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## **APPENDICES**

## **APPENDIX A**

**Raw data and Statistical Tests to determine whether there are any significant differences in HGA performances between current Gimbal bond method and proposed Gimbal bond method.**

Gimbal Bond is one of the critical operation in HGA assembly process. There are five majors that are evaluated and need to have data collection procedures, i.e. Mechanical defect in part of Gimbal Bond criteria, Gimbal Bond shear strength, Roll Static Attitude (RSA)/Pitch Static Attitude (PSA), and Fly Performance.

In term of functional effect evaluation, functional effects include RSA, PSA, Fly performance and shear strength. This evaluation need to be run with more quantity of HGAs to compare the performance of three factors such as RSA/PSA, Fly test, and Shear test between current method and proposed method as the instructions below.

2.1) Build 250 pair of HGAs (250 up tab HGAs and 250 down tab HGAs) with current method through HGA assembly process. This group is celled “Control Group”.

2.2) Build more 250 HGAs (250 up tab HGAs and 250 down tab HGAs) with new method for Gimbal bond operation and build them through other operations with current method. This group is called “ Eval Group”.

2.3) Separately record RSA/PSA data of both groups.

2.4) 100% Fly test of both groups and separately record fly test data.

2.5) Randomly select 70 HGAs of each group for Gimbal shear test. Because Gimbal bond shear test is destructive test, therefore, this test is performed on only 70 HGAs per group.

Data of evaluation are analyzed by statistical tests as followings;

Current method for UP tab

NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA
1	-0.19	51	-0.26	101	0	151	-0.91	201	-0.5
2	-0.31	52	-0.02	102	-0.98	152	0.68	202	-0.07
3	-0.36	53	-0.21	103	-0.07	153	-0.33	203	0.34
4	-0.71	54	-0.38	104	-0.83	154	0.99	204	-0.25
5	0.8	55	-0.35	105	-0.26	155	-0.58	205	0.21
6	-0.45	56	0.68	106	0.46	156	-0.07	206	-0.2
7	0.15	57	0.49	107	-0.31	157	-0.4	207	0.75
8	-0.19	58	-0.5	108	0.29	158	0.12	208	0.32
9	-0.07	59	-0.77	109	-0.1	159	0.21	209	-0.33
10	-0.95	60	-0.25	110	-0.3	160	0.41	210	0.18
11	0.19	61	0.41	111	-0.36	161	-0.24	211	-0.28
12	0.2	62	0.16	112	-0.46	162	0.02	212	-0.19
13	1.1	63	-0.5	113	0.16	163	-0.3	213	0.05
14	-0.02	64	-0.1	114	0.46	164	-0.2	214	-0.26
15	-0.79	65	0	115	-0.31	165	-0.02	215	-0.18
16	0.49	66	0.11	116	-0.36	166	0.2	216	-0.21
17	0.03	67	0.61	117	0.44	167	0.24	217	-0.09
18	-0.1	68	-0.02	118	-0.48	168	-0.76	218	-0.17
19	-0.48	69	-0.84	119	-0.02	169	-1.01	219	0.25
20	0.2	70	-0.43	120	-0.07	170	-0.07	220	-0.24
21	0.41	71	-0.03	121	0.29	171	-0.7	221	-0.15
22	-0.15	72	-0.38	122	-0.26	172	-0.59	222	0
23	-0.05	73	-0.02	123	0.24	173	-0.29	223	-0.33
24	-0.33	74	0.52	124	-0.48	174	0.07	224	-0.53
25	-0.15	75	-0.62	125	0.3	175	-0.2	225	-0.5
26	0.24	76	0.03	126	0.2	176	-0.2	226	0.56
27	0.17	77	-0.33	127	-0.38	177	-0.26	227	0.49
28	-0.04	78	-0.02	128	0.27	178	-0.76	228	0.26
29	-0.14	79	0.29	129	0.82	179	-0.97	229	0.1
30	-0.01	80	-0.02	130	0.32	180	-0.98	230	-0.19
31	0.18	81	0.29	131	-0.46	181	-0.14	231	0.22
32	-0.02	82	-0.17	132	0.27	182	0.34	232	0
33	0	83	0.7	133	0.03	183	-0.41	233	0.01
34	-0.38	84	0.46	134	-0.38	184	0.21	234	0.22
35	-0.04	85	0.55	135	-0.38	185	-0.76	235	-0.77
36	-0.31	86	0.2	136	0.49	186	0.54	236	-0.12
37	-0.41	87	-0.47	137	0.12	187	-0.38	237	0.87
38	-0.18	88	-0.4	138	-0.66	188	0.23	238	0.02
39	0.16	89	0.28	139	-0.47	189	-0.19	239	-0.31
40	-0.41	90	-0.05	140	-0.65	190	0.21	240	-0.48
41	-0.07	91	0.23	141	0.08	191	-0.12	241	-0.33
42	0.12	92	-0.1	142	-0.71	192	-0.57	242	-0.05
43	0.26	93	-0.21	143	0.07	193	-0.12	243	0.26
44	-0.1	94	0	144	-0.43	194	0.27	244	0.7
45	-0.02	95	0.32	145	0.11	195	0.11	245	0.11
46	0.25	96	-0.09	146	-0.12	196	-0.08	246	-0.26
47	0.29	97	0.8	147	0.2	197	-0.48	247	-0.12
48	-0.41	98	-0.28	148	0.28	198	0.16	248	0.2
49	-0.24	99	0.32	149	0.36	199	0.18	249	0.12
50	-0.17	100	0.44	150	-0.35	200	-0.09	250	-0.21

Table A.1 Raw RSA data of Up tab that are produced with Current method.

**Proposed method for IP tab**

NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA
1	0.24	51	0.46	101	0.05	151	-0.12	201	0.1
2	-0.09	52	-0.87	102	-0.33	152	-0.02	202	0.03
3	0.15	53	-0.43	103	-0.12	153	0.05	203	-0.84
4	-0.43	54	-0.2	104	0.21	154	-0.14	204	-0.29
5	-0.19	55	0.41	105	0.05	155	0.44	205	-0.3
6	-0.48	56	-0.15	106	-0.18	156	0.99	206	0.17
7	-0.12	57	-0.1	107	-0.33	157	0.24	207	-0.04
8	0.1	58	-0.45	108	-0.28	158	-0.02	208	-0.92
9	-0.02	59	-0.53	109	-0.02	159	0.05	209	0.03
10	0.34	60	0.39	110	0.39	160	-0.33	210	-0.05
11	0.27	61	-0.41	111	-0.07	161	-0.48	211	0.32
12	0.15	62	1.08	112	0.18	162	0.29	212	-0.69
13	-0.18	63	-0.5	113	-0.23	163	-0.15	213	-0.33
14	0.7	64	0.03	114	-0.21	164	0.44	214	0.18
15	0.46	65	0.39	115	-0.15	165	0.1	215	-0.38
16	-0.48	66	0.7	116	0.41	166	-0.24	216	-0.15
17	0.56	67	0.32	117	-0.36	167	-0.48	217	-0.02
18	-0.77	68	0.64	118	0.16	168	0.27	218	0.22
19	-0.07	69	-0.33	119	-0.12	169	-0.02	219	0.05
20	0.08	70	0.29	120	0.24	170	-0.36	220	-0.33
21	-0.04	71	0.16	121	-0.56	171	-0.43	221	-0.83
22	-0.05	72	0.05	122	-0.07	172	-0.38	222	0.05
23	-0.31	73	0.46	123	-0.2	173	-0.24	223	-0.28
24	-0.58	74	-0.17	124	-0.28	174	-0.18	224	-0.48
25	-0.56	75	0	125	0.49	175	0.08	225	0.96
26	0.22	76	0.31	126	0.05	176	0.21	226	0.39
27	0.08	77	-0.67	127	-0.36	177	-0.5	227	-0.5
28	-0.48	78	0.46	128	-0.2	178	0.16	228	-0.15
29	-0.41	79	-0.29	129	-0.12	179	0.24	229	0.57
30	-0.07	80	0.2	130	0.13	180	-0.28	230	-0.94
31	-0.28	81	0	131	-0.09	181	-0.24	231	-0.85
32	0.05	82	0.15	132	-0.31	182	-0.59	232	-0.45
33	-0.55	83	-0.36	133	0.11	183	0.1	233	0.31
34	0.23	84	0.41	134	-0.09	184	0.11	234	-0.02
35	-0.41	85	-0.43	135	-0.02	185	-0.66	235	0.34
36	-0.29	86	-0.23	136	0.34	186	-0.07	236	-0.04
37	0.21	87	-0.09	137	-0.02	187	-0.33	237	-0.9
38	0.21	88	-0.1	138	0	188	-0.55	238	-0.26
39	-0.41	89	-0.23	139	0.31	189	0.05	239	0
40	-0.82	90	1.02	140	0.08	190	0.05	240	-0.04
41	-0.15	91	0.2	141	-0.12	191	0	241	-0.12
42	-0.24	92	-0.02	142	-0.28	192	-0.54	242	0.1
43	-0.25	93	-0.09	143	0.29	193	-0.37	243	-0.23
44	-0.36	94	0.32	144	-0.04	194	-0.41	244	0.05
45	-0.23	95	-0.24	145	-0.64	195	0.1	245	0.03
46	-0.26	96	-0.43	146	-0.26	196	-0.75	246	-0.48
47	0.23	97	-0.38	147	0.05	197	-0.07	247	-0.45
48	-0.38	98	0.16	148	0.49	198	-0.66	248	0.4
49	-0.02	99	0.03	149	0.65	199	-0.12	249	-0.02
50	-0.59	100	0.08	150	-0.05	200	-0.33	250	0.38

**Table A.2 Raw RSA data of Up tab that are produced with Proposed method.**

In determining whether there is a significant difference in RSA of Up tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for testing RSA of Up tab as followings;

$H_0$  : Assume there is no difference in RSA of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in RSA of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response    RSA\_Up  
 Factors      Method  
 ConfLvl     95.0000

Lower	Sigma	Upper	N	Factor Levels
0.327804	0.360816	0.400913	250	New
0.353101	0.388661	0.431853	250	Old

F-Test (normal distribution)

Test Statistic: 1.160

P-Value      : 0.241

Reviewing P-value that is above 0.05, there is not significant difference in RSA on Up tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference in RSA of Up tab between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for testing RSA of Up tab as followings;

$H_0$  : Assume there is no difference in RSA of Up tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in RSA of Up tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for RSA\_Old\_Up vs RSA\_New\_Up

	N	Mean	StDev	SE Mean
R_Old_Up	250	-0.066	0.389	0.025
R_New_Up	250	-0.078	0.361	0.023

95% CI for  $\mu$  RSA\_Old\_Up -  $\mu$  RSA\_New\_Up: (-0.053, 0.078)

T-Test  $\mu$  RSA\_Old\_Up =  $\mu$  RSA\_New\_Up (vs not =): T = 0.37 P = 0.71

DF = 498

Both use Pooled StDev = 0.375

Reviewing P-value that is above 0.05, there is not significant difference in RSA on Up tab between both populations' means.



