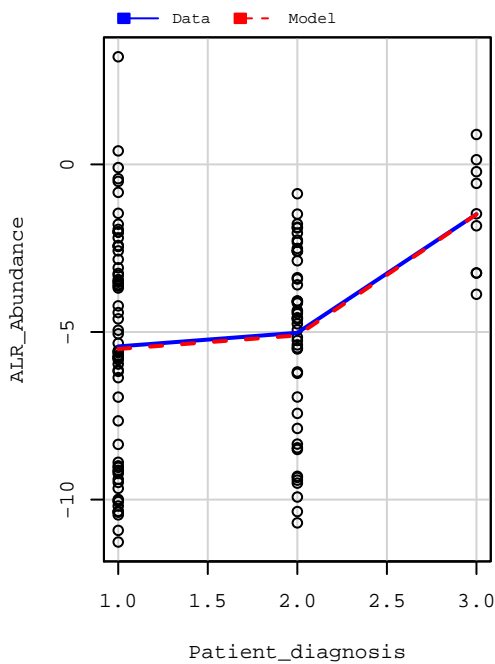
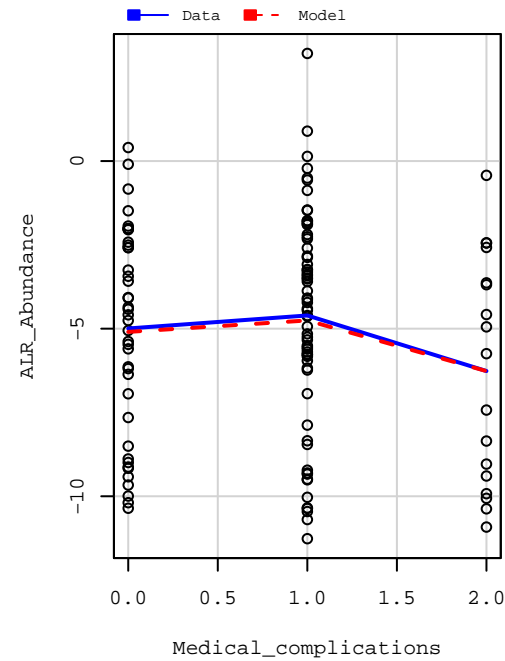
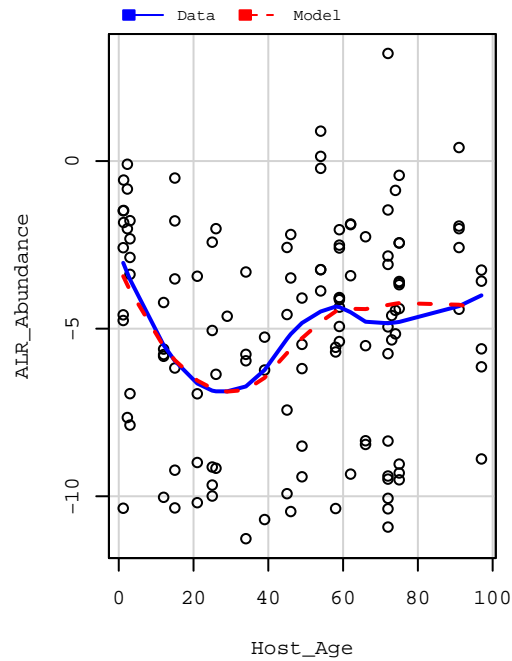
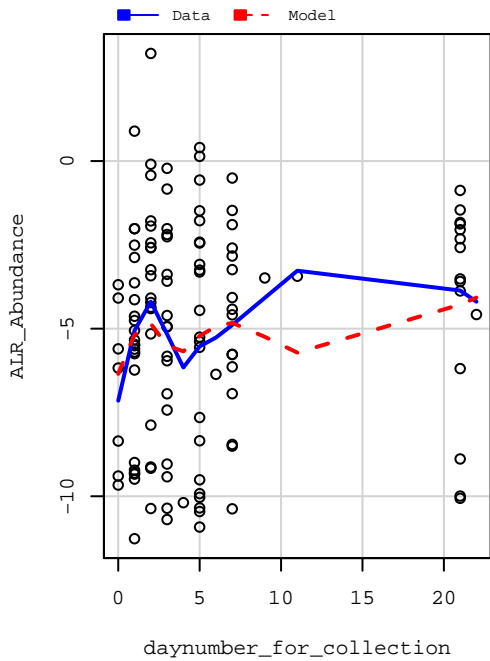
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	377.87	18.8934	2.2321	0.005277	**
daynumber_for_collection	1	8.13	8.1323	0.9608	0.329536	
Host_Age	1	27.05	27.0500	3.1957	0.077088	.
Host_Gender	1	1.84	1.8421	0.2176	0.641942	
Medical_complications	1	21.13	21.1267	2.4959	0.117535	
Patient_diagnosis	1	29.25	29.2508	3.4557	0.066195	.
Post_visit_treatment	1	4.72	4.7208	0.5577	0.457065	
Type	1	0.03	0.0326	0.0038	0.950662	
Vacc_status	1	0.61	0.6069	0.0717	0.789467	
Fever	1	0.11	0.1058	0.0125	0.911228	
SYMPTOM_COUGH	1	2.96	2.9606	0.3498	0.555678	
Residuals	93	787.19	8.4644			

---

Signif. codes: 0 '\*\*\*\*' 0.001 '\*\*\*' 0.01 '\*\*' 0.05 '.' 0.1 ' ' 1

# 9.) Streptococcus [2.4%]



# Univariate Regression:

10.) Dyella

Mean abundance: 1.9%

R^2: 0.4149

Adjusted R^2: 0.2261

## Analysis of Variance Table

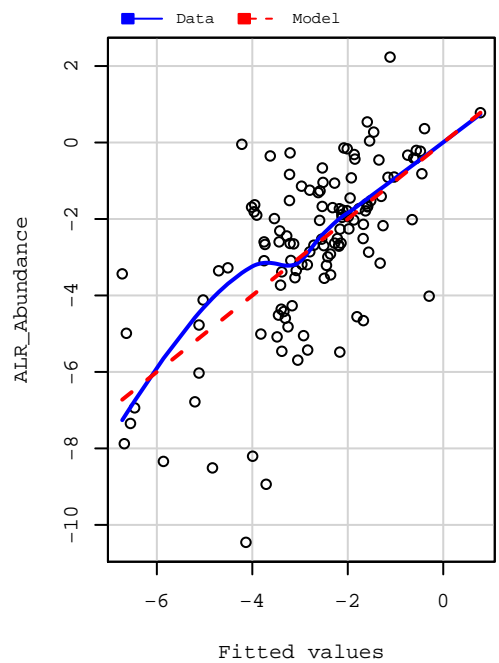
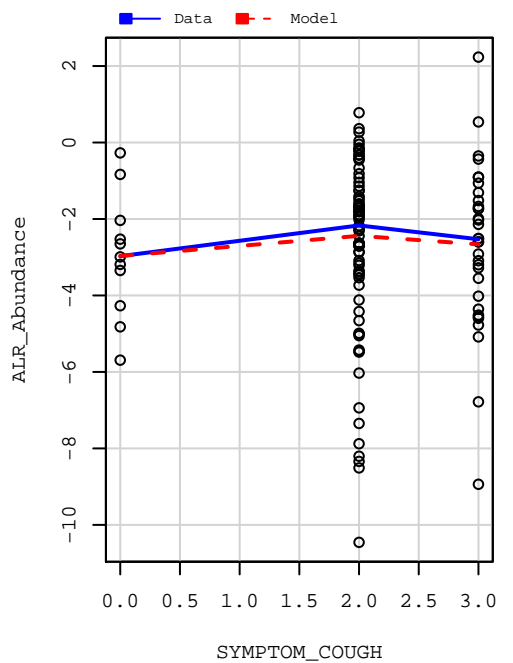
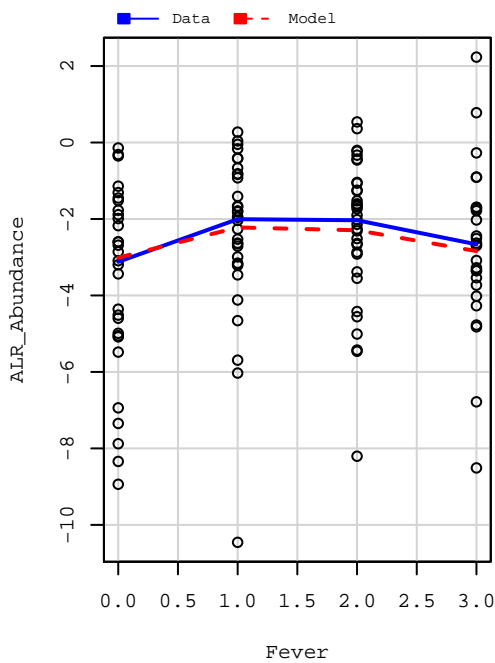
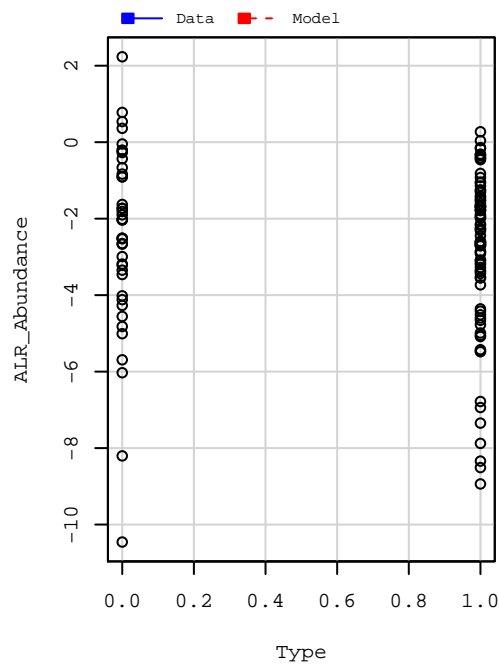
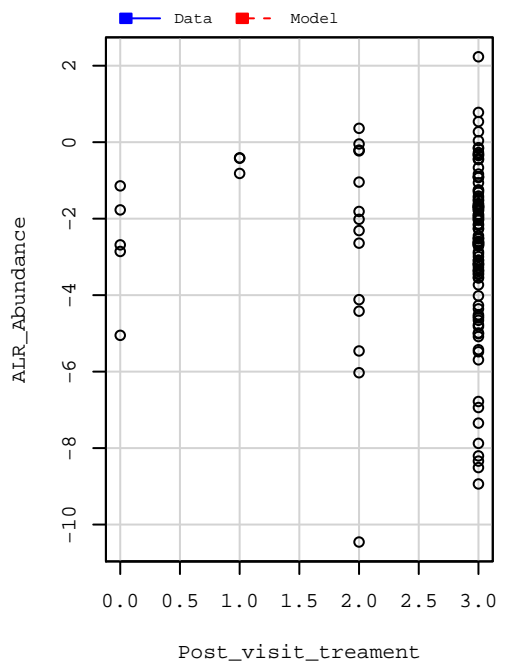
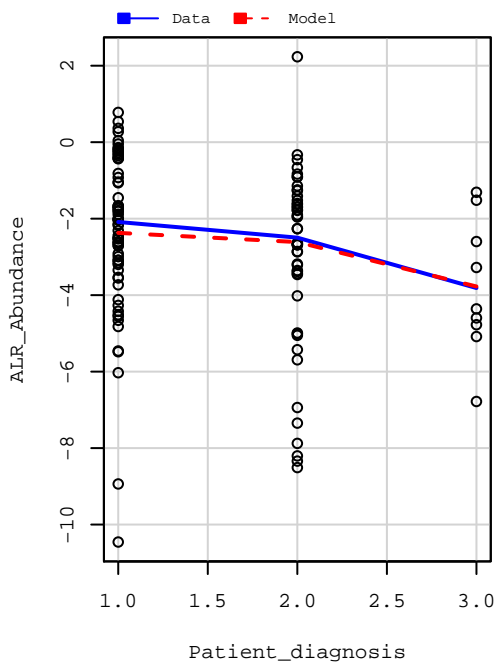
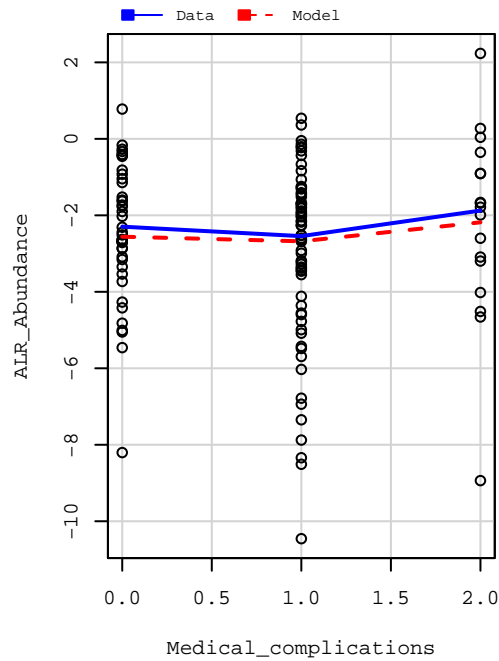
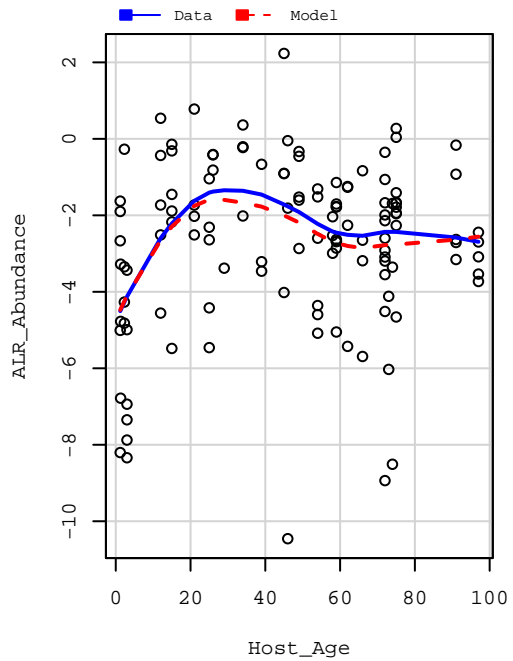
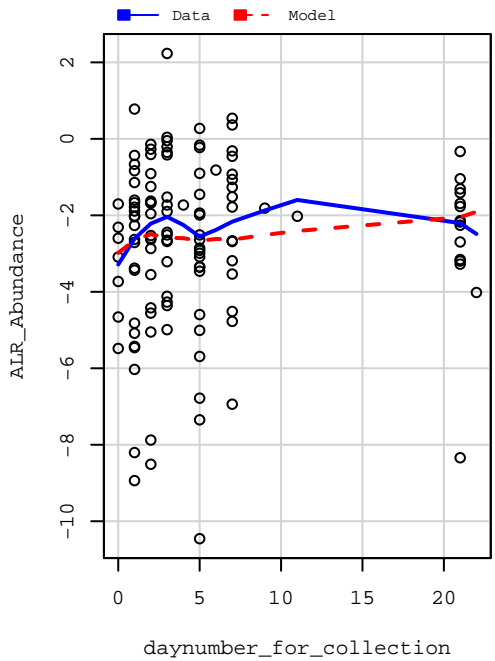
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	156.60	7.830	2.1043	0.009074	**
daynumber_for_collection	1	4.34	4.344	1.1676	0.282699	
Host_Age	1	3.02	3.016	0.8106	0.370275	
Host_Gender	1	8.23	8.232	2.2124	0.140288	
Medical_complications	1	0.03	0.028	0.0074	0.931515	
Patient_diagnosis	1	5.20	5.202	1.3979	0.240088	
Post_visit_treatment	1	0.31	0.312	0.0839	0.772734	
Type	1	16.77	16.765	4.5057	0.036439	*
Vacc_status	1	36.05	36.048	9.6879	0.002464	**
Fever	1	7.73	7.726	2.0762	0.152967	
SYMPTOM_COUGH	1	7.10	7.102	1.9086	0.170428	
Residuals	93	346.05	3.721			