Current method for UP tab

NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA
1	1.71	51	0.34	101	1.35	151	1.08	201	1.62
2	1.65	52	0.51	102	0.71	152	1.23	202	-0.05
3	0.54	53	0.47	103	0.59	153	0.79	203	0.51
4	0.86	54	1.18	104	0.65	154	0.74	204	1.25
5	1.53	55	1.38	105	1.15	155	0.39	205	0.58
6	0.32	56	-0.25	106	0.61	156	0.05	206	1.15
7	0.74	57	0.76	107	0.94	157	0.16	207	1.35
8	0.94	58	1.96	108	0.56	158	0.83	208	0.66
9	1.65	59	0.83	109	1.5	159	0.67	209	0.86
10	1.08	60	1.53	110	1.25	160	1.01	210	0.71
11	0.3	61	1.5	111	0.82	161	1.14	211	1.33
12	1.17	62	1.2	112	1.3	162	1.18	212	0.93
13	0.97	63	1.33	113	1.69	163	0.24	213	1.13
14	1.83	64	0.3	114	1.08	164	0.48	214	1.35
15	1.32	65	0.71	115	2.37	165	0.61	215	0.98
16	1.07	66	1.65	116	0.55	166	0.56	216	0.61
17	0.49	67	-0.12	117	0.93	167	1.04	217	0.81
18	1.27	68	1.86	118	0.86	168	0.62	218	1.2
19	0.92	69	0.69	119	1.23	169	0.2	219	1.02
20	0.69	70	0.24	120	0.99	170	1.83	220	0.74
21	1.55	71	1.96	121	2.11	171	1.25	221	0.59
22	1.35	72	1.28	122	0.99	172	0.31	222	1.02
23	1.15	73	1.08	123	0.34	173	0.42	223	0.51
24	1.4	74	1.83	124	2.06	174	0.11	224	1.68
25	1.96	75	1.08	125	0.35	175	1.78	225	1.06
26	1.58	76	1.01	126	0.49	176	0.86	226	1.35
27	1.55	77	1.98	127	1.11	177	1.06	227	1.1
28	1.99	78	1.65	128	0.81	178	-0.08	228	0.89
29	0.92	79	1.15	129	0.76	179	1.93	229	1.07
30	0.07	80	2.06	130	0.81	180	0.64	230	0.69
31	1.3	81	1.57	131	1.91	181	0.23	231	1.22
32	0.91	82	0.88	132	-0.03	182	1.42	232	2.06
33	0.64	83	1.42	133	0.79	183	0.15	233	2.29
34	1.37	84	1.33	134	1.23	184	1.3	234	0.07
35	1.25	85	0.16	135	1.68	185	0.23	235	1.55
36	0.86	86	1.12	136	1.15	186	0.84	236	0.96
37	0.37	87	0.33	137	0.32	187	-0.22	237	1.25
38	0.81	88	0.62	138	1.53	188	1.47	238	0.69
39	1.17	89	1.55	139	0.74	189	0.46	239	1.08
40	0.61	90	2.01	140	1.15	190	0.81	240	1.09
41	1.6	91	0.67	141	1.5	191	1.14	241	0.54
42	0.66	92	1.78	142	0.18	192	0.28	242	1.15
43	0.99	93	0.82	143	1.01	193	0.83	243	0.28
44	0.59	94	1.04	144	0.99	194	1.12	244	0.1
45	0.79	95	-0.03	145	0.72	195	1.25	245	0.3
46	-0.1	96	0.09	146	0.07	196	1.84	246	0.69
47	1.45	97	0.12	147	0.96	197	0.51	247	1.43
48	0.54	98	0.64	148	0.25	198	0.83	248	1.13
49	1.13	99	1.23	149	0.98	199	0.96	249	1.45
50	0.49	100	1.03	150	2.13	200	0.92	250	0.93

Table A.3 Raw PSA data of Up tab that are produced with Current method.

**Proposed method for IUP tab**

NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA
1	1.4	51	1.06	101	-0.08	151	1.2	201	0.83
2	0.76	52	1.48	102	0.43	152	1.4	202	0.89
3	1.42	53	0.39	103	0.44	153	1.25	203	0.95
4	1.35	54	1.53	104	0.74	154	0.32	204	1.69
5	1.62	55	0.29	105	1.01	155	2.34	205	1.03
6	1.32	56	1.07	106	0.56	156	0.12	206	1.93
7	1.01	57	0.69	107	1.65	157	1.45	207	0.98
8	0.59	58	0.51	108	0.71	158	1.68	208	0.74
9	1.07	59	1.96	109	1.79	159	1.02	209	0.54
10	0.69	60	1.3	110	0.94	160	0.64	210	0.79
11	0.22	61	1.3	111	0.79	161	0.86	211	1.4
12	1.35	62	1.14	112	1.17	162	1.52	212	0.58
13	0.69	63	1.28	113	1.17	163	1.2	213	1.15
14	1.18	64	1.3	114	1.52	164	1.4	214	-0.13
15	1.53	65	0.58	115	0.76	165	1.13	215	0.22
16	0.98	66	1.88	116	0.64	166	1.6	216	1.25
17	1.03	67	0.22	117	1.3	167	1.68	217	2.27
18	0.79	68	0.81	118	1.04	168	0.51	218	1.13
19	0.69	69	0.71	119	-0.03	169	1.47	219	0.99
20	0.08	70	1.18	120	0.2	170	0.69	220	1.58
21	0.79	71	1.55	121	1.2	171	0.98	221	1.18
22	1.09	72	0.86	122	0.74	172	1.6	222	1.88
23	1.84	73	1.76	123	1.83	173	0.39	223	2.2
24	1.5	74	1.13	124	0.71	174	1.17	224	1.88
25	1.3	75	1.08	125	1.42	175	-0.03	225	0.74
26	1.35	76	0.81	126	0.46	176	1.68	226	1.32
27	0.81	77	0.93	127	1.69	177	1.13	227	0.35
28	0.71	78	1.14	128	0	178	-0.15	228	0.38
29	2.24	79	1.2	129	0.15	179	1.03	229	0.82
30	2.11	80	1.42	130	0.99	180	1.96	230	0.2
31	0.81	81	0.28	131	1.4	181	0.39	231	1.01
32	1.35	82	0.49	132	0.32	182	1.17	232	0.93
33	1.18	83	1.12	133	0.79	183	0.91	233	0.61
34	0.56	84	0.51	134	2.09	184	1.43	234	0.61
35	1.57	85	0.71	135	0.79	185	1.77	235	0.57
36	1.1	86	1.25	136	0.81	186	0.37	236	1.25
37	0.92	87	1.1	137	0.69	187	1.55	237	0.99
38	0.92	88	0.81	138	2.28	188	1.55	238	0.86
39	0.79	89	1.12	139	1.27	189	1.03	239	-0.18
40	-0.03	90	0.61	140	1.69	190	1.37	240	0.91
41	1.45	91	0.42	141	1.22	191	1.08	241	0.33
42	0.51	92	-0.08	142	1.83	192	1.57	242	1.01
43	1.32	93	1.35	143	0.74	193	1.72	243	1.12
44	0.24	94	1.15	144	0.98	194	1.65	244	2.18
45	1.6	95	0.54	145	0.94	195	1.42	245	1.3
46	0.81	96	0.86	146	1.23	196	0.78	246	-0.27
47	0.48	97	0.91	147	1.96	197	0.86	247	0.4
48	1.55	98	1.73	148	1.72	198	1.13	248	0.83
49	0.74	99	1.14	149	0.56	199	1.13	249	0.58
50	0.64	100	0.91	150	1.81	200	0.98	250	1.13

**Table A.4** Raw PSA data of Up tab that are produced with Proposed method.

In determining whether there is a significant difference in PSA of Up tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for testing PSA of Up tab as followings;

$H_0$  : Assume there is no difference in PSA of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in PSA of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response    PSA\_Up  
 Factors    {    Method  
 ConfLvl    95.0000

Lower	Sigma	Upper	N	Factor Levels
0.477622	0.525722	0.584145	250	New
0.486346	0.535325	0.594814	250	Old

F-Test (normal distribution)

Test Statistic: 1.037

P-Value    : 0.775

Reviewing P-value that is above 0.05, there is not significant difference in PSA on Up tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for testing PSA of Up tab as followings;

$H_0$  : Assume there is no difference in RSA of Up tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in RSA of Up tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for PSA\_Old\_Up vs PSA\_New\_Up

	N	Mean	StDev	SE Mean
PSA_Old_Up	250	0.969	0.535	0.034
PSA_New_Up	250	1.030	0.526	0.033

95% CI for  $\mu$  PSA\_Old\_Up -  $\mu$  PSA\_New\_Up: (-0.155, 0.032)

T-Test  $\mu$  PSA\_Old\_Up =  $\mu$  PSA\_New\_Up (vs not =): T = -1.30 P = 0.20

DF = 498

Both use Pooled StDev = 0.531

Reviewing P-value that is above 0.05, there is not significant difference in PSA on Up tab between both populations' means.

Current method for DN tab

NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA
1	-0.47	51	-0.19	101	0.19	151	-0.45	201	0.05
2	-0.33	52	0	102	0.38	152	0.18	202	0.03
3	0.72	53	-0.6	103	-0.3	153	-0.57	203	0.24
4	-1.02	54	0.25	104	-0.44	154	-0.31	204	-0.09
5	-0.12	55	-0.02	105	-0.12	155	0.03	205	0.42
6	-0.31	56	-0.62	106	-0.14	156	0.5	206	0.4
7	0.43	57	-0.07	107	0.16	157	0.17	207	0.53
8	0	58	0.6	108	0.07	158	0.63	208	0.27
9	-0.55	59	0.1	109	-0.5	159	-0.26	209	0.24
10	-0.38	60	0.23	110	-0.04	160	-0.62	210	0.07
11	-0.5	61	-0.33	111	-0.19	161	-0.3	211	0.38
12	0.07	62	-0.4	112	-0.08	162	0.12	212	-0.13
13	-0.15	63	-0.3	113	-0.28	163	-0.04	213	0.31
14	0.1	64	0	114	-0.45	164	0.23	214	-0.35
15	0.05	65	0.13	115	-0.02	165	-0.63	215	-0.35
16	0.24	66	-0.16	116	-0.09	166	-0.16	216	-0.67
17	-0.12	67	0.05	117	-0.66	167	0.23	217	-0.26
18	-0.41	68	-0.5	118	-0.09	168	0.2	218	-0.05
19	0.24	69	-0.83	119	-0.26	169	-0.4	219	0.55
20	-0.83	70	0.79	120	0.07	170	0.2	220	0.03
21	-0.19	71	-0.28	121	0.48	171	0.58	221	-0.26
22	-0.62	72	0.27	122	-0.26	172	0.4	222	-0.16
23	-0.14	73	-0.17	123	0.22	173	-0.63	223	-0.11
24	-0.11	74	-0.5	124	0.09	174	0.55	224	-0.07
25	0.15	75	-0.52	125	0.36	175	0.49	225	0.17
26	-0.54	76	0.1	126	-0.4	176	-0.55	226	0.16
27	-0.72	77	-0.12	127	0.03	177	0.72	227	-0.95
28	0.91	78	-0.27	128	0.24	178	0.2	228	0.19
29	-0.23	79	0.19	129	0.29	179	0.1	229	0
30	-0.26	80	1.1	130	-0.28	180	-0.12	230	-0.57
31	0.42	81	-0.67	131	-0.59	181	1.12	231	0.31
32	0.05	82	0.65	132	-0.08	182	-0.72	232	0.55
33	-0.55	83	0.1	133	0.62	183	-0.42	233	0.16
34	-0.9	84	0.48	134	-0.08	184	0.62	234	-0.45
35	-0.11	85	-0.38	135	0.1	185	0.29	235	0.38
36	0.03	86	-0.17	136	0	186	0.28	236	-0.45
37	0	87	0.07	137	-0.02	187	0.07	237	-0.11
38	0.58	88	-0.52	138	-0.57	188	0.75	238	0.25
39	-0.7	89	0.62	139	0.05	189	0.7	239	-0.21
40	-0.17	90	0.03	140	-0.17	190	-0.26	240	-0.07
41	0.53	91	0.07	141	0.34	191	0.27	241	0.29
42	-0.4	92	0.7	142	0.71	192	0.03	242	-0.19
43	-0.12	93	-0.47	143	-0.42	193	-0.42	243	0.03
44	-0.7	94	-0.3	144	-0.04	194	0.29	244	-0.12
45	0	95	-0.04	145	-0.52	195	0.19	245	0.31
46	-0.78	96	-0.27	146	0.29	196	-0.19	246	0.25
47	0	97	-0.28	147	0.33	197	0.36	247	0.12
48	0.96	98	-0.16	148	-0.37	198	0.05	248	0.05
49	-0.64	99	0.13	149	-0.78	199	0.27	249	0
50	0.45	100	0.03	150	-0.45	200	-0.22	250	0.72

Table A.5 Raw RSA data of Dn tab that are produced with Current method.