---

Signif. codes: 0 '\*\*\*\*' 0.001 '\*\*\*' 0.01 '\*\*' 0.05 '.' 0.1 ' ' 1

10.) Dyella [1.9%]





# Univariate Regression:

11.) Stenotrophomonas

Mean abundance: 1.9%

R^2: 0.5818

Adjusted R^2: 0.4468

## Analysis of Variance Table

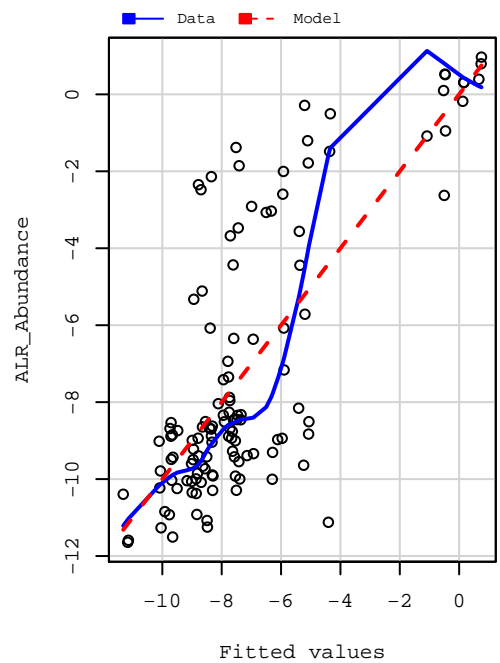
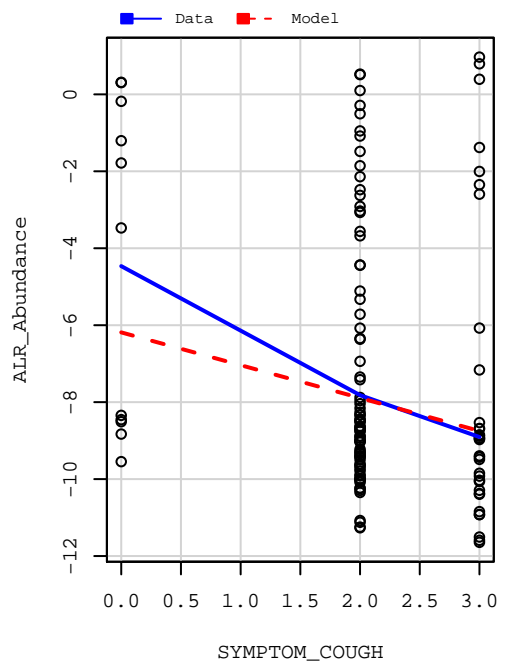
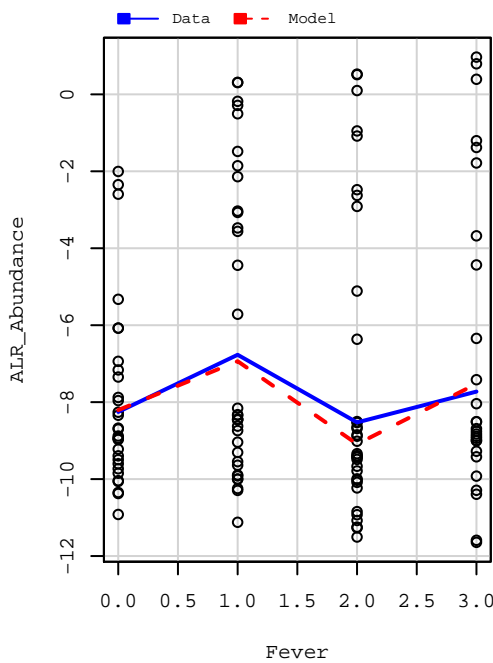
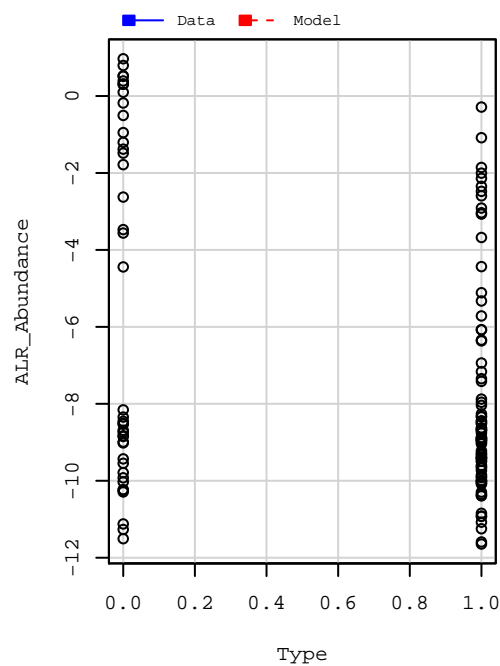
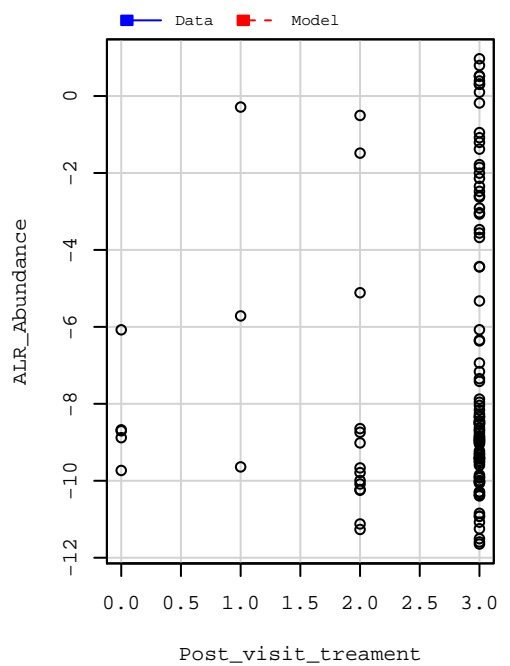
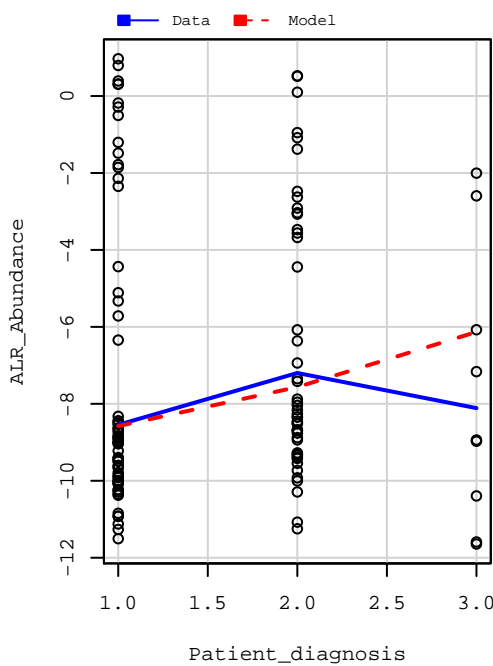
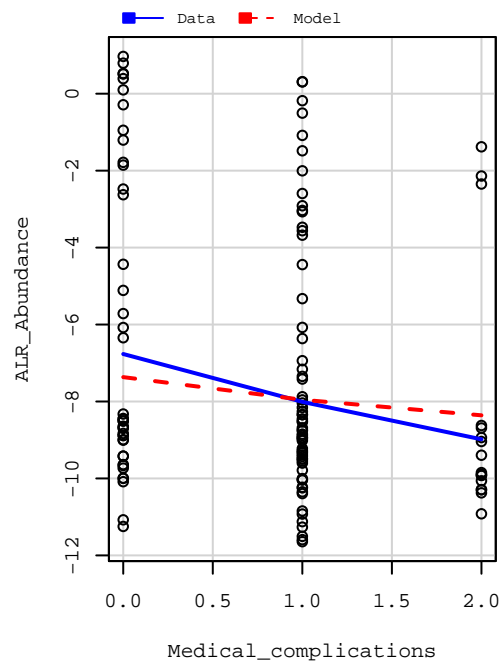
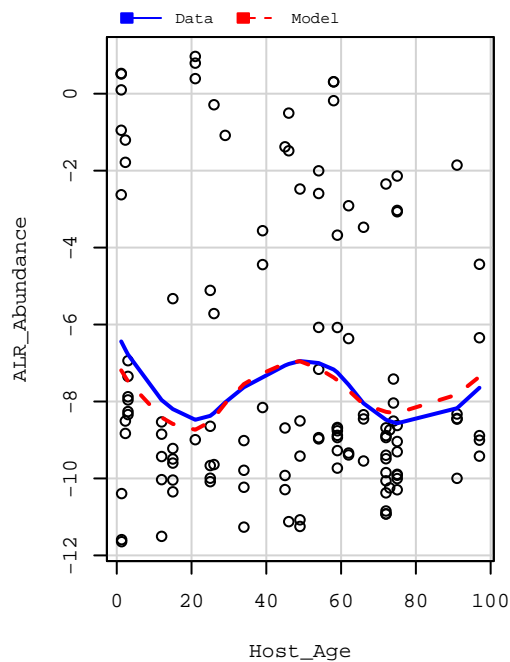
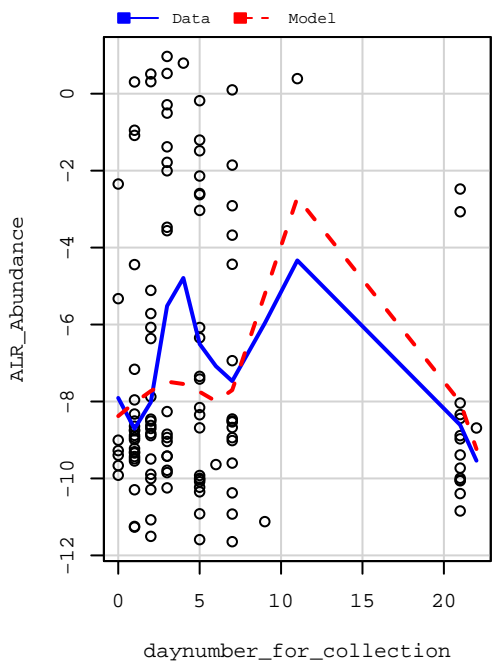
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	586.60	29.330	4.0917	1.691e-06	***
daynumber_for_collection	1	0.68	0.683	0.0953	0.7582357	
Host_Age	1	80.65	80.652	11.2515	0.0011526	**
Host_Gender	1	9.40	9.399	1.3113	0.2551052	
Medical_complications	1	12.86	12.862	1.7943	0.1836715	
Patient_diagnosis	1	3.84	3.837	0.5353	0.4662450	
Post_visit_treatment	1	94.02	94.016	13.1158	0.0004767	***
Type	1	35.70	35.705	4.9810	0.0280290	*
Vacc_status	1	11.30	11.299	1.5763	0.2124344	
Fever	1	21.02	21.024	2.9330	0.0901195	.
SYMPTOM_COUGH	1	71.20	71.197	9.9324	0.0021855	**
Residuals	93	666.64	7.168			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 11.) Stenotrophomonas [1.9%]



Univariate Regression:

12.) order:Rhizobiales

Mean abundance: 1.8%

R<sup>2</sup>: 0.5493

Adjusted R<sup>2</sup>: 0.4039

Analysis of Variance Table

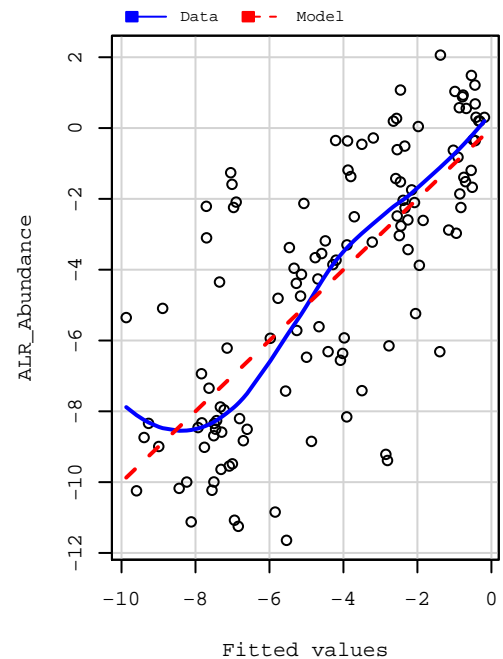
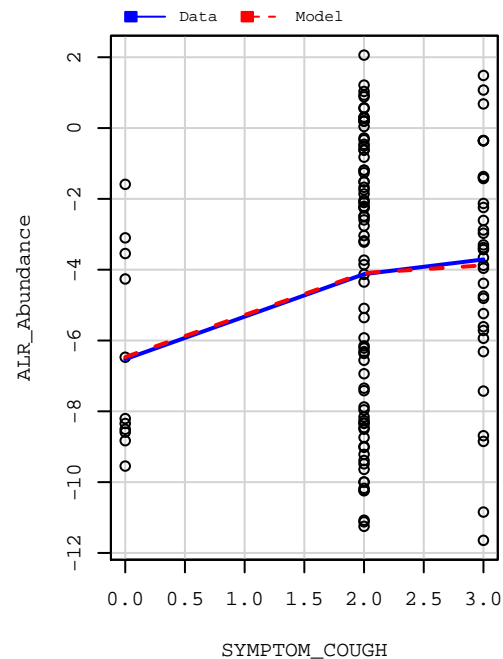
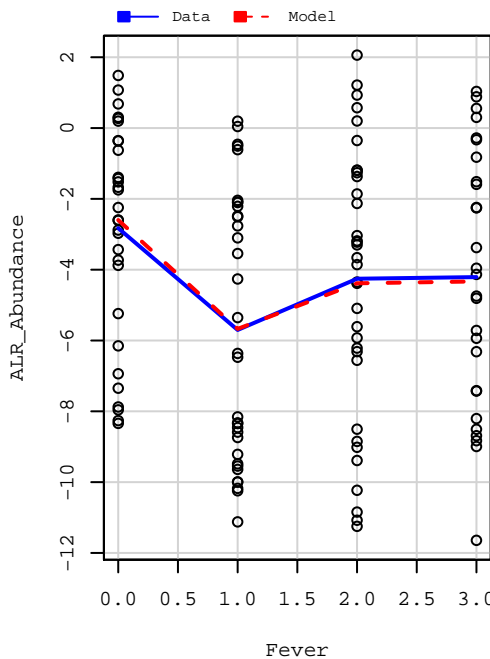
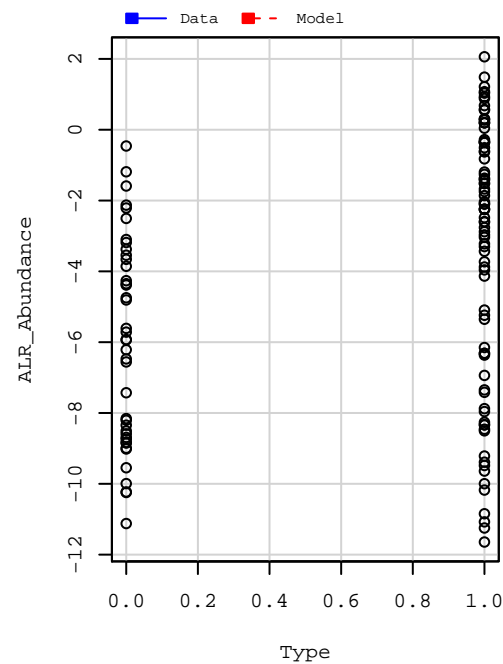
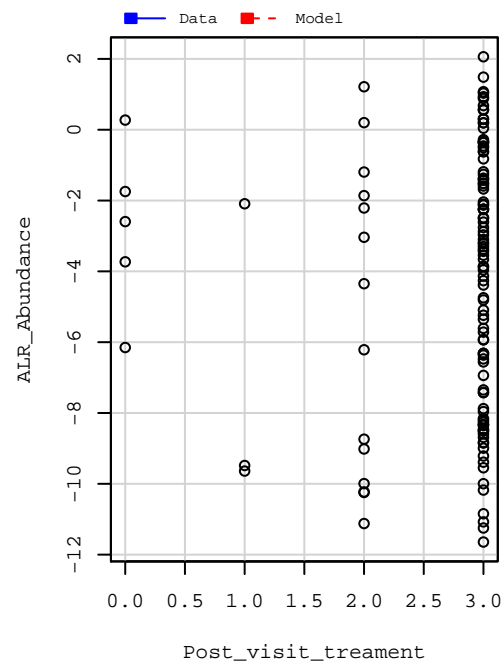
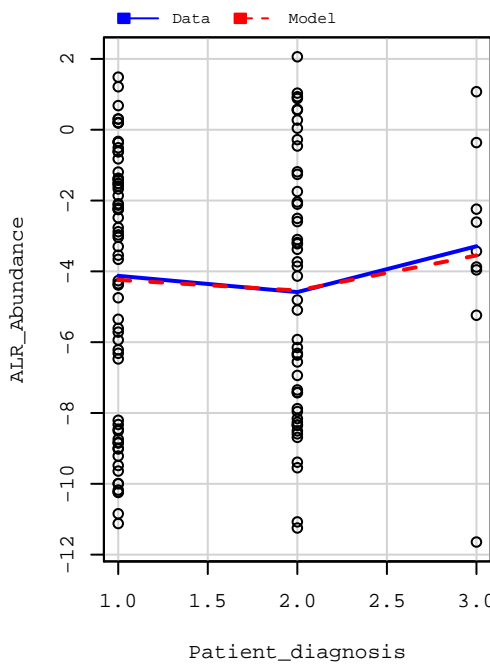
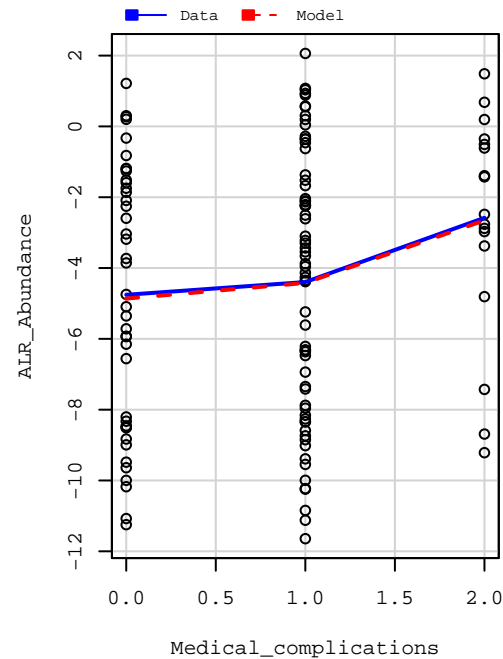
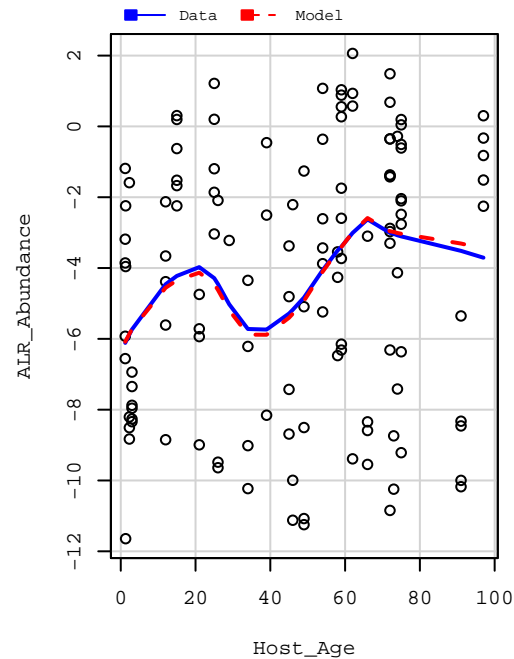
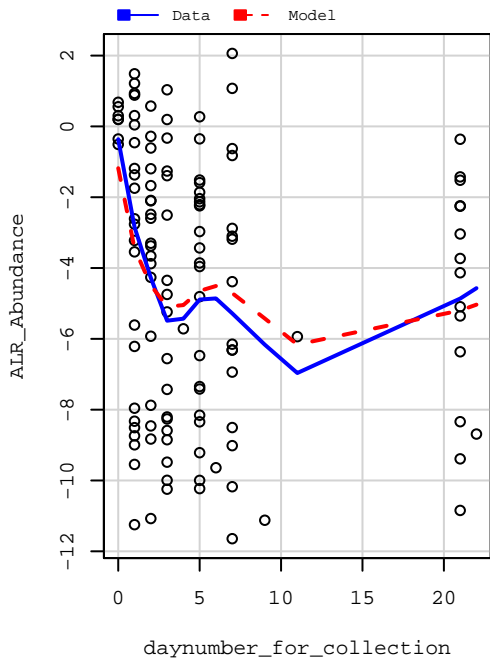
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	508.68	25.434	3.1378	0.0001023	***
daynumber_for_collection	1	24.13	24.134	2.9774	0.0877581	.
Host_Age	1	152.82	152.817	18.8529	3.592e-05	***
Host_Gender	1	13.95	13.947	1.7206	0.1928387	
Medical_complications	1	0.91	0.913	0.1126	0.7379233	
Patient_diagnosis	1	32.42	32.417	3.9992	0.0484391	*
Post_visit_treatment	1	2.90	2.900	0.3578	0.5511824	
Type	1	168.05	168.049	20.7321	1.598e-05	***
Vacc_status	1	0.10	0.098	0.0120	0.9128788	
Fever	1	2.54	2.540	0.3133	0.5769924	
SYMPTOM_COUGH	1	12.17	12.172	1.5017	0.2235029	
Residuals	93	753.84	8.106			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 12.) order:Rhizobiales [1.8%]



# Univariate Regression:

13.) Dolosigranulum

Mean abundance: 1.5%

R^2: 0.6283

Adjusted R^2: 0.5084

## Analysis of Variance Table

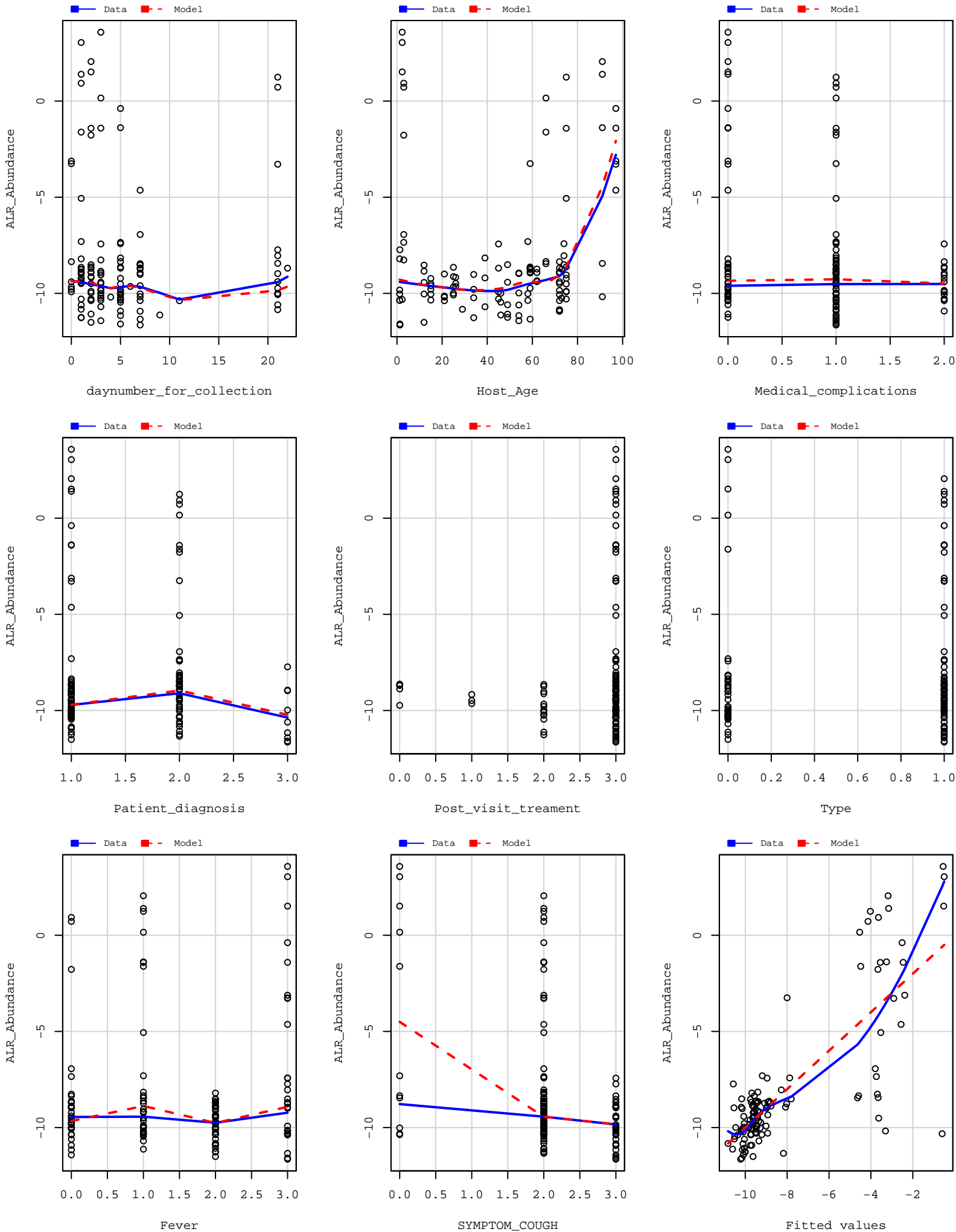
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	955.03	47.752	7.6550	2.434e-12	***
daynumber_for_collection	1	3.41	3.414	0.5473	0.4613	
Host_Age	1	1.13	1.135	0.1819	0.6707	
Host_Gender	1	0.30	0.302	0.0484	0.8264	
Medical_complications	1	4.43	4.428	0.7099	0.4017	
Patient_diagnosis	1	0.00	0.003	0.0005	0.9821	
Post_visit_treatment	1	2.60	2.597	0.4163	0.5204	
Type	1	0.22	0.224	0.0359	0.8501	
Vacc_status	1	12.40	12.399	1.9876	0.1619	
Fever	1	0.14	0.139	0.0224	0.8815	
SYMPTOM_COUGH	1	0.94	0.936	0.1501	0.6993	
Residuals	93	580.13	6.238			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 13.) Dolosigranulum [1.5%]