**Proposed method for DN tab**

NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA	NO.	RSA
1	0.53	51	0.11	101	0.03	151	0.38	201	0.4
2	0.24	52	-0.35	102	0	152	-0.52	202	0.65
3	0.27	53	0.03	103	-0.16	153	0.34	203	-0.21
4	-0.28	54	0.29	104	-0.35	154	-0.44	204	-0.24
5	1.1	55	0.38	105	-0.78	155	0.24	205	-0.12
6	-0.42	56	-0.28	106	-0.15	156	0.38	206	-0.19
7	-0.41	57	0.33	107	-0.65	157	-0.37	207	-0.02
8	-0.35	58	0	108	-0.28	158	0.38	208	-0.26
9	-0.33	59	0.4	109	-0.59	159	-1.12	209	0.25
10	-0.04	60	0.23	110	-0.97	160	-0.12	210	0.53
11	0.2	61	0.29	111	0.03	161	-0.59	211	0.22
12	-0.46	62	0.4	112	-0.25	162	0.72	212	-0.71
13	0.1	63	-0.35	113	0.07	163	-0.28	213	0.24
14	-0.37	64	-0.22	114	-0.16	164	0.13	214	-0.72
15	-0.46	65	-0.35	115	-0.02	165	0.1	215	0
16	0.38	66	-0.24	116	0.03	166	0.22	216	0.1
17	0.35	67	-0.45	117	-0.28	167	-0.17	217	-0.08
18	-0.44	68	-0.35	118	0.36	168	-0.14	218	0.29
19	0.41	69	-0.57	119	0.2	169	0.38	219	0.46
20	-0.02	70	-0.47	120	-0.25	170	-0.12	220	-0.33
21	0.69	71	0.27	121	0.28	171	-1.1	221	-0.67
22	0.1	72	0.05	122	0.43	172	-0.83	222	-0.06
23	0.11	73	0.48	123	0.22	173	0.1	223	-0.43
24	-0.05	74	0.38	124	0.05	174	-0.62	224	0.24
25	0.05	75	0.14	125	-0.07	175	-0.19	225	0.17
26	-0.22	76	-0.07	126	0.48	176	0.1	226	0.31
27	-0.13	77	0.11	127	-0.12	177	0.72	227	-0.37
28	0.31	78	0.22	128	-0.11	178	-0.78	228	0.24
29	-0.2	79	0.18	129	-0.08	179	1.06	229	0.84
30	0.62	80	0.07	130	-0.47	180	0	230	-0.62
31	0.44	81	-0.66	131	0.46	181	0.53	231	0.03
32	-0.12	82	-0.14	132	0.13	182	-0.57	232	-0.52
33	0.14	83	0.03	133	-0.09	183	0.07	233	-0.17
34	-0.28	84	0.03	134	0	184	-0.02	234	0.15
35	0.18	85	0.05	135	-0.15	185	-0.22	235	0.78
36	-0.04	86	-0.63	136	-0.02	186	0.22	236	0
37	0.18	87	0.07	137	0.19	187	-0.13	237	-0.23
38	0.03	88	-0.35	138	0.11	188	-0.43	238	0.62
39	0.14	89	-0.35	139	0.15	189	0.05	239	-0.08
40	-0.1	90	-0.43	140	0.79	190	0	240	0.63
41	0.62	91	0	141	0.38	191	-0.32	241	-0.45
42	0.07	92	0.14	142	0.46	192	0.22	242	0.36
43	-0.27	93	0.05	143	0.09	193	-0.35	243	-0.15
44	0.79	94	-0.05	144	0.29	194	-0.08	244	0.1
45	-0.19	95	0.53	145	-0.15	195	0.31	245	-0.33
46	0.72	96	0.27	146	-0.26	196	0.11	246	-0.08
47	0.19	97	-0.15	147	0.72	197	0.05	247	-1.05
48	-0.15	98	0.1	148	0.17	198	-0.64	248	0.72
49	0.24	99	0.16	149	0.34	199	-0.07	249	0.12
50	-0.32	100	-0.68	150	-0.4	200	0.07	250	0.1

**Table A.6 Raw RSA data of Dn tab that are produced with Proposed method.**

In determining whether there is a significant difference in RSA of Dn tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for testing RSA of Dn tab as followings;

$H_0$  : Assume there is no difference in RSA of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in RSA of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response RSA\_Dn

Factors Method

ConfLvl 95.0000

Lower	Sigma	Upper	N	Factor Levels
0.348611	0.383719	0.426361	250	New
0.363889	0.400536	0.445046	250	Old

F-Test (normal distribution)

Test Statistic: 1.090

P-Value : 0.499

Reviewing P-value that is above 0.05, there is not significant difference in RSA on Dn tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for testing RSA of Dn tab as followings;

$H_0$  : Assume there is no difference in RSA of Dn tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in RSA of Dn tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for RSA\_Old\_Dn vs RSA\_New\_Dn

	N	Mean	StDev	SE Mean
RSA_Old_Dn	250	-0.031	0.401	0.025
RSA_New_Dn	250	-0.004	0.384	0.024

95% CI for  $\mu$  RSA\_Old\_Dn -  $\mu$  RSA\_New\_Dn: (-0.096, 0.042)

T-Test  $\mu$  RSA\_Old\_Dn =  $\mu$  RSA\_New\_Dn (vs not =): T = -0.78 P = 0.44

DF = 498

Both use Pooled StDev = 0.392

Reviewing P-value that is above 0.05, there is not significant difference in RSA on Dn tab between both populations' means.



Current method for DN tab

NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA
1	1.14	51	1.27	101	0.56	151	0.79	201	1.52
2	0.94	52	1.25	102	1.42	152	0.84	202	1.01
3	-0.08	53	1.04	103	1.86	153	1.81	203	0.85
4	0.89	54	0.84	104	1.1	154	1.48	204	1.4
5	1.27	55	0.89	105	0.62	155	0.43	205	0.84
6	0.53	56	1.14	106	1.3	156	0.74	206	1.27
7	0.69	57	0.69	107	1.25	157	1.17	207	0.46
8	0.47	58	1.98	108	1.14	158	1.42	208	1.76
9	0.94	59	0.4	109	0.61	159	0.11	209	1.27
10	1.16	60	-0.08	110	1.08	160	1.52	210	1.04
11	1.42	61	0.79	111	0.81	161	1.18	211	1.12
12	1.22	62	1.45	112	1.16	162	1.12	212	1.16
13	1.08	63	1.46	113	0.89	163	1.73	213	1.51
14	0.94	64	0.32	114	1.3	164	0.71	214	0.02
15	2.39	65	2	115	1.22	165	0.93	215	1.33
16	-0.21	66	1.02	116	0.61	166	0.76	216	0.3
17	2.16	67	0.57	117	1.78	167	1.72	217	1.08
18	1.73	68	1.16	118	1.78	168	1.25	218	1.12
19	0.99	69	1.45	119	0.8	169	1.07	219	0.59
20	1.7	70	0.36	120	0.36	170	1.59	220	1.42
21	1.33	71	1.4	121	0.94	171	0.36	221	0.69
22	0.48	72	-0.02	122	2.16	172	1.07	222	0.23
23	1.02	73	1.79	123	0.66	173	0.8	223	0.62
24	1.29	74	1.78	124	1.93	174	1.32	224	1.18
25	1.55	75	0.67	125	1.64	175	1.03	225	0.58
26	1.43	76	1.32	126	1.57	176	1.38	226	1.08
27	1.4	77	1.48	127	0.84	177	1.66	227	0.33
28	1.62	78	1.22	128	0.77	178	0.73	228	1.83
29	0.43	79	1.14	129	1.51	179	1.32	229	0.97
30	0.94	80	-0.02	130	0.58	180	1.32	230	0.11
31	1.78	81	0.8	131	1.31	181	1.76	231	1.46
32	1.25	82	0.77	132	0.89	182	0.84	232	0.56
33	2.18	83	1.27	133	1.3	183	0.6	233	1.64
34	1.98	84	1.86	134	1.25	184	2.27	234	0.38
35	1.38	85	0.61	135	1.02	185	1.77	235	1.45
36	0.79	86	0.89	136	1.5	186	1.42	236	1.32
37	1.4	87	0.28	137	0.99	187	0.43	237	1.64
38	1.55	88	0.99	138	0.97	188	0.11	238	1.36
39	0.58	89	1.98	139	1.81	189	1.38	239	1.84
40	1.59	90	1.4	140	1.65	190	0.3	240	1.91
41	1.64	91	0.53	141	2.04	191	0.86	241	1.38
42	0.82	92	1.46	142	0.45	192	2.03	242	0.97
43	-0.03	93	0.71	143	1.23	193	1.13	243	0.97
44	-0.05	94	1.83	144	0.93	194	1.25	244	1.83
45	1.02	95	1.1	145	1.02	195	1.58	245	1.69
46	0.84	96	0.89	146	1.32	196	0.79	246	0.71
47	1.12	97	1.73	147	1.66	197	1.05	247	0.79
48	1.09	98	0.45	148	1.12	198	0.98	248	1.29
49	0.08	99	1.52	149	1.68	199	1.45	249	0.61
50	0.97	100	2.19	150	0.95	200	1.1	250	1.14

Table A.7 Raw PSA data of Dn tab that are produced with Current method.

**Proposed method for DN tab**

NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA	NO.	PSA
1	0.71	51	0.11	101	1.73	151	0.86	201	0.47
2	0.97	52	1.12	102	1.12	152	1.92	202	1.02
3	0.9	53	0.94	103	1.35	153	1.27	203	1.43
4	0.71	54	0.97	104	1.4	154	0.62	204	0.64
5	1.1	55	0.75	105	0.81	155	0.58	205	1.04
6	0.57	56	-0.08	106	1.18	156	0.97	206	1.46
7	1.46	57	0.45	107	1.04	157	1.57	207	0.79
8	0.52	58	0.58	108	0.23	158	0.13	208	0.46
9	1.79	59	0.88	109	0.84	159	0.77	209	0.89
10	2.14	60	1.18	110	0.43	160	1.02	210	1.22
11	1.38	61	0.18	111	1.53	161	1.88	211	1.18
12	1.27	62	1.03	112	1.08	162	1.04	212	1.4
13	0.66	63	1.07	113	0.89	163	0.52	213	0.97
14	1.74	64	1.14	114	1.65	164	0.4	214	0.67
15	1.42	65	1.32	115	0.84	165	1.78	215	1.4
16	0.81	66	0.99	116	1.13	166	1.66	216	0.99
17	0.74	67	1.65	117	1.74	167	1.45	217	1.12
18	0.64	68	0.9	118	1.71	168	0.51	218	0.97
19	1.58	69	1.79	119	1.1	169	0.77	219	1.4
20	2.23	70	0.99	120	2.13	170	1.81	220	1.27
21	1.29	71	1.16	121	0.99	171	1.89	221	1.16
22	0.76	72	1.3	122	0.84	172	0.33	222	1.59
23	0.99	73	1.35	123	0.2	173	1.91	223	0.81
24	1.69	74	1.16	124	1.79	174	0.62	224	1.48
25	1.27	75	1.38	125	0.97	175	1.9	225	1.86
26	1.04	76	1.09	126	0.82	176	1.21	226	2.05
27	1.31	77	1.66	127	1.14	177	2.16	227	0.77
28	1.29	78	1.45	128	1.27	178	-0.21	228	2.19
29	1.47	79	1.72	129	1.38	179	0.9	229	0.95
30	1.44	80	1.5	130	1.52	180	1.71	230	1.55
31	1.46	81	-0.02	131	0.61	181	1.64	231	1.76
32	1.35	82	1.45	132	1.04	182	0.61	232	1.25
33	1.42	83	0.32	133	1.3	183	0.23	233	1.59
34	1.33	84	0.89	134	1.04	184	1.81	234	0.58
35	1.72	85	1.07	135	-0.67	185	1.55	235	1.08
36	1.98	86	0.71	136	0.53	186	0.53	236	1.73
37	2.25	87	1.09	137	1.22	187	1.57	237	0.56
38	0.39	88	1.17	138	0.82	188	0.89	238	1.98
39	0.43	89	1.21	139	1.11	189	1.4	239	2.22
40	1.25	90	0.53	140	1.3	190	1.25	240	1.84
41	1.65	91	1.18	141	1.16	191	0.84	241	0.15
42	0.8	92	0.95	142	1.63	192	0.86	242	1.37
43	1.93	93	1.81	143	2.18	193	1.78	243	1.93
44	0.69	94	1.55	144	0.36	194	1.7	244	0.79
45	0.82	95	1.66	145	1.74	195	0.3	245	1.3
46	1.55	96	-0.02	146	1.32	196	1.51	246	2
47	1.27	97	1.4	147	0.3	197	0.89	247	1.5
48	1.42	98	0.56	148	1.4	198	1.12	248	0.94
49	1.27	99	0.69	149	0.99	199	0.6	249	1.3
50	1.4	100	1.12	150	2.08	200	1.09	250	1.2