# Univariate Regression:

14.) Achromobacter

Mean abundance: 1.4%

R^2: 0.5318

Adjusted R^2: 0.3808

## Analysis of Variance Table

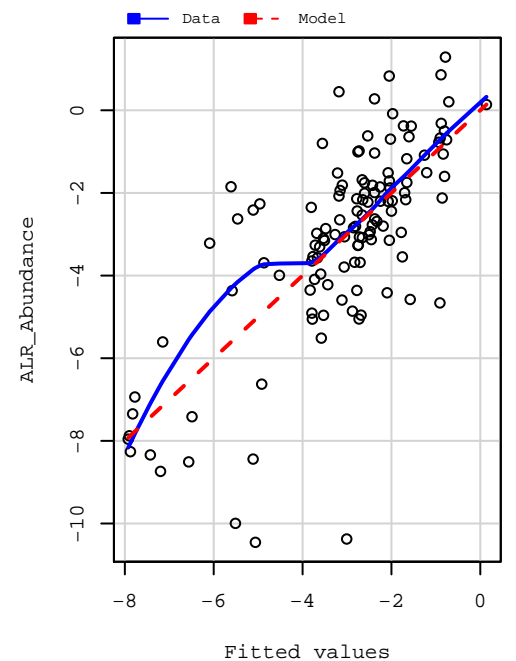
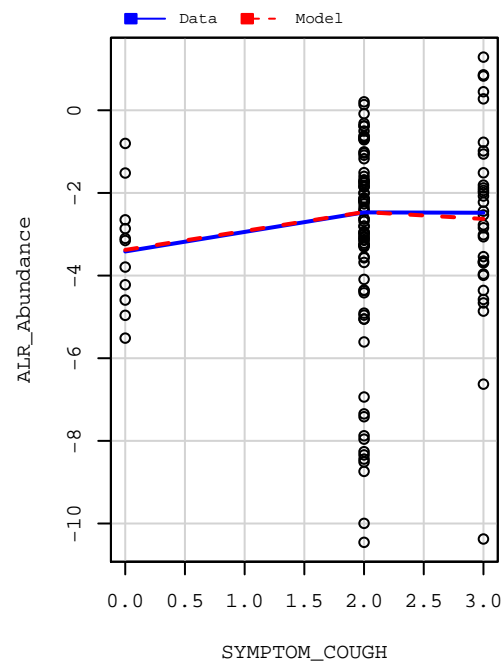
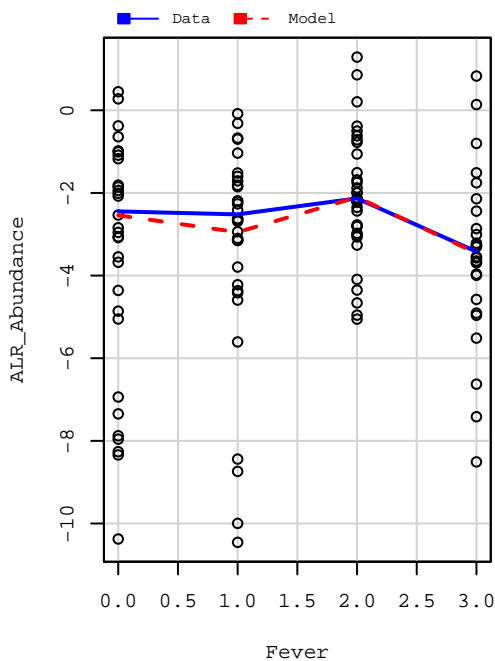
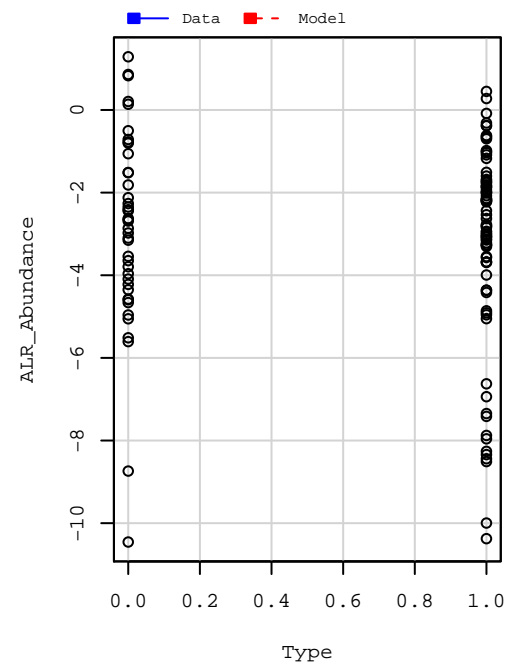
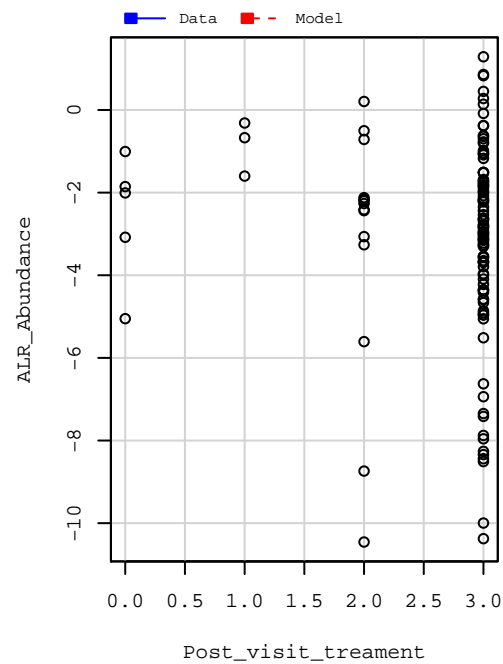
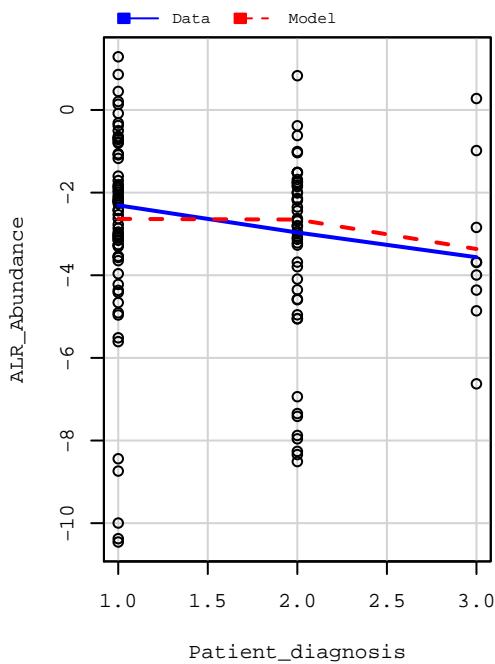
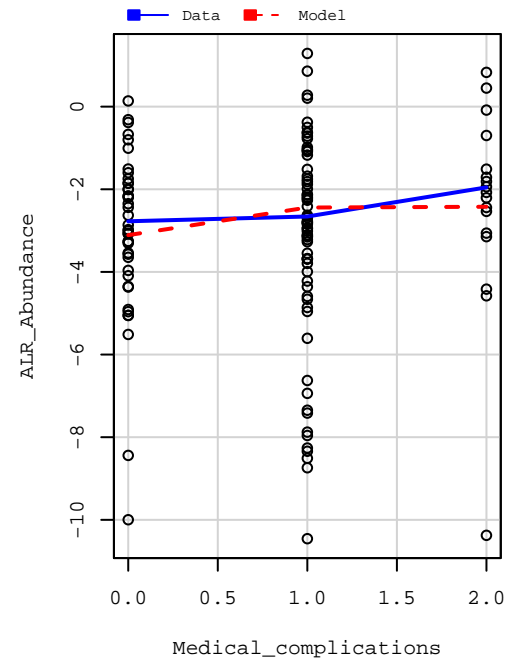
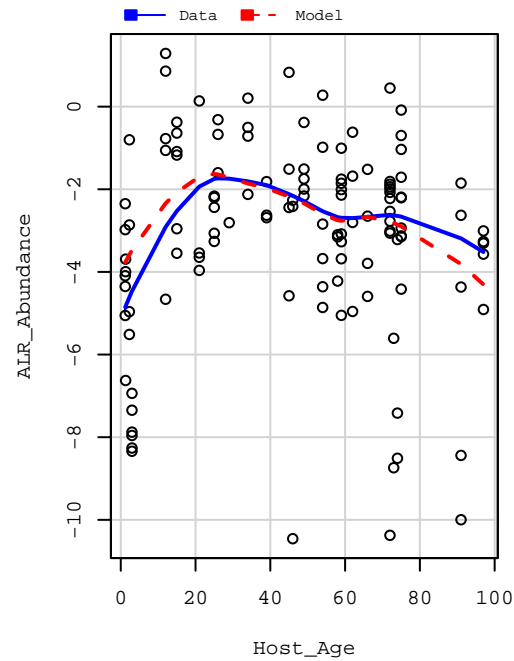
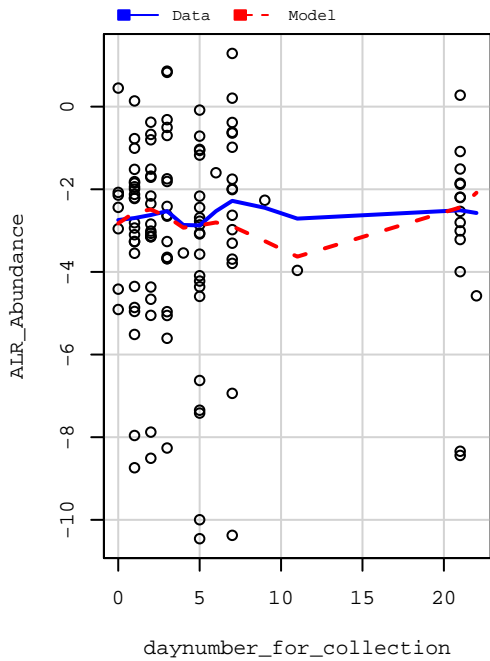
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	311.86	15.5929	4.4049	4.572e-07	***
daynumber_for_collection	1	0.68	0.6833	0.1930	0.661425	
Host_Age	1	3.27	3.2739	0.9249	0.338695	
Host_Gender	1	11.80	11.8022	3.3341	0.071067	.
Medical_complications	1	0.66	0.6643	0.1877	0.665862	
Patient_diagnosis	1	3.49	3.4934	0.9869	0.323088	
Post_visit_treatment	1	0.42	0.4196	0.1185	0.731410	
Type	1	0.15	0.1482	0.0419	0.838346	
Vacc_status	1	28.85	28.8534	8.1510	0.005307	**
Fever	1	0.93	0.9256	0.2615	0.610313	
SYMPTOM_COUGH	1	11.82	11.8249	3.3405	0.070800	.
Residuals	93	329.21	3.5399			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 14.) *Achromobacter* [1.4%]