**Table A.8** Raw PSA data of Dn tab that are produced with Proposed method.

In determining whether there is a significant difference in PSA of Dn tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for testing PSA of Dn tab as followings;

$H_0$  : Assume there is no difference in PSA of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in PSA of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response	PSA_Dn			
Factors	Method			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
0.456764	0.502764	0.558635	250	New
0.466875	0.513893	0.571001	250	Old

F-Test (normal distribution)

Test Statistic: 1.045

P-Value : 0.730

Reviewing P-value that is above 0.05, there is not significant difference in PSA on Dn tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference in PSA of Dn tab between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for testing in PSA of Dn tab as followings;

$H_0$  : Assume there is no difference in PSA of Dn tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in PSA of Dn tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for PSA\_Old\_Dn vs PSA\_New\_Dn

	N	Mean	StDev	SE Mean
PSA_Old_Dn	250	1.113	0.514	0.033
PSA_New_Dn	250	1.157	0.503	0.032

95% CI for  $\mu$  PSA\_Old\_Dn -  $\mu$  PSA\_New\_Dn: (-0.134, 0.045)

T-Test  $\mu$  PSA\_Old\_Dn =  $\mu$  PSA\_New\_Dn (vs not =): T = -0.97 P = 0.33

DF = 498

Both use Pooled StDev = 0.508

Reviewing P-value that is above 0.05, there is not significant difference in PSA on Dn tab between both populations' means.

**CRTE\_ID UP Current Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.6998	51	1.7834	101	1.4949	151	1.4867	201	1.5741
2	1.6288	52	1.6958	102	1.6523	152	1.777	202	1.5197
3	1.6807	53	1.4928	103	1.4977	153	1.5907	203	1.8702
4	1.551	54	1.6588	104	1.6555	154	1.4712	204	1.4451
5	1.7604	55	1.7636	105	1.7595	155	1.7005	205	1.4512
6	1.7203	56	1.6615	106	1.4443	156	1.4879	206	1.6371
7	1.6201	57	1.5977	107	1.6347	157	1.4188	207	1.7014
8	1.6047	58	1.7153	108	1.7749	158	1.7802	208	1.6346
9	1.6296	59	1.6507	109	1.5329	159	1.5992	209	1.5462
10	1.5726	60	1.7393	110	1.4985	160	1.7664	210	1.748
11	1.6181	61	1.6357	111	1.6009	161	1.6397	211	1.5388
12	1.6738	62	1.5792	112	1.6667	162	1.725	212	1.6831
13	1.694	63	1.7883	113	1.5551	163	1.741	213	1.6225
14	1.6688	64	1.7766	114	1.5138	164	1.6598	214	1.443
15	1.7589	65	1.7565	115	1.6304	165	1.5786	215	1.5384
16	1.7597	66	1.6819	116	1.7046	166	1.3989	216	1.6344
17	1.4811	67	1.7043	117	1.5168	167	1.7408	217	1.6722
18	1.5447	68	1.6312	118	1.6527	168	1.5052	218	1.5009
19	1.7209	69	1.7862	119	1.7846	169	1.6111	219	1.5654
20	1.7372	70	1.5048	120	1.5799	170	1.6213	220	1.7154
21	1.631	71	1.5851	121	1.5879	171	1.4457	221	1.7841
22	1.621	72	1.7078	122	1.653	172	1.552	222	1.6379
23	1.5908	73	1.5761	123	1.7353	173	1.604	223	1.9089
24	1.6367	74	1.6736	124	1.5153	174	1.7986	224	1.6714
25	1.6204	75	1.7293	125	1.5325	175	1.6441	225	1.5926
26	1.6709	76	1.647	126	1.6262	176	1.4816	226	1.4282
27	1.6167	77	1.6383	127	1.5984	177	1.6602	227	1.5824
28	1.7678	78	1.5823	128	1.6772	178	1.687	228	1.7627
29	1.5647	79	1.649	129	1.577	179	1.6157	229	1.7357
30	1.5748	80	1.6706	130	1.5144	180	1.6767	230	1.7491
31	1.5255	81	1.6001	131	1.5048	181	1.659	231	1.5934
32	1.4664	82	1.7113	132	1.5133	182	1.5874	232	1.549
33	1.775	83	1.4613	133	1.5002	183	1.5072	233	1.7526
34	1.8266	84	1.5777	134	1.6685	184	1.6881	234	1.7204
35	1.5563	85	1.6584	135	1.5732	185	1.7302	235	1.654
36	1.6852	86	1.6265	136	1.5959	186	1.6764	236	1.6234
37	1.7116	87	1.684	137	1.9287	187	1.6255	237	1.5524
38	1.7163	88	1.6755	138	1.5871	188	1.5174	238	1.4806
39	1.5166	89	1.6434	139	1.6393	189	1.4881	239	1.7576
40	1.6099	90	1.6643	140	1.6017	190	1.6023	240	1.8888
41	1.477	91	1.6965	141	1.6102	191	1.5956	241	1.5603
42	1.5126	92	1.6758	142	1.4094	192	1.6206	242	1.5811
43	1.7813	93	1.5425	143	1.5932	193	1.5318	243	1.5458
44	1.4495	94	1.6033	144	1.6653	194	1.5482	244	1.5396
45	1.6615	95	1.7365	145	1.763	195	1.7732	245	1.9017
46	1.5591	96	1.5084	146	1.5758	196	1.5289	246	1.6458
47	1.653	97	2.0394	147	1.688	197	1.7401	247	1.6111
48	1.57	98	1.5653	148	1.7565	198	1.6488	248	1.6989
49	1.5873	99	1.78	149	1.532	199	1.5228	249	1.6962
50	1.6247	100	1.4527	150	1.7285	200	1.6815	250	1.6486

Table A.9 Raw CRTE\_ID data of Up tab that are produced with Current method.

**CRTE ID Up New Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.7009	51	1.7853	101	1.496	151	1.4878	201	1.5752
2	1.6299	52	1.6969	102	1.6534	152	1.8976	202	1.5208
3	1.6818	53	1.4939	103	1.4988	153	1.5918	203	1.8713
4	1.5521	54	1.6599	104	1.6566	154	1.4723	204	1.4462
5	1.7615	55	1.7647	105	1.7606	155	1.7016	205	1.4523
6	1.7214	56	1.6626	106	1.4454	156	1.489	206	1.6382
7	1.6212	57	1.5988	107	1.6358	157	1.4199	207	1.7025
8	1.6058	58	1.7164	108	1.776	158	1.7821	208	1.6357
9	1.6307	59	1.6518	109	1.534	159	1.6003	209	1.5473
10	1.5737	60	1.7404	110	1.4996	160	1.7675	210	1.7491
11	1.6192	61	1.6368	111	1.602	161	1.6408	211	1.5399
12	1.6749	62	1.5803	112	1.6678	162	1.7261	212	1.6842
13	1.6951	63	1.412	113	1.5562	163	1.7421	213	1.6236
14	1.6699	64	1.4438	114	1.5149	164	1.6609	214	1.4441
15	1.76	65	1.7576	115	1.6315	165	1.5797	215	1.5395
16	1.7608	66	1.683	116	1.7057	166	1.4	216	1.6355
17	1.4822	67	1.7054	117	1.5179	167	1.7419	217	1.6733
18	1.5458	68	1.6323	118	1.6538	168	1.5063	218	1.502
19	1.722	69	1.7881	119	1.8021	169	1.6122	219	1.5665
20	1.7383	70	1.5059	120	1.581	170	1.6224	220	1.7165
21	1.6321	71	1.5862	121	1.589	171	1.4468	221	1.786
22	1.6221	72	1.7089	122	1.6541	172	1.5531	222	1.639
23	1.5919	73	1.5772	123	1.7364	173	1.6051	223	1.91
24	1.6378	74	1.6747	124	1.5164	174	1.4229	224	1.6725
25	1.6215	75	1.7304	125	1.5336	175	1.6452	225	1.5937
26	1.672	76	1.6481	126	1.6273	176	1.4827	226	1.4293
27	1.6178	77	1.6394	127	1.5995	177	1.6613	227	1.5835
28	1.7689	78	1.5834	128	1.6783	178	1.6881	228	1.7638
29	1.5658	79	1.6501	129	1.5781	179	1.6168	229	1.7368
30	1.5759	80	1.6717	130	1.5155	180	1.6778	230	1.7502
31	1.5266	81	1.6012	131	1.5059	181	1.6601	231	1.5945
32	1.4675	82	1.7124	132	1.5144	182	1.5885	232	1.5501
33	1.902	83	1.4624	133	1.5013	183	1.5083	233	1.7537
34	1.8277	84	1.5788	134	1.6696	184	1.6892	234	1.7215
35	1.5574	85	1.6595	135	1.5743	185	1.7313	235	1.6551
36	1.6863	86	1.6276	136	1.597	186	1.6775	236	1.6245
37	1.7127	87	1.6851	137	1.9298	187	1.6266	237	1.5535
38	1.7174	88	1.6766	138	1.5882	188	1.5185	238	1.4817
39	1.5177	89	1.6445	139	1.6404	189	1.4892	239	1.7587
40	1.611	90	1.6654	140	1.6028	190	1.6034	240	1.8899
41	1.4781	91	1.6976	141	1.6113	191	1.5967	241	1.5614
42	1.5137	92	1.6769	142	1.4105	192	1.6217	242	1.5822
43	1.431	93	1.5436	143	1.5943	193	1.5329	243	1.5469
44	1.4506	94	1.6044	144	1.6664	194	1.5493	244	1.5407
45	1.6626	95	1.7376	145	1.7641	195	1.8557	245	1.9028
46	1.5602	96	1.5095	146	1.5769	196	1.53	246	1.6469
47	1.6541	97	2.0405	147	1.6891	197	1.7412	247	1.6122
48	1.5711	98	1.5664	148	1.7576	198	1.6499	248	1.7
49	1.5884	99	1.7819	149	1.5331	199	1.5239	249	1.6973
50	1.6258	100	1.4538	150	1.7296	200	1.6826	250	1.6497

**Table A.10** Raw CRTE\_ID data of Up tab that are produced with Proposed method.

In determining whether there is a significant difference in CRTE\_ID of Up tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for CRTE\_ID of Up tab as followings;

$H_0$  : Assume there is no difference in CRTE\_ID of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_ID of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response FHID\_Up

Factors Methods

ConfLvl 95.0000

Lower	Sigma	Upper	N	Factor Levels
9.76E-02	0.107483	0.119428	250	New
9.41E-02	0.103573	0.115083	250	Old

F-Test (normal distribution)

Test Statistic: 1.077

P-Value : 0.559

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_ID on Up tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for CRTE\_ID of Up tab as followings;

$H_0$  : Assume there is no difference in CRTE\_ID of Up tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_ID of Up tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for CRTE\_ID\_Old\_Up vs CRTE\_ID\_New\_Up

	N	Mean	StDev	SE Mean
CRTE_ID_Old	250	1.632	0.104	0.0066
CRTE_ID_New	250	1.628	0.107	0.0068

95% CI for  $\mu$  CRTE\_ID\_Old -  $\mu$  CRTE\_ID\_New: ( -0.0153, 0.0218)

T-Test  $\mu$  CRTE\_ID\_Old=  $\mu$  CRTE\_ID\_New (vs not =): T = 0.35 P = 0.73

DF = 498

Both use Pooled StDev = 0.106

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_ID on Up tab between both populations' means.