# Univariate Regression:

15.) Propionibacterium

Mean abundance: 0.9%

R^2: 0.4139

Adjusted R^2: 0.2248

## Analysis of Variance Table

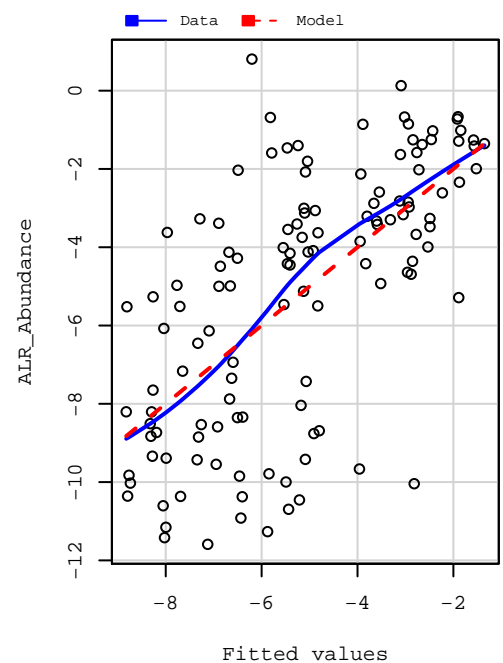
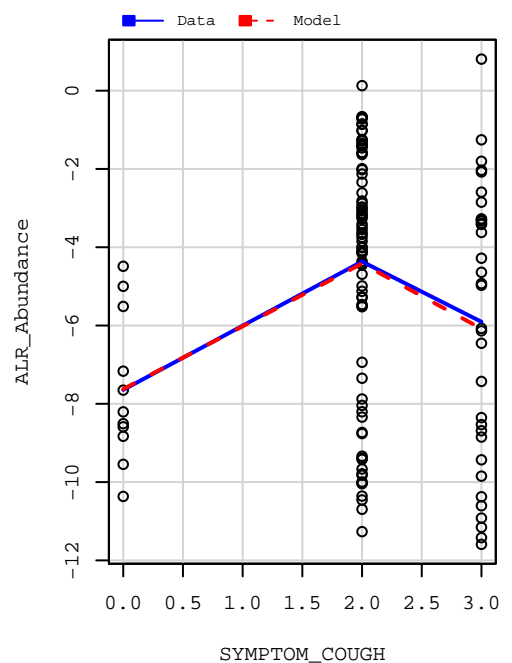
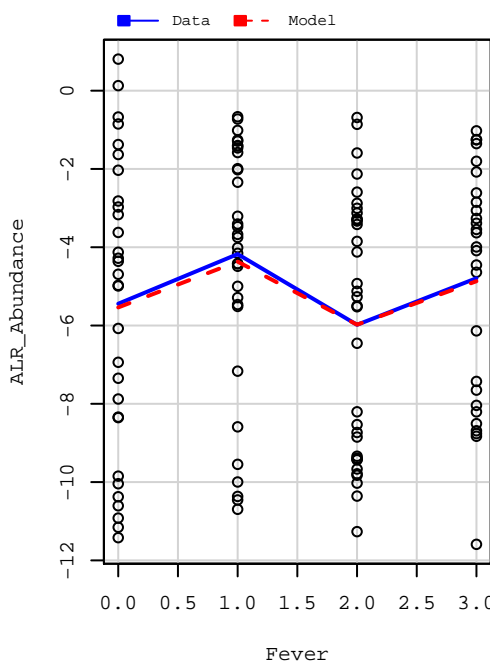
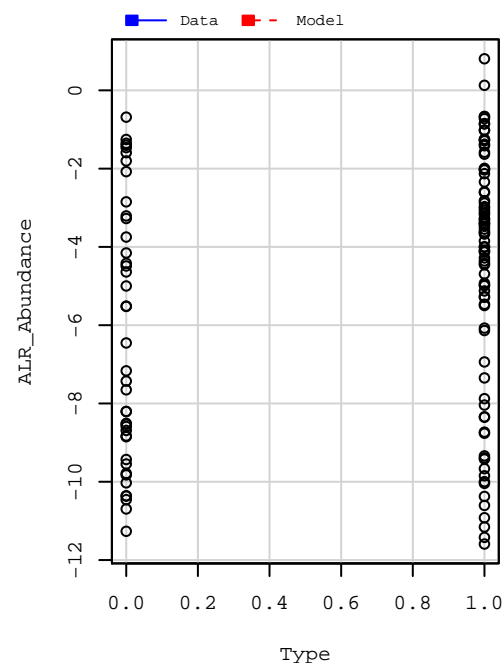
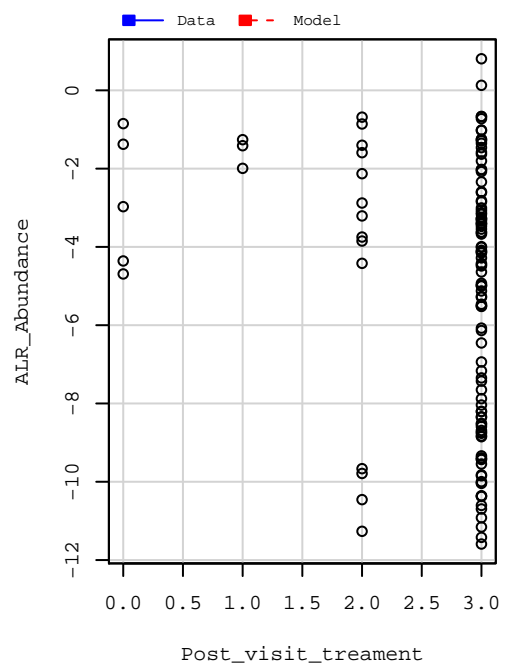
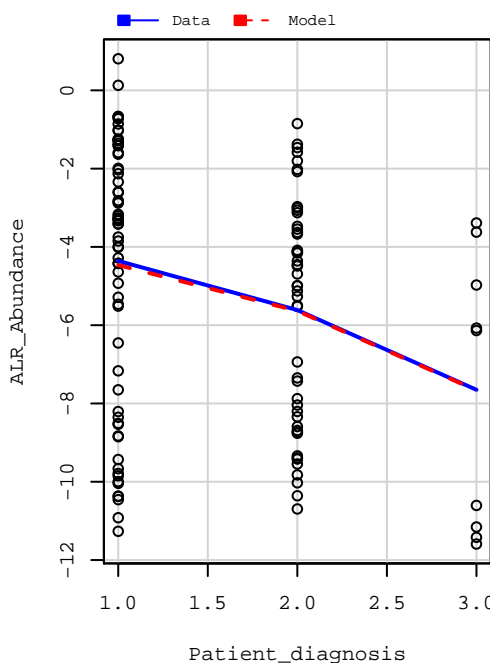
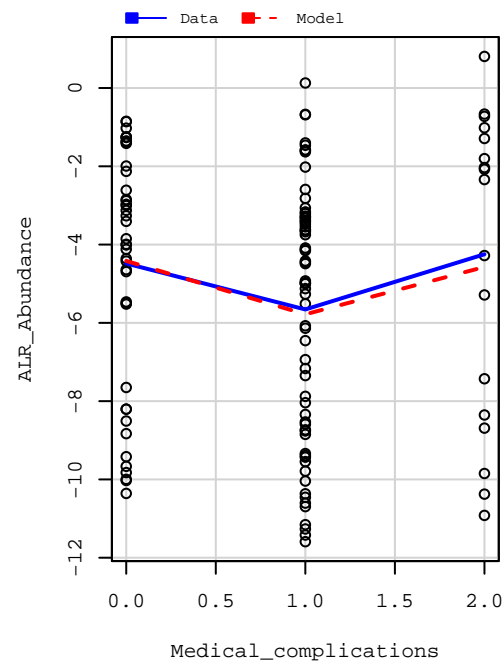
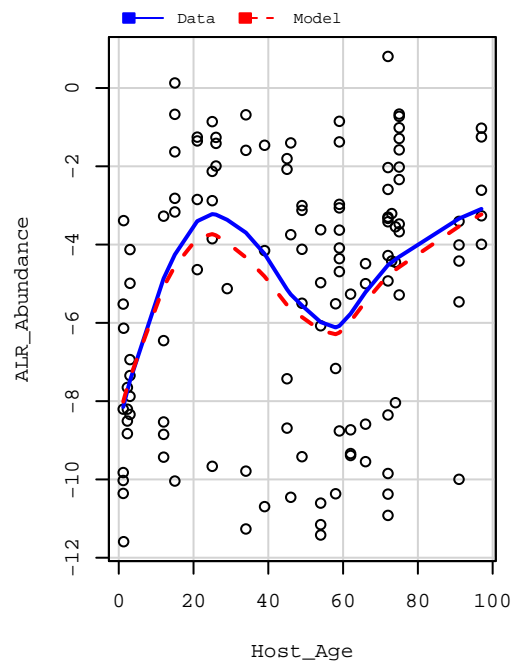
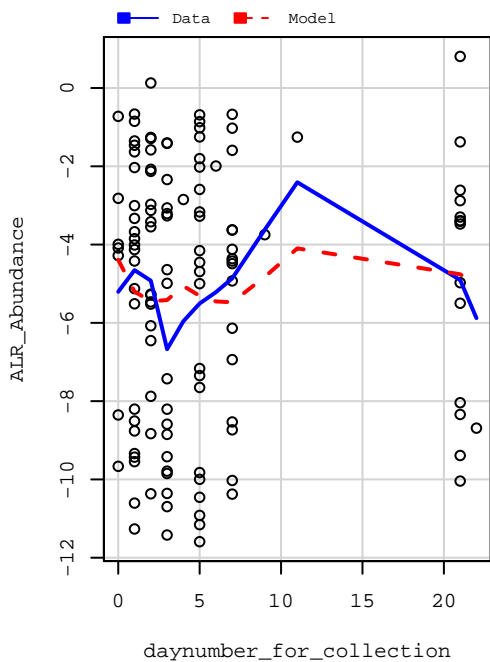
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	356.07	17.804	2.1047	0.009061	**
daynumber_for_collection	1	3.38	3.380	0.3996	0.528838	
Host_Age	1	84.26	84.255	9.9602	0.002156	**
Host_Gender	1	11.88	11.885	1.4049	0.238918	
Medical_complications	1	0.01	0.014	0.0016	0.968178	
Patient_diagnosis	1	0.21	0.210	0.0248	0.875112	
Post_visit_treatment	1	26.69	26.693	3.1555	0.078941	.
Type	1	28.65	28.655	3.3874	0.068884	.
Vacc_status	1	1.81	1.809	0.2138	0.644862	
Fever	1	40.54	40.539	4.7924	0.031089	*
SYMPTOM_COUGH	1	1.99	1.993	0.2356	0.628523	
Residuals	93	786.70	8.459			

---

Signif. codes: 0 '\*\*\*\*' 0.001 '\*\*\*' 0.01 '\*\*' 0.05 '.' 0.1 ' ' 1

# 15.) Propionibacterium [0.9%]



# Univariate Regression:

16.) Rhizobium

Mean abundance: 0.9%

R^2: 0.4558

Adjusted R^2: 0.2802

## Analysis of Variance Table

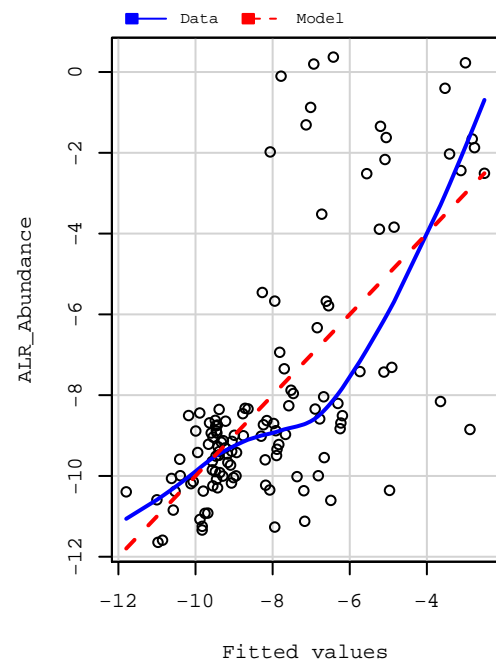
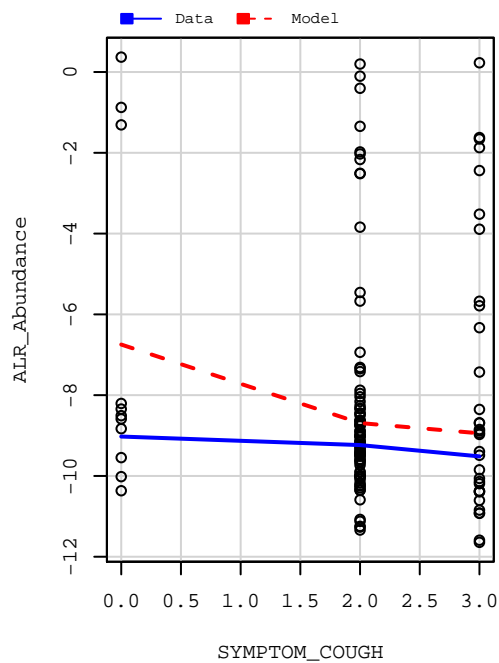
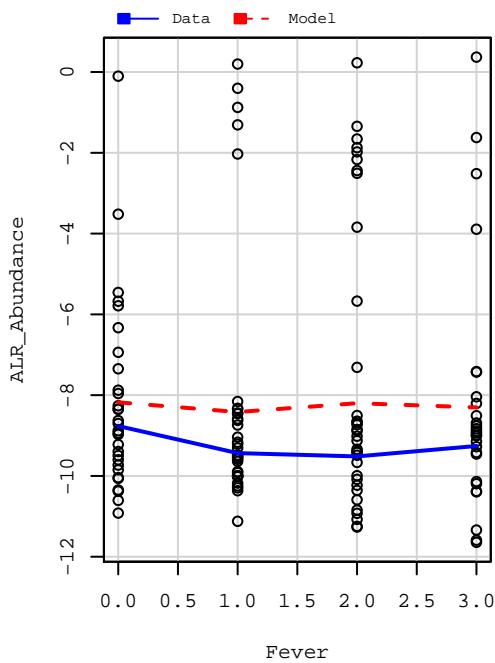
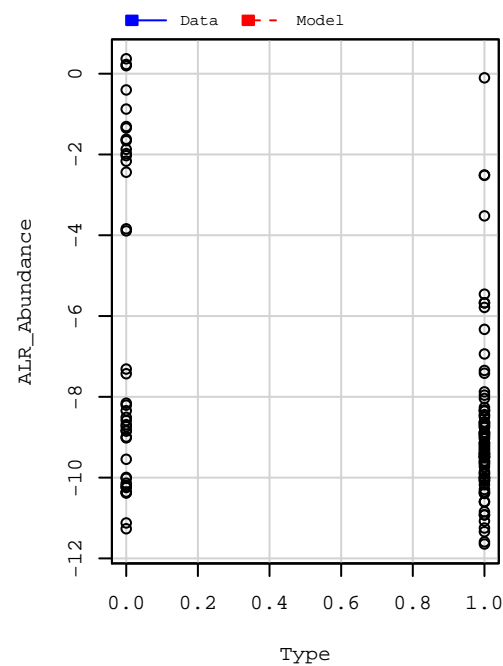
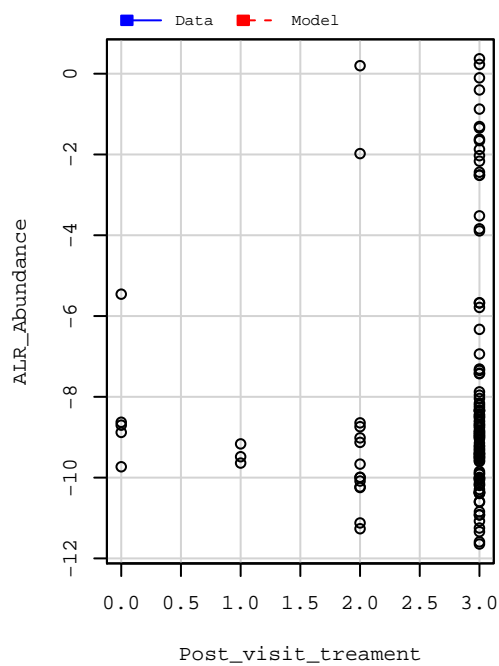
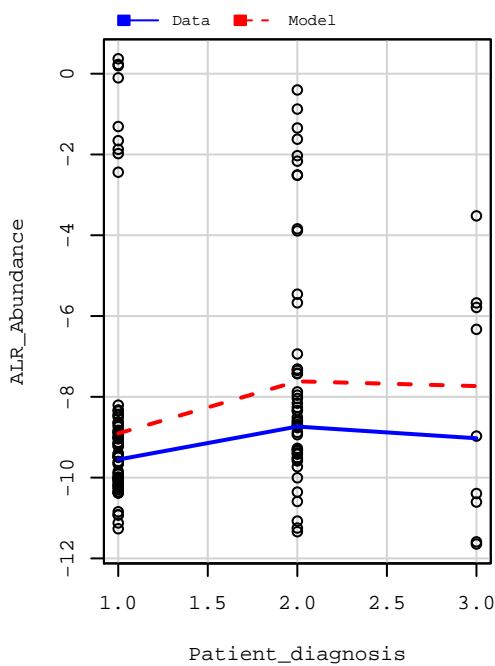
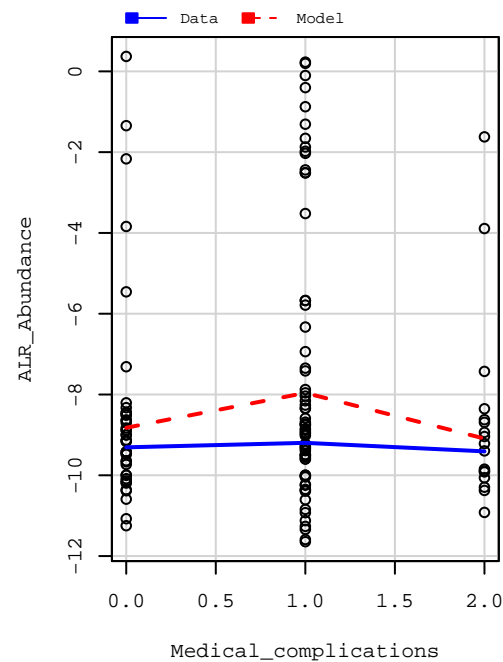
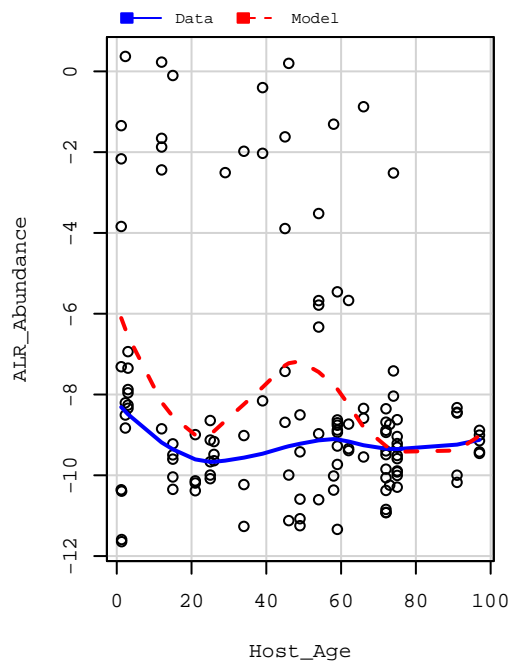
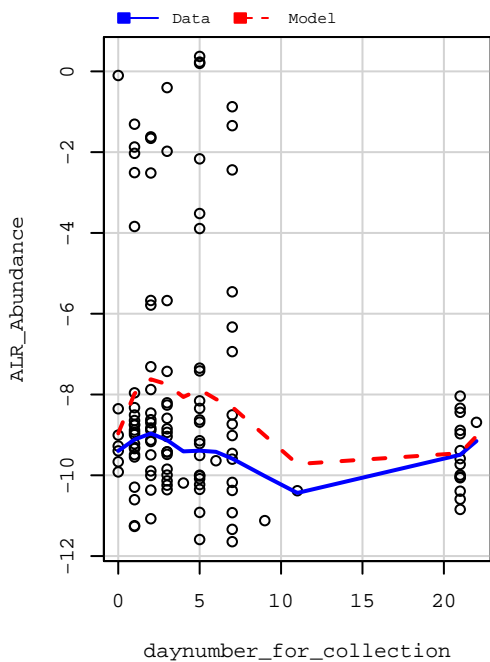
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	266.34	13.317	1.9805	0.015219	*
daynumber_for_collection	1	24.76	24.761	3.6825	0.058054	.
Host_Age	1	57.99	57.990	8.6242	0.004181	**
Host_Gender	1	125.82	125.824	18.7123	3.819e-05	***
Medical_complications	1	2.46	2.464	0.3664	0.546423	
Patient_diagnosis	1	0.09	0.085	0.0127	0.910573	
Post_visit_treatment	1	32.88	32.878	4.8895	0.029471	*
Type	1	6.88	6.877	1.0228	0.314483	
Vacc_status	1	5.67	5.670	0.8432	0.360845	
Fever	1	0.11	0.108	0.0160	0.899580	
SYMPTOM_COUGH	1	0.67	0.675	0.1003	0.752152	
Residuals	93	625.34	6.724			

---

Signif. codes: 0 '\*\*\*\*' 0.001 '\*\*\*' 0.01 '\*\*' 0.05 '.' 0.1 ' ' 1

# 16.) Rhizobium [0.9%]



# Univariate Regression:

17.) Moraxella

Mean abundance: 0.7%

R^2: 0.6514

Adjusted R^2: 0.5390

## Analysis of Variance Table

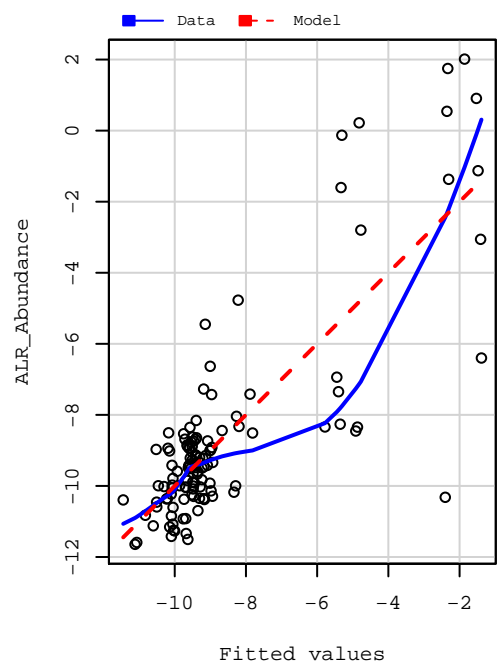
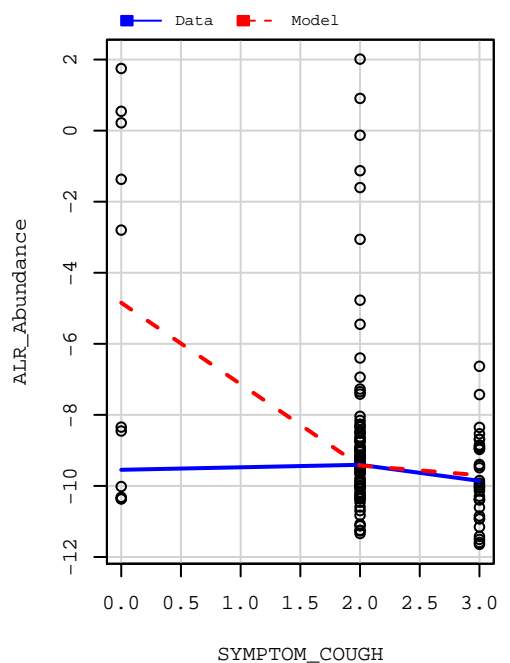
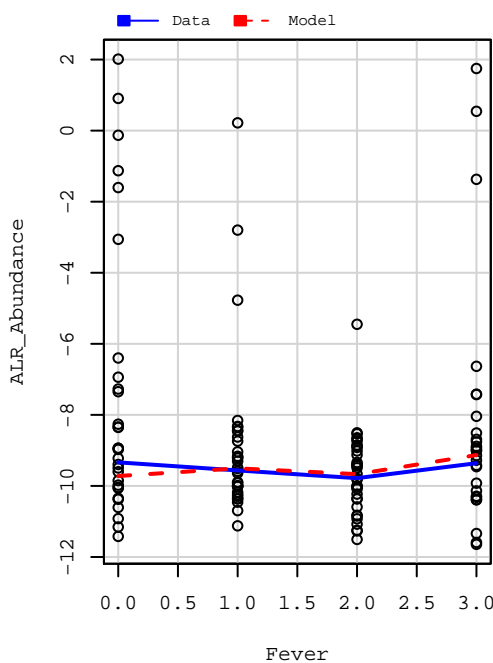
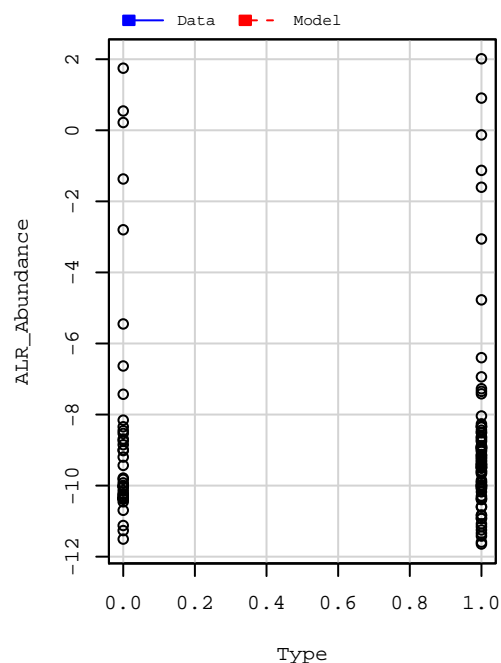
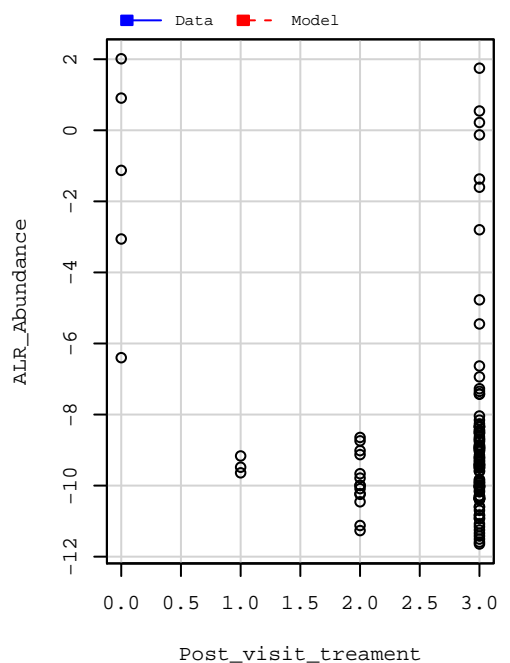
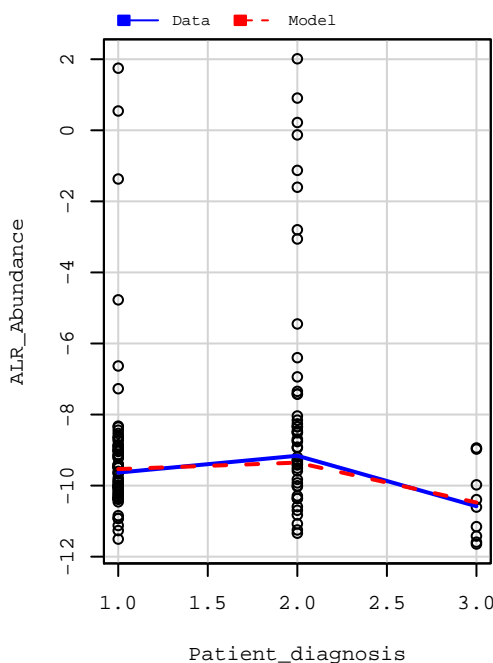
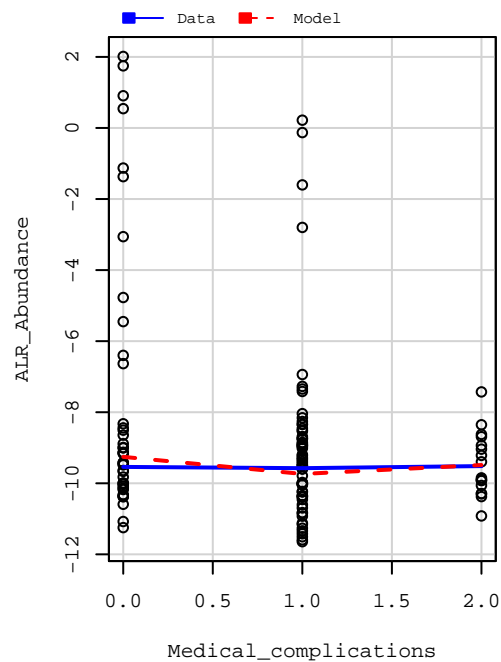
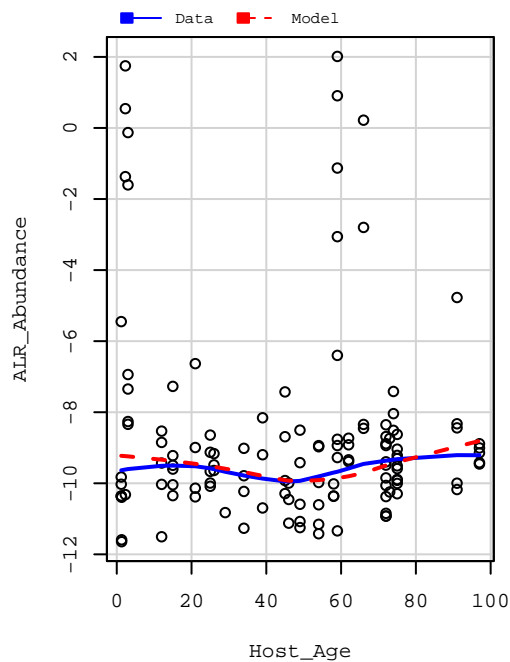
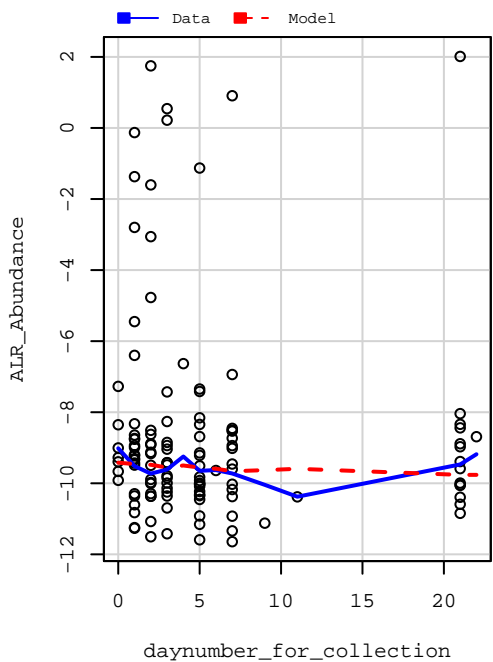
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	543.60	27.180	7.1682	1.277e-11	***
daynumber_for_collection	1	6.34	6.338	1.6716	0.199252	
Host_Age	1	63.75	63.752	16.8135	8.822e-05	***
Host_Gender	1	0.01	0.011	0.0028	0.957618	
Medical_complications	1	6.40	6.403	1.6886	0.197002	
Patient_diagnosis	1	7.97	7.969	2.1018	0.150494	
Post_visit_treatment	1	0.00	0.003	0.0008	0.976839	
Type	1	1.78	1.782	0.4699	0.494743	
Vacc_status	1	28.92	28.922	7.6277	0.006926	**
Fever	1	0.19	0.192	0.0505	0.822672	
SYMPTOM_COUGH	1	0.00	0.003	0.0007	0.978618	
Residuals	93	352.63	3.792			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 17.) Moraxella [0.7%]