**CRTE OD Up Current Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.6654	51	1.7607	101	1.4566	151	1.4518	201	1.5427
2	1.5934	52	1.6608	102	1.621	152	1.7558	202	1.4952
3	1.6531	53	1.4548	103	1.4591	153	1.5653	203	1.8426
4	1.5197	54	1.6264	104	1.6242	154	1.4351	204	1.4138
5	1.7365	55	1.7436	105	1.736	155	1.6676	205	1.4194
6	1.6884	56	1.6316	106	1.4116	156	1.453	206	1.6047
7	1.589	57	1.5704	107	1.6031	157	1.3686	207	1.6689
8	1.5783	58	1.6765	108	1.7524	158	1.7571	208	1.6028
9	1.5979	59	1.6168	109	1.5083	159	1.5716	209	1.5177
10	1.5378	60	1.7122	110	1.4601	160	1.7453	210	1.7252
11	1.5885	61	1.6033	111	1.5734	161	1.6092	211	1.5112
12	1.6445	62	1.553	112	1.6363	162	1.6946	212	1.6564
13	1.6607	63	1.7756	113	1.5227	163	1.7206	213	1.5913
14	1.6393	64	1.7537	114	1.4851	164	1.6285	214	1.3847
15	1.7351	65	1.7308	115	1.5983	165	1.5486	215	1.5108
16	1.7363	66	1.6557	116	1.6728	166	1.3393	216	1.6007
17	1.4452	67	1.6689	117	1.489	167	1.7134	217	1.644
18	1.5162	68	1.5999	118	1.6214	168	1.4776	218	1.4739
19	1.6933	69	1.767	119	1.7636	169	1.5835	219	1.5331
20	1.7089	70	1.4771	120	1.5548	170	1.5905	220	1.6767
21	1.5992	71	1.5614	121	1.5651	171	1.4181	221	1.761
22	1.5893	72	1.6729	122	1.6231	172	1.5207	222	1.6054
23	1.5656	73	1.5456	123	1.7059	173	1.5776	223	1.9023
24	1.6046	74	1.6442	124	1.4886	174	1.7847	224	1.6425
25	1.5891	75	1.7004	125	1.5057	175	1.6113	225	1.5658
26	1.6403	76	1.6117	126	1.5931	176	1.4503	226	1.3834
27	1.5881	77	1.6071	127	1.5708	177	1.6302	227	1.5609
28	1.7456	78	1.5575	128	1.6518	178	1.659	228	1.739
29	1.5324	79	1.6165	129	1.5464	179	1.5879	229	1.7077
30	1.5431	80	1.6401	130	1.4861	180	1.6517	230	1.7284
31	1.4976	81	1.5733	131	1.4772	181	1.6274	231	1.5669
32	1.4337	82	1.6733	132	1.484	182	1.5646	232	1.5196
33	1.7532	83	1.4214	133	1.4701	183	1.4796	233	1.73
34	1.7868	84	1.5468	134	1.6389	184	1.6604	234	1.6895
35	1.5275	85	1.6254	135	1.5387	185	1.7017	235	1.6231
36	1.6568	86	1.5932	136	1.5692	186	1.6502	236	1.5921
37	1.6738	87	1.6567	137	1.9293	187	1.5927	237	1.5215
38	1.6841	88	1.6454	138	1.5617	188	1.4934	238	1.4413
39	1.4887	89	1.6108	139	1.6089	189	1.4542	239	1.7314
40	1.5786	90	1.634	140	1.5747	190	1.5767	240	1.8575
41	1.4389	91	1.6621	141	1.5792	191	1.568	241	1.5287
42	1.482	92	1.6459	142	1.3498	192	1.5892	242	1.5557
43	1.7601	93	1.5152	143	1.5666	193	1.4995	243	1.5174
44	1.4182	94	1.5775	144	1.6354	194	1.5182	244	1.513
45	1.6302	95	1.708	145	1.7407	195	1.7457	245	1.8813
46	1.5278	96	1.4817	146	1.5437	196	1.4979	246	1.6117
47	1.6223	97	2.04	147	1.6596	197	1.7132	247	1.5862
48	1.5335	98	1.5326	148	1.7313	198	1.6157	248	1.6645
49	1.5632	99	1.757	149	1.5008	199	1.4955	249	1.6608
50	1.5925	100	1.421	150	1.6968	200	1.6539	250	1.614

**Table A.11 Raw CRTE\_OD data of Up tab that are produced with Current method.**

**CRTE OD Up New Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.673	51	1.7605	101	1.4664	151	1.4577	201	1.5451
2	1.6031	52	1.6676	102	1.6239	152	1.8658	202	1.4969
3	1.6544	53	1.4664	103	1.4701	153	1.5648	203	1.8499
4	1.5259	54	1.6334	104	1.6305	154	1.4465	204	1.4161
5	1.7362	55	1.7424	105	1.7351	155	1.6762	205	1.43
6	1.6951	56	1.6365	106	1.4144	156	1.4646	206	1.6135
7	1.5908	57	1.5708	107	1.6085	157	1.3906	207	1.6793
8	1.5816	58	1.6881	108	1.7497	158	1.7513	208	1.6083
9	1.6039	59	1.6238	109	1.5107	159	1.5734	209	1.5211
10	1.5435	60	1.715	110	1.4716	160	1.7433	210	1.7214
11	1.59	61	1.6097	111	1.5751	161	1.6172	211	1.5122
12	1.6485	62	1.5558	112	1.6404	162	1.6988	212	1.6602
13	1.6654	63	1.3875	113	1.5302	163	1.72	213	1.5978
14	1.6423	64	1.4096	114	1.4869	164	1.6342	214	1.4114
15	1.7291	65	1.7263	115	1.6044	165	1.5538	215	1.5112
16	1.7361	66	1.6573	116	1.6803	166	1.3743	216	1.608
17	1.4566	67	1.6803	117	1.4961	167	1.719	217	1.6451
18	1.5169	68	1.606	118	1.6264	168	1.4806	218	1.4746
19	1.6972	69	1.7677	119	1.7697	169	1.5855	219	1.5388
20	1.7128	70	1.4771	120	1.5561	170	1.5959	220	1.689
21	1.6054	71	1.5594	121	1.5621	171	1.4248	221	1.7667
22	1.5942	72	1.6811	122	1.6285	172	1.5282	222	1.6139
23	1.565	73	1.5482	123	1.7047	173	1.5806	223	1.8814
24	1.6109	74	1.648	124	1.4883	174	1.3931	224	1.645
25	1.5914	75	1.7039	125	1.5052	175	1.618	225	1.5658
26	1.644	76	1.6189	126	1.6007	176	1.4567	226	1.4053
27	1.5888	77	1.6145	127	1.5729	177	1.6352	227	1.5593
28	1.7462	78	1.5575	128	1.6539	178	1.6627	228	1.7394
29	1.5386	79	1.6232	129	1.5498	179	1.5883	229	1.7059
30	1.5464	80	1.6423	130	1.4877	180	1.6529	230	1.7243
31	1.4988	81	1.5743	131	1.4782	181	1.634	231	1.5676
32	1.4361	82	1.6833	132	1.4861	182	1.5621	232	1.5219
33	1.8776	83	1.433	133	1.4735	183	1.4815	233	1.7244
34	1.8101	84	1.5523	134	1.6421	184	1.6654	234	1.696
35	1.5317	85	1.6324	135	1.5441	185	1.7044	235	1.6289
36	1.6611	86	1.6028	136	1.5704	186	1.6519	236	1.5983
37	1.6858	87	1.6604	137	1.9122	187	1.5996	237	1.529
38	1.691	88	1.6502	138	1.5596	188	1.4965	238	1.4499
39	1.4935	89	1.6177	139	1.6154	189	1.4651	239	1.7279
40	1.5827	90	1.6393	140	1.5774	190	1.5791	240	1.8575
41	1.4493	91	1.6705	141	1.5837	191	1.5682	241	1.5381
42	1.4831	92	1.6502	142	1.3824	192	1.5934	242	1.5567
43	1.4092	93	1.5159	143	1.5671	193	1.5032	243	1.5193
44	1.4265	94	1.5798	144	1.6395	194	1.5212	244	1.5153
45	1.6363	95	1.7088	145	1.7398	195	1.8195	245	1.88
46	1.5325	96	1.482	146	1.5473	196	1.5016	246	1.6181
47	1.6271	97	2.0043	147	1.6637	197	1.7178	247	1.5858
48	1.541	98	1.5387	148	1.7277	198	1.6217	248	1.6727
49	1.5608	99	1.7498	149	1.5037	199	1.4976	249	1.6678
50	1.5992	100	1.4324	150	1.7021	200	1.6555	250	1.6206

**Table A.12** Raw CRTE\_OD data of Up tab that are produced with Proposed method.

In determining whether there is a significant difference in CRTE\_OD of Up tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for CRTE\_OD of Up tab as followings;

$H_0$  : Assume there is no difference in CRTE\_OD of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_OD of Up tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response	FHOD_Up			
Factors	Methods			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
9.78E-02	0.107645	0.119608	250	New
9.74E-02	0.107206	0.119120	250	Old
F-Test (normal distribution)				
Test Statistic: 1.008				
P-Value : 0.949				

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_OD on Up tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for CRTE\_OD of Up tab as followings;

$H_0$  : Assume there is no difference in CRTE\_OD of Up tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_OD of Up tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for CRTE\_OD\_Old\_Up vs CRTE\_OD\_New\_Up

	N	Mean	StDev	SE Mean
CRTE_OD_Old	250	1.602	0.107	0.0068
CRTE_OD_New	250	1.601	0.108	0.0068

95% CI for mu CRTE\_OD\_Old - mu CRTE\_OD\_New: (-0.0182, 0.0196)

T-Test mu CRTE\_OD\_Old= mu CRTE\_OD\_New(vs not =): T = 0.07 P = 0.94

DF = 498

Both use Pooled StDev = 0.107

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_OD on Up tab between both populations' means.