# Univariate Regression:

18.) Prevotella

Mean abundance: 0.6%

R^2: 0.5037

Adjusted R^2: 0.3435

## Analysis of Variance Table

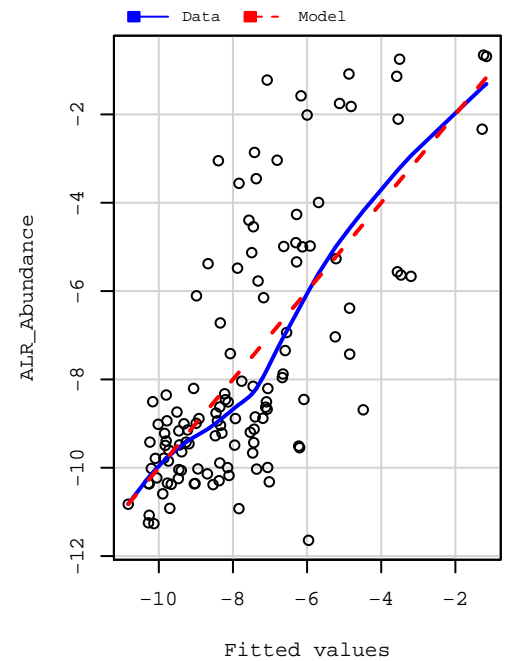
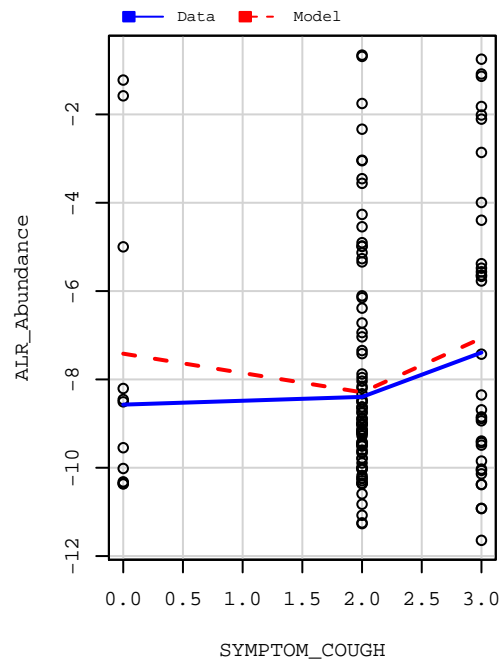
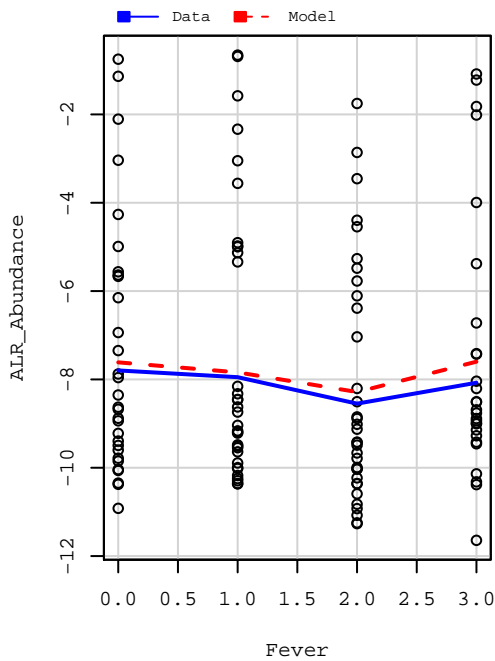
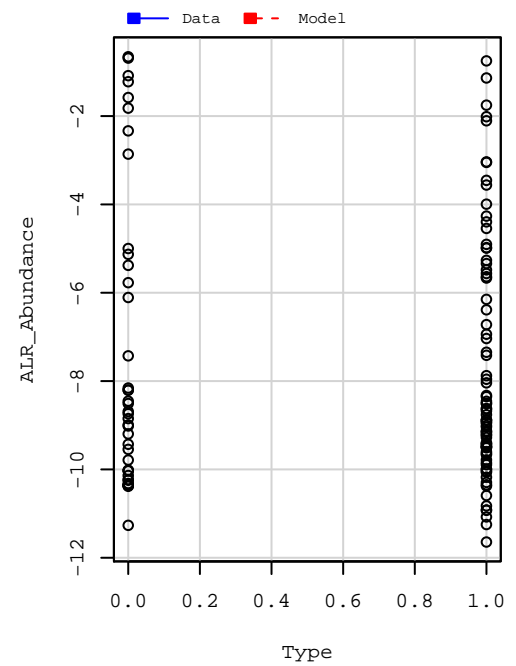
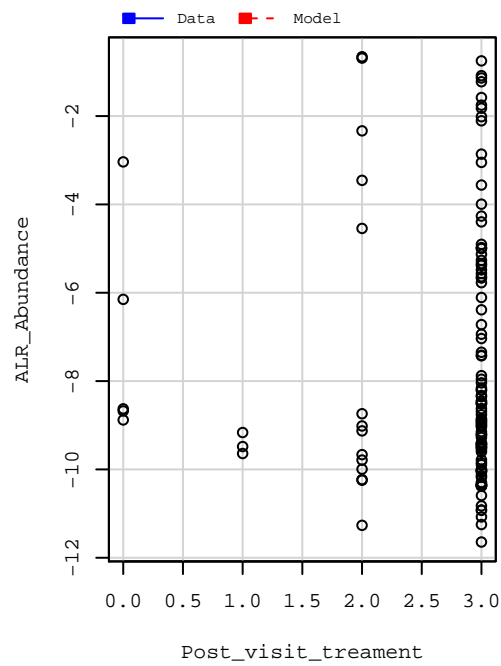
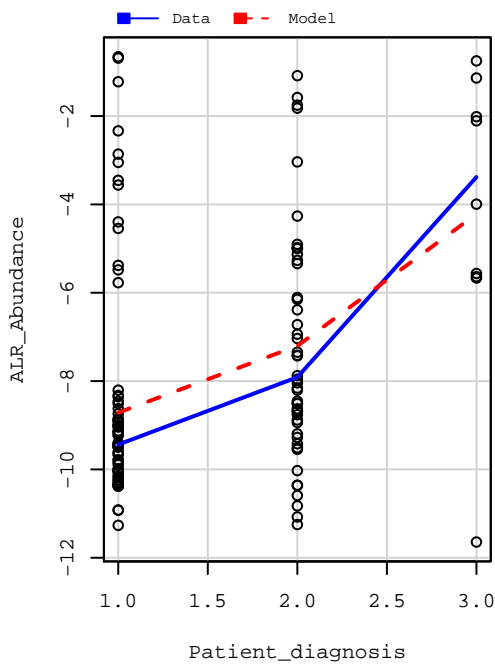
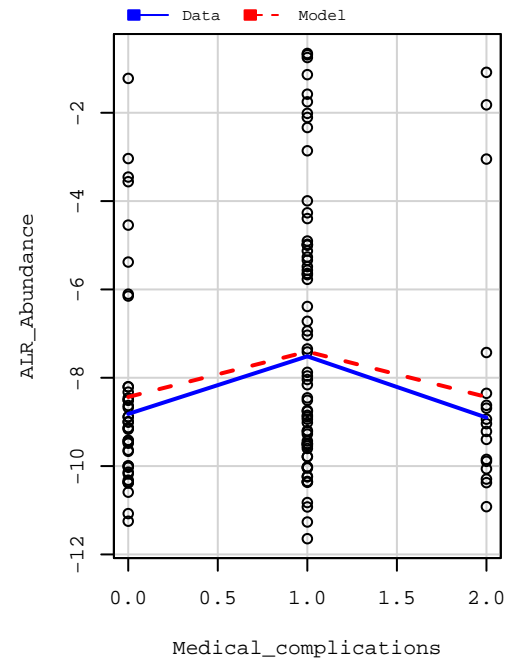
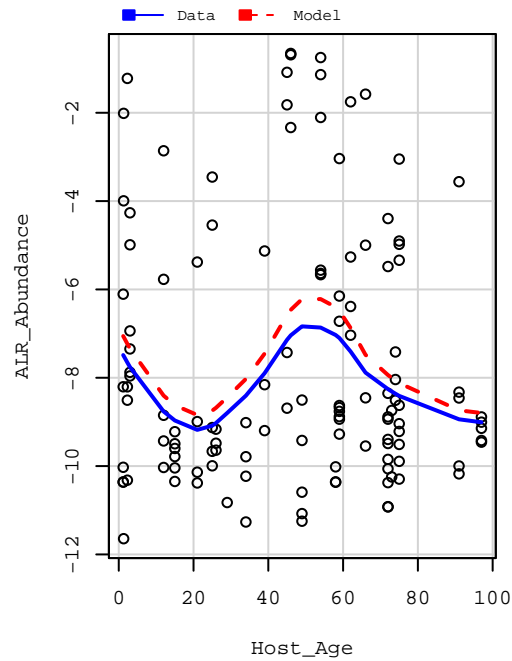
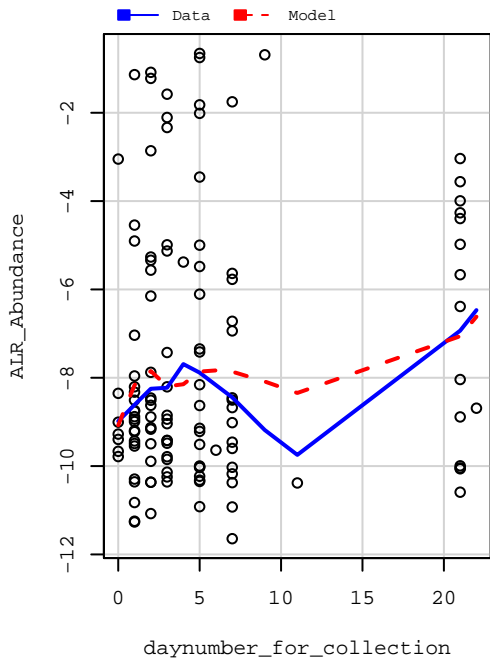
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	366.02	18.301	3.3381	4.274e-05	***
daynumber_for_collection	1	3.34	3.337	0.6086	0.43729	
Host_Age	1	36.39	36.392	6.6379	0.01156	*
Host_Gender	1	19.28	19.276	3.5159	0.06392	.
Medical_complications	1	5.90	5.902	1.0765	0.30217	
Patient_diagnosis	1	12.09	12.095	2.2060	0.14085	
Post_visit_treatment	1	33.88	33.882	6.1800	0.01471	*
Type	1	28.84	28.838	5.2600	0.02407	*
Vacc_status	1	6.72	6.719	1.2256	0.27112	
Fever	1	4.87	4.869	0.8880	0.34846	
SYMPTOM_COUGH	1	0.05	0.052	0.0094	0.92284	
Residuals	93	509.87	5.482			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

18.) Prevotella [0.6%]





# Univariate Regression:

19.) order:Actinomycetales

Mean abundance: 0.6%

R^2: 0.5465

Adjusted R^2: 0.4002

## Analysis of Variance Table

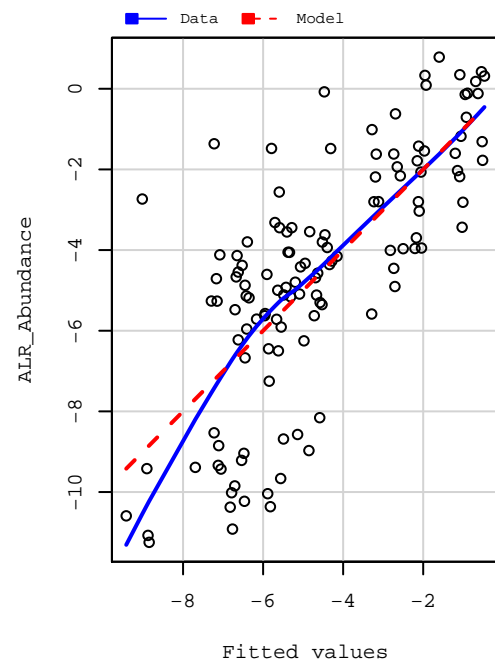
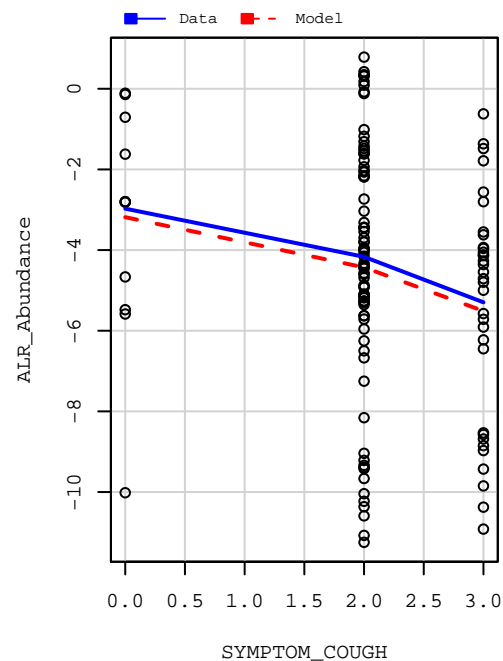
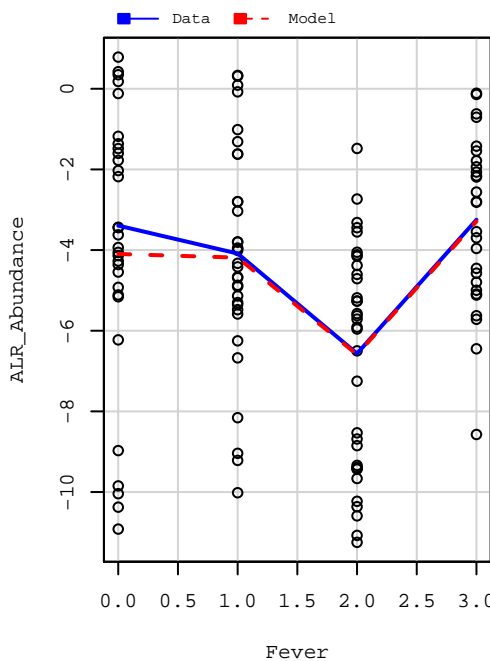
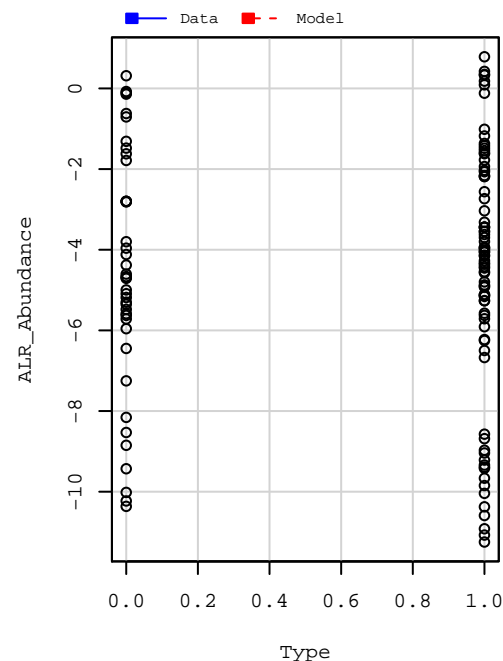
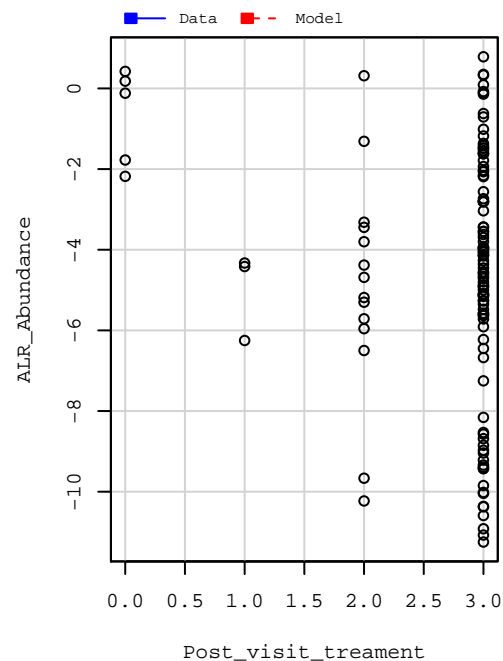
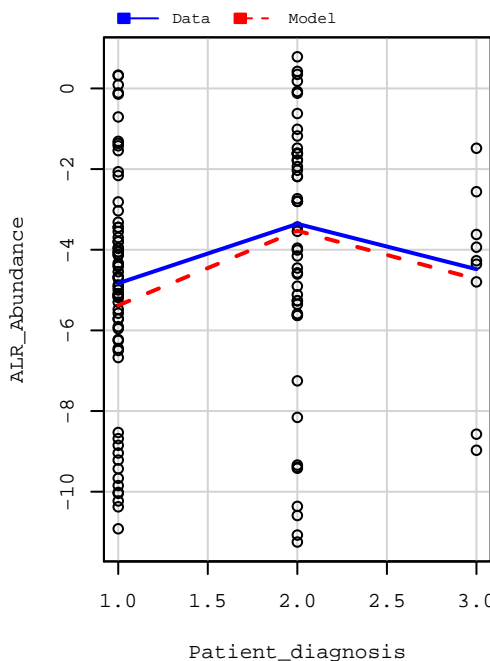
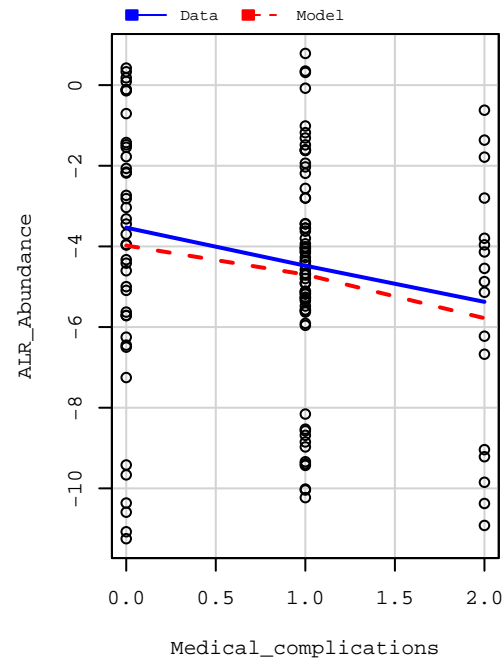
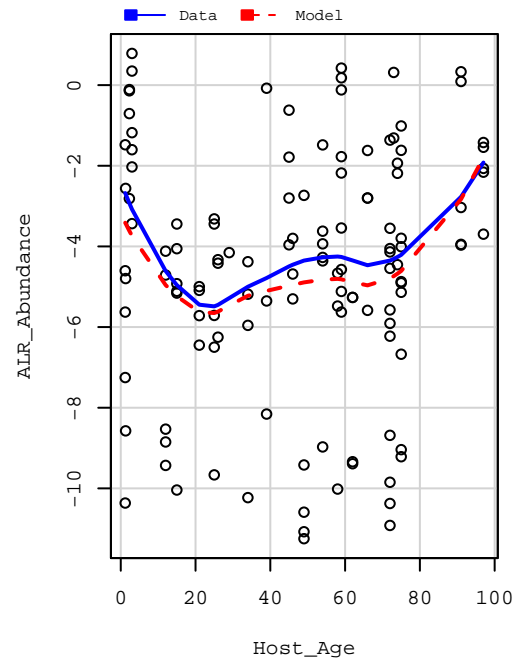
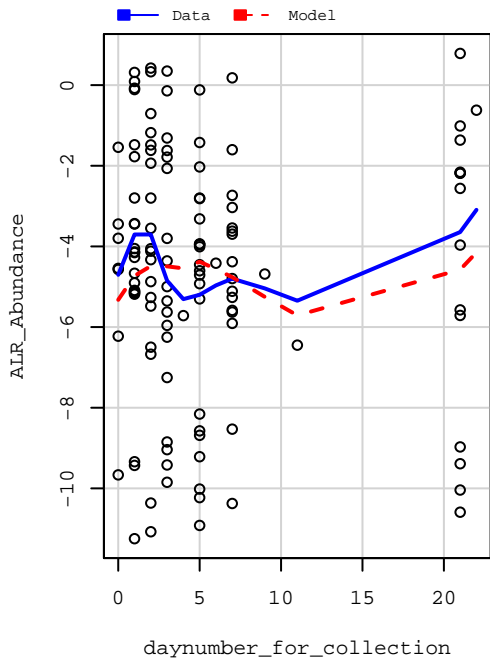
Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	532.29	26.6143	4.8381	7.79e-08	***
daynumber_for_collection	1	1.96	1.9608	0.3564	0.55194	
Host_Age	1	9.13	9.1337	1.6604	0.20075	
Host_Gender	1	2.31	2.3125	0.4204	0.51835	
Medical_complications	1	10.42	10.4183	1.8939	0.17207	
Patient_diagnosis	1	4.05	4.0539	0.7369	0.39285	
Post_visit_treatment	1	14.91	14.9140	2.7111	0.10302	
Type	1	17.81	17.8089	3.2374	0.07522	.
Vacc_status	1	1.67	1.6659	0.3028	0.58343	
Fever	1	21.78	21.7843	3.9601	0.04953	*
SYMPTOM_COUGH	1	0.18	0.1770	0.0322	0.85801	
Residuals	93	511.59	5.5010			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

19.) order:Actinomycetales [0.6%]



# Univariate Regression:

20.) Rhodococcus

Mean abundance: 0.5%

R^2: 0.4955

Adjusted R^2: 0.3328

## Analysis of Variance Table

Response: ALR\_Abundance

	Df	Sum Sq	Mean Sq	F value	Pr(>F)	
Patient	20	488.92	24.4462	3.7728	6.549e-06	***
daynumber_for_collection	1	2.75	2.7477	0.4241	0.51653	
Host_Age	1	21.63	21.6280	3.3378	0.07091	.
Host_Gender	1	23.18	23.1846	3.5781	0.06166	.
Medical_complications	1	0.61	0.6059	0.0935	0.76045	
Patient_diagnosis	1	0.82	0.8161	0.1260	0.72347	
Post_visit_treatment	1	25.37	25.3719	3.9156	0.05080	.
Type	1	0.43	0.4345	0.0671	0.79624	
Vacc_status	1	27.18	27.1844	4.1954	0.04335	*
Fever	1	0.04	0.0358	0.0055	0.94089	
SYMPTOM_COUGH	1	1.04	1.0387	0.1603	0.68980	
Residuals	93	602.61	6.4797			

---

Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

# 20.) Rhodococcus [0.5%]