**CRTE ID Dn Current Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.7759	51	1.6362	101	1.5509	151	1.5644	201	1.6204
2	1.6178	52	1.6213	102	1.5795	152	1.5689	202	1.4988
3	1.7604	53	1.6195	103	1.5743	153	1.5862	203	1.6642
4	1.91	54	1.6335	104	1.4868	154	1.7421	204	1.6634
5	1.5783	55	1.6891	105	1.6599	155	1.6514	205	1.5802
6	1.6971	56	1.5865	106	1.5163	156	1.7364	206	1.5739
7	1.7195	57	1.6256	107	1.6518	157	1.7894	207	1.5766
8	1.5862	58	1.8877	108	1.7241	158	1.4516	208	1.5471
9	1.7535	59	1.6049	109	1.6744	159	1.6761	209	1.7025
10	1.6624	60	1.6731	110	1.7361	160	1.7639	210	1.5
11	1.5945	61	1.7154	111	1.7311	161	1.6366	211	1.7366
12	1.5177	62	1.7471	112	1.6192	162	1.5533	212	1.6541
13	1.4434	63	1.5473	113	1.6727	163	1.5888	213	1.7276
14	1.6593	64	1.5779	114	1.7554	164	1.6358	214	1.6611
15	1.7613	65	1.6212	115	1.6301	165	1.7007	215	1.5935
16	1.5122	66	1.7016	116	1.5434	166	1.9026	216	1.6501
17	1.5612	67	1.7382	117	1.7793	167	1.4484	217	1.5499
18	1.5073	68	1.5142	118	1.6443	168	1.4805	218	1.6266
19	1.7977	69	1.6851	119	1.5882	169	1.6604	219	1.6656
20	1.7035	70	1.682	120	1.6201	170	1.7755	220	1.6703
21	1.741	71	1.8713	121	1.7419	171	1.6406	221	1.6356
22	1.7667	72	1.398	122	1.5041	172	1.7845	222	1.6333
23	1.5278	73	1.76	123	1.7574	173	1.6392	223	1.4937
24	1.4976	74	1.6551	124	1.67	174	1.7824	224	1.7143
25	1.6449	75	1.5995	125	1.6036	175	1.6755	225	1.5129
26	1.6747	76	1.5239	126	1.7616	176	1.6168	226	1.5329
27	1.7587	77	1.5582	127	1.6234	177	1.7104	227	1.6949
28	1.6279	78	1.6695	128	1.5083	178	1.9296	228	1.687
29	1.5574	79	1.5665	129	1.6479	179	1.6122	229	1.6305
30	1.7759	80	1.6006	130	1.4703	180	1.7586	230	1.6459
31	1.5948	81	1.6579	131	1.7743	181	1.4468	231	1.6253
32	1.5059	82	1.5338	132	1.6587	182	1.4085	232	1.444
33	1.4273	83	1.6003	133	1.4521	183	1.5814	233	1.4653
34	1.6756	84	1.6947	134	1.5788	184	1.5117	234	1.681
35	1.6544	85	1.5385	135	1.7125	185	1.6676	235	1.4624
36	1.4797	86	1.6014	136	1.5334	186	1.602	236	1.5188
37	1.7857	87	1.5395	137	1.6521	187	1.7871	237	1.785
38	1.7811	88	1.5656	138	1.5919	188	1.6452	238	1.5479
39	1.556	89	1.6679	139	1.6088	189	1.5327	239	1.4958
40	1.6861	90	1.4197	140	1.4878	190	1.5011	240	1.489
41	1.7482	91	1.7144	141	1.637	191	1.7194	241	1.7647
42	1.6024	92	1.4779	142	1.6818	192	1.5835	242	1.6976
43	1.5986	93	1.6477	143	1.5943	193	1.575	243	1.5399
44	1.7653	94	1.4421	144	1.601	194	1.7304	244	1.7376
45	1.5717	95	1.7067	145	1.7054	195	1.6727	245	1.6978
46	1.5438	96	1.612	146	1.5749	196	1.6111	246	1.5916
47	1.6841	97	1.7738	147	2.0403	197	1.5039	247	1.577
48	1.6404	98	1.482	148	1.6518	198	1.5177	248	1.6223
49	1.5135	99	1.6315	149	1.6804	199	1.5266	249	1.6238
50	1.8257	100	1.722	150	1.6319	200	1.5469	250	1.5967

**Table A.13** Raw CRTE\_ID data of Dn tab that are produced with Current method.

**CRTE ID Dn New Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.4539	51	1.7554	101	1.7418	151	1.5571	201	1.4875
2	1.5263	52	1.871	102	1.7639	152	1.4507	202	1.5301
3	1.4839	53	1.5532	103	1.6356	153	1.7416	203	1.6165
4	1.6548	54	1.6218	104	1.7145	154	1.6973	204	1.5001
5	1.7623	55	1.4435	105	1.6239	155	1.6257	205	1.574
6	1.6175	56	1.6515	106	1.6059	156	1.6209	206	1.6811
7	1.7195	57	1.5165	107	1.5474	157	1.663	207	1.6379
8	1.6449	58	1.5954	108	1.5964	158	1.769	208	1.7196
9	1.6498	59	1.6864	109	1.5236	159	1.7026	209	1.5803
10	1.6827	60	1.7483	110	1.6324	160	1.4117	210	1.7001
11	1.7384	61	1.6	111	1.5396	161	1.5357	211	1.7405
12	1.6025	62	1.5784	112	1.7593	162	1.7597	212	1.5408
13	1.675	63	1.7155	113	1.7166	163	1.4985	213	1.6893
14	1.7277	64	1.7802	114	1.9037	164	1.7472	214	1.6767
15	1.5935	65	1.4621	115	1.5916	165	1.5866	215	1.645
16	1.6862	66	1.6635	116	1.5769	166	1.503	216	1.699
17	1.677	67	2.0422	117	1.6779	167	1.5096	217	1.4828
18	1.5645	68	1.6567	118	1.4086	168	1.7144	218	1.5196
19	1.628	69	1.6401	119	1.6618	169	1.6068	219	1.648
20	1.5118	70	1.6482	120	1.5522	170	1.5814	220	1.4307
21	1.5064	71	1.5992	121	1.513	171	1.7013	221	1.6355
22	1.5174	72	1.661	122	1.4891	172	1.4274	222	1.5832
23	1.5579	73	1.5675	123	1.8018	173	1.5811	223	1.575
24	1.421	74	1.4422	124	1.7385	174	1.6338	224	1.6522
25	1.6848	75	1.5789	125	1.5907	175	1.574	225	1.6726
26	1.6253	76	1.4909	126	1.675	176	1.5789	226	1.7577
27	1.6411	77	1.8258	127	1.454	177	1.5466	227	1.6189
28	1.6538	78	1.7584	128	1.6029	178	1.6246	228	1.4798
29	1.785	79	1.7217	129	1.6718	179	1.7816	229	1.6139
30	1.7898	80	1.4216	130	1.7658	180	1.5186	230	1.4977
31	1.7373	81	1.9315	131	1.6679	181	1.7761	231	1.5718
32	1.4704	82	1.5798	132	1.6888	182	1.6756	232	1.5348
33	1.9045	83	1.6968	133	1.6312	183	1.6665	233	1.6728
34	1.658	84	1.668	134	1.5863	184	1.5189	234	1.5631
35	1.508	85	1.5392	135	1.594	185	1.6815	235	1.7644
36	1.8554	86	1.6263	136	1.6119	186	1.5583	236	1.7242
37	1.6612	87	1.6254	137	1.7022	187	1.7676	237	1.5859
38	1.4676	88	1.7609	138	1.5439	188	1.5971	238	1.6017
39	1.697	89	1.6202	139	1.709	189	1.7429	239	1.9097
40	1.6643	90	1.4465	140	1.5712	190	1.613	240	1.4798
41	1.89	91	1.5901	141	1.5552	191	1.6324	241	1.4977
42	1.6462	92	1.6425	142	1.7301	192	1.5353	242	1.6515
43	1.7058	93	1.6677	143	1.6843	193	1.6358	243	1.4956
44	1.5145	94	1.7051	144	1.8977	194	1.5942	244	1.5056
45	1.5815	95	1.6029	145	1.7105	195	1.6784	245	1.6478
46	1.6371	96	1.7361	146	1.5453	196	1.6519	246	1.6385
47	1.5662	97	1.6005	147	1.6232	197	1.4463	247	1.6111
48	1.3981	98	1.6701	148	1.6015	198	1.7632	248	1.5346
49	1.6627	99	1.6363	149	1.6205	199	1.7877	249	1.733
50	1.549	100	1.5502	150	1.504	200	1.4439	250	1.5136

**Table A.14** Raw CRTE\_ID data of Dn tab that are produced with Proposed meth

In determining whether there is a significant difference in CRTE\_ID of Dn tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for CRTE\_ID of Dn tab as followings;

$H_0$  : Assume there is no difference in CRTE\_ID of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_ID of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response	FHID_Dn			
Factors	Methods			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
9.78E-02	0.107606	0.119564	250	New
9.42E-02	0.103645	0.115163	250	Old

F-Test (normal distribution)

Test Statistic: 1.078

P-Value : 0.554

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_ID on Dn tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for CRTE\_ID of Dn tab as followings;

$H_0$  : Assume there is no difference in CRTE\_ID of Dn tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_ID of Dn tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for CRTE\_ID\_Old\_Dn vs CRTE\_ID\_New\_Dn

	N	Mean	StDev	SE Mean
CRTE_ID_Old	250	1.632	0.104	0.0066
CRTE_ID_New	250	1.628	0.108	0.0068

95% CI for  $\mu$  CRTE\_ID\_Old -  $\mu$  CRTE\_ID\_New: (-0.0152, 0.0219)

T-Test  $\mu$  CRTE\_ID\_Old =  $\mu$  CRTE\_ID\_New(vs not =): T = 0.36 P = 0.72

DF = 498

Both use Pooled StDev = 0.106

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_ID on Dn tab between both populations' means.



**CRTE OD Dn Current Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.7552	51	1.6035	101	1.5208	151	1.5307	201	1.5887
2	1.5876	52	1.5906	102	1.5538	152	1.5341	202	1.4588
3	1.7377	53	1.5882	103	1.5412	153	1.5611	203	1.6355
4	1.902	54	1.6028	104	1.4515	154	1.7203	204	1.6321
5	1.5503	55	1.6605	105	1.6291	155	1.6165	205	1.5549
6	1.6624	56	1.5627	106	1.4887	156	1.7077	206	1.5384
7	1.6876	57	1.5922	107	1.6195	157	1.7753	207	1.5469
8	1.5606	58	1.8576	108	1.693	158	1.4211	208	1.5171
9	1.7311	59	1.5787	109	1.6457	159	1.6519	209	1.6686
10	1.6319	60	1.6455	110	1.7056	160	1.7424	210	1.4718
11	1.5675	61	1.6822	111	1.7034	161	1.6047	211	1.709
12	1.4907	62	1.7233	112	1.5878	162	1.5232	212	1.622
13	1.4097	63	1.5194	113	1.6446	163	1.5653	213	1.6949
14	1.6286	64	1.5481	114	1.7314	164	1.6029	214	1.6319
15	1.7382	65	1.5893	115	1.598	165	1.6671	215	1.5668
16	1.4832	66	1.6673	116	1.5143	166	1.883	216	1.6162
17	1.5304	67	1.7123	117	1.7559	167	1.4183	217	1.5198
18	1.4793	68	1.4884	118	1.6109	168	1.4469	218	1.5924
19	1.7828	69	1.6569	119	1.5649	169	1.6317	219	1.6364
20	1.6686	70	1.6564	120	1.5886	170	1.7538	220	1.6423
21	1.7131	71	1.8423	121	1.7149	171	1.6098	221	1.6028
22	1.7454	72	1.3374	122	1.4769	172	1.7604	222	1.6009
23	1.498	73	1.7364	123	1.7317	173	1.6086	223	1.4565
24	1.4583	74	1.6243	124	1.6402	174	1.7598	224	1.6755
25	1.611	75	1.5713	125	1.5784	175	1.6483	225	1.4841
26	1.646	76	1.4952	126	1.7391	176	1.5874	226	1.5025
27	1.7348	77	1.5272	127	1.5912	177	1.673	227	1.6618
28	1.593	78	1.6384	128	1.4801	178	1.931	228	1.6593
29	1.5259	79	1.5336	129	1.6138	179	1.5859	229	1.5996
30	1.7549	80	1.5731	130	1.4338	180	1.7325	230	1.6121
31	1.5677	81	1.6245	131	1.7525	181	1.4178	231	1.5915
32	1.4777	82	1.51	132	1.6271	182	1.3479	232	1.4139
33	1.3815	83	1.5721	133	1.4211	183	1.5556	233	1.4332
34	1.6518	84	1.6609	134	1.5511	184	1.4818	234	1.6538
35	1.6228	85	1.5105	135	1.6746	185	1.637	235	1.4211
36	1.4406	86	1.5748	136	1.5074	186	1.575	236	1.4935
37	1.7633	87	1.5109	137	1.6212	187	1.7687	237	1.7627
38	1.7567	88	1.5328	138	1.5666	188	1.6118	238	1.5197
39	1.5244	89	1.6374	139	1.5793	189	1.5012	239	1.4582
40	1.6571	90	1.3703	140	1.4531	190	1.472	240	1.4559
41	1.7265	91	1.6768	141	1.605	191	1.6865	241	1.7433
42	1.5756	92	1.4394	142	1.654	192	1.5598	242	1.6625
43	1.5705	93	1.6125	143	1.567	193	1.5444	243	1.5131
44	1.7454	94	1.3828	144	1.5748	194	1.7001	244	1.7094
45	1.5359	95	1.6729	145	1.6714	195	1.6426	245	1.6646
46	1.5163	96	1.5852	146	1.5418	196	1.5809	246	1.5663
47	1.6565	97	1.7457	147	2.0417	197	1.4752	247	1.5473
48	1.6088	98	1.4504	148	1.6191	198	1.4933	248	1.5908
49	1.4842	99	1.6	149	1.6528	199	1.4973	249	1.5913
50	1.7849	100	1.6927	150	1.6008	200	1.5169	250	1.5693

**Table A.15** Raw CRTE\_OD data of Dn tab that are produced with Current method.

**CRTE OD Dn New Method**

No.	FLY	No.	FLY	No.	FLY	No.	FLY	No.	FLY
1	1.4317	51	1.7261	101	1.7195	151	1.5307	201	1.4583
2	1.4985	52	1.8496	102	1.7395	152	1.4266	202	1.5017
3	1.4574	53	1.5283	103	1.6082	153	1.7187	203	1.588
4	1.6286	54	1.5935	104	1.6875	154	1.6695	204	1.4727
5	1.7368	55	1.4097	105	1.5973	155	1.5995	205	1.5445
6	1.5885	56	1.6229	106	1.5817	156	1.5931	206	1.6541
7	1.6932	57	1.4884	107	1.5193	157	1.6369	207	1.6116
8	1.6177	58	1.5675	108	1.5679	158	1.7463	208	1.6941
9	1.622	59	1.6612	109	1.4978	159	1.679	209	1.5548
10	1.6556	60	1.7224	110	1.6061	160	1.3872	210	1.6728
11	1.7085	61	1.5726	111	1.5124	161	1.5109	211	1.7151
12	1.5772	62	1.5499	112	1.728	162	1.7288	212	1.515
13	1.6486	63	1.6891	113	1.6891	163	1.4698	213	1.6655
14	1.7002	64	1.7495	114	1.8793	164	1.7197	214	1.6503
15	1.5665	65	1.4327	115	1.5647	165	1.5602	215	1.6187
16	1.6608	66	1.6374	116	1.5468	166	1.4752	216	1.6702
17	1.6503	67	2.006	117	1.653	167	1.4812	217	1.4568
18	1.5385	68	1.6306	118	1.3805	168	1.6862	218	1.4973
19	1.6012	69	1.6151	119	1.6357	169	1.5823	219	1.6194
20	1.4821	70	1.6198	120	1.526	170	1.5556	220	1.4089
21	1.4807	71	1.5725	121	1.485	171	1.6747	221	1.6081
22	1.4932	72	1.6341	122	1.4647	172	1.4034	222	1.5577
23	1.5314	73	1.5403	123	1.7694	173	1.5555	223	1.5454
24	1.3912	74	1.4095	124	1.7129	174	1.6071	224	1.6266
25	1.6603	75	1.5515	125	1.5638	175	1.5438	225	1.6451
26	1.5988	76	1.4668	126	1.6468	176	1.5524	226	1.7276
27	1.6162	77	1.8082	127	1.4325	177	1.519	227	1.5897
28	1.6268	78	1.7278	128	1.5775	178	1.5984	228	1.448
29	1.7602	79	1.6969	129	1.6424	179	1.7498	229	1.5872
30	1.7694	80	1.3923	130	1.7421	180	1.495	230	1.4681
31	1.7076	81	1.9139	131	1.6404	181	1.7494	231	1.5416
32	1.4446	82	1.5539	132	1.6634	182	1.65	232	1.5054
33	1.8811	83	1.6671	133	1.6041	183	1.6396	233	1.6461
34	1.6315	84	1.6405	134	1.5591	184	1.4966	234	1.5368
35	1.4812	85	1.5119	135	1.5668	185	1.6554	235	1.7415
36	1.8192	86	1.6009	136	1.5854	186	1.5319	236	1.6969
37	1.6343	87	1.5993	137	1.6759	187	1.7434	237	1.559
38	1.4362	88	1.7362	138	1.5154	188	1.5705	238	1.576
39	1.6677	89	1.5905	139	1.6812	189	1.7195	239	1.8817
40	1.638	90	1.4245	140	1.5411	190	1.5855	240	1.451
41	1.8576	91	1.5625	141	1.5306	191	1.6056	241	1.4697
42	1.6189	92	1.6162	142	1.7036	192	1.5069	242	1.6235
43	1.6804	93	1.6402	143	1.6601	193	1.6084	243	1.4681
44	1.4862	94	1.68	144	1.8659	194	1.5673	244	1.4779
45	1.5562	95	1.5779	145	1.6814	195	1.654	245	1.619
46	1.6114	96	1.7061	146	1.5176	196	1.6245	246	1.612
47	1.5398	97	1.5731	147	1.594	197	1.4162	247	1.5828
48	1.3724	98	1.6421	148	1.5748	198	1.7379	248	1.5049
49	1.6366	99	1.611	149	1.5923	199	1.7684	249	1.7044
50	1.522	100	1.5228	150	1.4752	200	1.4125	250	1.4858

**Table A.16** Raw CRTE\_OD data of Dn tab that are produced with Proposed method.

In determining whether there is a significant difference in CRTE\_OD of Dn tab between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for CRTE\_OD of Dn tab as followings;

H<sub>0</sub> : Assume there is no difference in CRTE\_OD of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

H<sub>a</sub> : Assume there is significant difference in CRTE\_OD of Dn tab between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response	FHOD_Dn			
Factors	Methods			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
9.79E-02	0.107771	0.119747	250	New
9.75E-02	0.107304	0.119229	250	Old
F-Test (normal distribution)				
Test Statistic: 1.009				
P-Value : 0.946				

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_OD on Dn tab between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for CRTE\_OD of Dn tab as followings;

$H_0$  : Assume there is no difference in CRTE\_OD of Dn tab between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in CRTE\_OD of Dn tab between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for CRTE\_OD\_Old\_Dn vs CRTE\_OD\_New\_Dn

	N	Mean	StDev	SE Mean
CRTE_OD_Old	250	1.602	0.107	0.0068
CRTE_OD_New	250	1.601	0.108	0.0068

95% CI for  $\mu$  CRTE\_OD\_Old -  $\mu$  CRTE\_OD\_New: (-0.0182, 0.0196)

T-Test  $\mu$  CRTE\_OD\_Old =  $\mu$  CRTE\_OD\_New (vs not =): T = 0.07 P = 0.94

DF = 498

Both use Pooled StDev = 0.108

Reviewing P-value that is above 0.05, there is not significant difference in CRTE\_OD on Dn tab between both populations' means.

**Current Method**

No.	Shear Test	No.	Shear Test
1	380	36	230
2	350	37	390
3	380	38	390
4	455	39	270
5	280	40	345
6	345	41	375
7	355	42	350
8	295	43	290
9	370	44	380
10	330	45	285
11	295	46	270
12	250	47	340
13	220	48	325
14	325	49	250
15	380	50	410
16	250	51	310
17	285	52	315
18	250	53	350
19	395	54	315
20	350	55	340
21	375	56	290
22	380	57	310
23	260	58	440
24	240	59	300
25	325	60	335
26	335	61	355
27	370	62	375
28	315	63	275
29	270	64	285
30	380	65	315
31	295	66	350
32	255	67	360
33	215	68	250
34	330	69	340
35	325	70	345

**Proposed Method**

No.	Shear Test	No.	Shear Test
1	430	36	250
2	325	37	325
3	380	38	360
4	320	39	330
5	290	40	365
6	260	41	360
7	275	42	300
8	330	43	335
9	285	44	370
10	350	45	310
11	320	46	275
12	260	47	385
13	300	48	325
14	345	49	290
15	260	50	310
16	350	51	370
17	260	52	335
18	285	53	375
19	330	54	330
20	250	55	350
21	355	56	380
22	235	57	310
23	320	58	255
24	220	59	325
25	350	60	315
26	300	61	380
27	380	62	320
28	245	63	220
29	315	64	355
30	365	65	350
31	275	66	265
32	280	67	325
33	280	68	290
34	245	69	300
35	325	70	245

**Table A.17** Raw Shear test data that are produced with Current Method vs Proposed method.

In determining whether there is a significant difference in Shear Strength between the two populations' variances. The test begins by specifying Null Hypothesis and alternative hypothesis for Shear strength as followings;

$H_0$  : Assume there is no difference in Shear strength between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in Shear strength between population standard deviation of New Gimbal bond method and Current Gimbal bond Method.

### Homogeneity of Variance

Response	Shear			
Factors	Method			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
38.3368	45.6800	56.3233	70	New
44.0651	52.5056	64.7391	70	Old
F-Test (normal distribution)				
Test Statistic: 1.321				
P-Value : 0.250				

Reviewing P-value that is above 0.05, there is not significant difference in Shear strength between both populations' variances.

As same as the Hypothesis testing of standard deviation, In order to know whether there is a significant difference between two populations' means, the test begins by specifying Null hypothesis and alternative hypothesis for Shear strength as followings;

$H_0$  : Assume there is no difference in Shear strength between population means of New Gimbal bond method and Current Gimbal bond Method.

$H_a$  : Assume there is significant difference in Shear strength between population means of New Gimbal bond method and Current Gimbal bond.

### Two Sample T-Test and Confidence Interval

Two sample T for Old vs New

	N	Mean	StDev	SE Mean
Old	70	323.8	52.5	6.3
New	70	314.0	45.7	5.5

95% CI for  $\mu$  Old -  $\mu$  New: (-6.7, 26.2)

T-Test  $\mu$  Old =  $\mu$  New (vs not =): T = 1.18 P = 0.24 DF = 138

Both use Pooled StDev = 49.2

Reviewing P-value that is above 0.05, there is not significant difference in Shear strength between both populations' means.

## Summarized Result of Testing:

### Homogeneity of Variance

By applying the statistical test, Homogeneity of variance test, to all evaluation factors of both groups, current gimbal bond method and proposed gimbal bond method, the result of Homogeneity of variance test are summarized and shown in TableA.18

Factors	F-Test	P-Value	Result
RSA_UP	1.160	0.241	Not Significant
RSA_DN	1.090	0.499	Not Significant
PSA_UP	1.037	0.775	Not Significant
PSA_DN	1.045	0.730	Not Significant
FHID_UP	1.077	0.559	Not Significant
FHID_DN	1.078	0.554	Not Significant
FHOD_UP	1.008	0.949	Not Significant
FHOD_DN	1.009	0.946	Not Significant
Shear Test	1.321	0.250	Not Significant

**Table A.18** Summarized Results of Homogeneity of variance test.

Decision making on the results is performed on P-Value of each evaluation factor. For Hypothesis testing, the Confidential Interval of each factor was set at 95% (0.95). Therefore, P-Value of Homogeneity of variance test of each evaluation factor will be compared to 0.05 that is shown that difference is out of 95% Confidential Interval. From review each P-Value of each test of each factor, all of them are above 0.05. The result of F-Test of each evaluation factor shows that H0 are accepted while Ha are rejected. This implies there are **no significant difference** between two populations' variances of each evaluation factors. The statistical testing results conclude that the proposed gimbal bond method does not impact to *variances* of current HGA performances.



## Two Sample T-Test

By applying the same statistical test to all evaluation factors of both groups, current gimbal bond method and proposed gimbal bond method, the result of T-Tests are summarized and shown in TableA.19.

Factors	T-Test	P-Value	Result
RSA_UP	0.370	0.710	Not Significant
RSA_DN	-0.780	0.440	Not Significant
PSA_UP	-1.300	0.200	Not Significant
PSA_DN	-0.970	0.330	Not Significant
FHID_UP	0.350	0.730	Not Significant
FHID_DN	0.360	0.720	Not Significant
FHOD_UP	0.070	0.940	Not Significant
FHOD_DN	0.070	0.940	Not Significant
Shear Test	1.180	0.240	Not Significant

**Table A.19** Summarized Results of two samples T-test.

Decision making on the results is performed on P-Value of each evaluation factor. For Hypothesis testing, the Confidential Interval of each factor was set at 95% (0.95). Therefore, P-Value of Two samples T-Test of each evaluation factor will be compared to 0.05 that is shown that difference is out of 95% Confidential Interval. From review each P-Value of each test of each factor, all of them are above 0.05. The result of T-Test of each evaluation factor shows that H<sub>0</sub> are accepted while H<sub>a</sub> are rejected. This implies there are **no significant difference** between two populations' means of each evaluation factors. The statistical testing results conclude that the proposed gimbal bond method does not impact to *means* of current HGA performances.

## **APPENDIX B**

Raw data and Statistical Test to determine whether there is a significant difference in Gramload between HGAs with tack tail and HGAs without tack tail.

Gramload is one factor that needs to be evaluated for this proposal. Autogrammer is a machine or tester to adjust gramload of HGA to target limits before fly and electrical testing on HGA process. Every single HGA will be first measured gramload (called Gram\_In) and compared to  $2.5 \pm 0.10$  grams called target limits. Any HGA gramload is out target limits, that part will be adjusted by autogrammer. Any HGA gramload is between target limits, such HGA will be passed to next operation. The measurement and adjustment process may be repeated from 1 to 9 times (depend on gramload after adjustment). Final measurement at tenth will be last and compared to HGA gramload spec at  $2.5 + 0.4$  grams called gramload specs, any HGA gramload is out of HGA gramload specs will be scrapped.

Gramload data was collected from 250 pairs HGAs per group. Moreover gramload of 250 pairs of incoming flexures were measured to study effect of operation to gramload (Gram\_In).

Gramload data were collected and were analyzed through ANOVA in Minitab Software. This analysis is to study difference in mean and standard deviation among raw flexure, HGA with tack tail, and HGA without tack tail.

**Raw Flexure Up**

NO	Gram	NO	Gram	NO	Gram	NO	Gram	NO	Gram
1	2.52	51	2.49	101	2.44	151	2.5	201	2.55
2	2.48	52	2.48	102	2.5	152	2.62	202	2.57
3	2.57	53	2.47	103	2.51	153	2.61	203	2.51
4	2.37	54	2.39	104	2.44	154	2.56	204	2.51
5	2.47	55	2.53	105	2.47	155	2.53	205	2.64
6	2.41	56	2.58	106	2.5	156	2.45	206	2.46
7	2.57	57	2.56	107	2.45	157	2.55	207	2.49
8	2.47	58	2.52	108	2.43	158	2.5	208	2.54
9	2.51	59	2.49	109	2.47	159	2.56	209	2.51
10	2.36	60	2.42	110	2.53	160	2.46	210	2.53
11	2.42	61	2.47	111	2.59	161	2.5	211	2.51
12	2.46	62	2.56	112	2.53	162	2.51	212	2.58
13	2.54	63	2.51	113	2.42	163	2.47	213	2.47
14	2.4	64	2.49	114	2.54	164	2.43	214	2.46
15	2.47	65	2.42	115	2.46	165	2.37	215	2.47
16	2.62	66	2.6	116	2.47	166	2.47	216	2.48
17	2.42	67	2.44	117	2.47	167	2.48	217	2.52
18	2.43	68	2.47	118	2.51	168	2.48	218	2.45
19	2.52	69	2.57	119	2.52	169	2.41	219	2.47
20	2.46	70	2.46	120	2.49	170	2.62	220	2.54
21	2.54	71	2.44	121	2.51	171	2.5	221	2.51
22	2.57	72	2.53	122	2.51	172	2.54	222	2.47
23	2.48	73	2.49	123	2.55	173	2.5	223	2.61
24	2.5	74	2.49	124	2.57	174	2.51	224	2.48
25	2.52	75	2.49	125	2.55	175	2.43	225	2.43
26	2.42	76	2.49	126	2.55	176	2.53	226	2.52
27	2.55	77	2.53	127	2.53	177	2.58	227	2.52
28	2.49	78	2.57	128	2.52	178	2.57	228	2.38
29	2.53	79	2.53	129	2.48	179	2.57	229	2.41
30	2.45	80	2.42	130	2.58	180	2.55	230	2.48
31	2.4	81	2.58	131	2.45	181	2.5	231	2.53
32	2.6	82	2.5	132	2.51	182	2.52	232	2.5
33	2.51	83	2.57	133	2.49	183	2.55	233	2.49
34	2.63	84	2.48	134	2.56	184	2.55	234	2.51
35	2.48	85	2.51	135	2.51	185	2.43	235	2.39
36	2.5	86	2.45	136	2.57	186	2.56	236	2.45
37	2.5	87	2.47	137	2.6	187	2.46	237	2.49
38	2.48	88	2.49	138	2.5	188	2.52	238	2.52
39	2.46	89	2.53	139	2.54	189	2.54	239	2.45
40	2.5	90	2.52	140	2.45	190	2.42	240	2.55
41	2.48	91	2.58	141	2.52	191	2.43	241	2.48
42	2.56	92	2.52	142	2.53	192	2.59	242	2.43
43	2.53	93	2.58	143	2.46	193	2.49	243	2.48
44	2.59	94	2.56	144	2.5	194	2.57	244	2.5
45	2.41	95	2.45	145	2.44	195	2.6	245	2.4
46	2.49	96	2.5	146	2.52	196	2.5	246	2.45
47	2.57	97	2.54	147	2.48	197	2.46	247	2.46
48	2.6	98	2.46	148	2.53	198	2.48	248	2.51
49	2.5	99	2.51	149	2.46	199	2.55	249	2.4
50	2.57	100	2.45	150	2.53	200	2.54	250	2.47

**Table B.1** Raw gramload data of incoming flexure on Up tab.

**Current Process Up**

NO	Gram	NO	Gram	NO	Gram	NO	Gram	NO	Gram
1	2.63	51	2.59	101	2.55	151	2.59	201	2.66
2	2.59	52	2.59	102	2.61	152	2.73	202	2.68
3	2.68	53	2.58	103	2.62	153	2.72	203	2.62
4	2.48	54	2.5	104	2.55	154	2.67	204	2.62
5	2.5	55	2.64	105	2.58	155	2.64	205	2.75
6	2.52	56	2.69	106	2.53	156	2.56	206	2.57
7	2.68	57	2.67	107	2.56	157	2.66	207	2.72
8	2.58	58	2.63	108	2.54	158	2.61	208	2.65
9	2.74	59	2.53	109	2.58	159	2.67	209	2.62
10	2.47	60	2.53	110	2.64	160	2.57	210	2.64
11	2.53	61	2.58	111	2.7	161	2.52	211	2.52
12	2.57	62	2.67	112	2.64	162	2.62	212	2.69
13	2.65	63	2.62	113	2.53	163	2.58	213	2.58
14	2.51	64	2.6	114	2.65	164	2.54	214	2.57
15	2.58	65	2.53	115	2.57	165	2.48	215	2.58
16	2.73	66	2.71	116	2.58	166	2.58	216	2.59
17	2.53	67	2.55	117	2.58	167	2.61	217	2.63
18	2.54	68	2.58	118	2.62	168	2.59	218	2.56
19	2.63	69	2.68	119	2.63	169	2.52	219	2.58
20	2.57	70	2.57	120	2.6	170	2.73	220	2.65
21	2.65	71	2.55	121	2.62	171	2.61	221	2.35
22	2.68	72	2.64	122	2.62	172	2.65	222	2.58
23	2.48	73	2.6	123	2.66	173	2.79	223	2.72
24	2.47	74	2.52	124	2.68	174	2.62	224	2.59
25	2.63	75	2.6	125	2.66	175	2.54	225	2.54
26	2.43	76	2.73	126	2.66	176	2.64	226	2.63
27	2.66	77	2.64	127	2.64	177	2.69	227	2.63
28	2.46	78	2.68	128	2.63	178	2.68	228	2.49
29	2.64	79	2.64	129	2.59	179	2.68	229	2.52
30	2.56	80	2.74	130	2.69	180	2.66	230	2.59
31	2.51	81	2.69	131	2.56	181	2.61	231	2.4
32	2.71	82	2.77	132	2.76	182	2.63	232	2.42
33	2.59	83	2.68	133	2.6	183	2.66	233	2.6
34	2.74	84	2.59	134	2.67	184	2.66	234	2.62
35	2.59	85	2.62	135	2.77	185	2.54	235	2.5
36	2.61	86	2.56	136	2.68	186	2.67	236	2.56
37	2.75	87	2.58	137	2.71	187	2.57	237	2.6
38	2.59	88	2.62	138	2.47	188	2.63	238	2.63
39	2.57	89	2.64	139	2.65	189	2.65	239	2.56
40	2.77	90	2.63	140	2.56	190	2.71	240	2.66
41	2.59	91	2.69	141	2.75	191	2.54	241	2.59
42	2.67	92	2.76	142	2.64	192	2.7	242	2.54
43	2.64	93	2.69	143	2.57	193	2.6	243	2.47
44	2.7	94	2.67	144	2.61	194	2.68	244	2.61
45	2.52	95	2.56	145	2.55	195	2.71	245	2.51
46	2.7	96	2.73	146	2.63	196	2.61	246	2.56
47	2.68	97	2.65	147	2.59	197	2.57	247	2.57
48	2.71	98	2.57	148	2.64	198	2.59	248	2.62
49	2.61	99	2.62	149	2.57	199	2.66	249	2.51
50	2.68	100	2.56	150	2.64	200	2.65	250	2.61

**Table B.2** Raw gramload data of HGAs with tack tail on Up tab.

**No tack tail Up**

NO	Gram	NO	Gram	NO	Gram	NO	Gram	NO	Gram
1	2.54	51	2.43	101	2.53	151	2.5	201	2.52
2	2.44	52	2.49	102	2.56	152	2.44	202	2.52
3	2.47	53	2.5	103	2.39	153	2.45	203	2.43
4	2.48	54	2.633	104	2.41	154	2.51	204	2.5
5	2.53	55	2.55	105	2.45	155	2.53	205	2.47
6	2.53	56	2.52	106	2.4	156	2.51	206	2.48
7	2.5	57	2.51	107	2.42	157	2.55	207	2.52
8	2.5	58	2.45	108	2.47	158	2.52	208	2.36
9	2.51	59	2.55	109	2.58	159	2.53	209	2.5
10	2.61	60	2.52	110	2.51	160	2.65	210	2.37
11	2.51	61	2.44	111	2.5	161	2.48	211	2.45
12	2.36	62	2.62	112	2.58	162	2.43	212	2.48
13	2.43	63	2.61	113	2.57	163	2.55	213	2.49
14	2.65	64	2.56	114	2.47	164	2.56	214	2.46
15	2.47	65	2.52	115	2.51	165	2.46	215	2.57
16	2.55	66	2.57	116	2.61	166	2.45	216	2.5
17	2.48	67	2.41	117	2.5	167	2.37	217	2.55
18	2.54	68	2.53	118	2.52	168	2.49	218	2.57
19	2.48	69	2.48	119	2.52	169	2.49	219	2.53
20	2.56	70	2.54	120	2.41	170	2.54	220	2.58
21	2.49	71	2.45	121	2.48	171	2.49	221	2.47
22	2.54	72	2.38	122	2.5	172	2.44	222	2.6
23	2.46	73	2.46	123	2.58	173	2.48	223	2.49
24	2.43	74	2.54	124	2.44	174	2.46	224	2.5
25	2.49	75	2.59	125	2.49	175	2.47	225	2.46
26	2.43	76	2.57	126	2.48	176	2.42	226	2.47
27	2.44	77	2.53	127	2.5	177	2.46	227	2.49
28	2.46	78	2.52	128	2.54	178	2.4	228	2.48
29	2.53	79	2.54	129	2.42	179	2.49	229	2.39
30	2.59	80	2.49	130	2.6	180	2.54	230	2.46
31	2.49	81	2.41	131	2.5	181	2.44	231	2.51
32	2.57	82	2.47	132	2.35	182	2.42	232	2.49
33	2.47	83	2.45	133	2.45	183	2.44	233	2.48
34	2.57	84	2.42	134	2.61	184	2.47	234	2.46
35	2.58	85	2.53	135	2.5	185	2.42	235	2.52
36	2.45	86	2.53	136	2.56	186	2.45	236	2.46
37	2.52	87	2.48	137	2.52	187	2.39	237	2.47
38	2.46	88	2.47	138	2.6	188	2.5	238	2.51
39	2.46	89	2.64	139	2.47	189	2.44	239	2.57
40	2.45	90	2.43	140	2.5	190	2.41	240	2.45
41	2.4	91	2.52	141	2.59	191	2.5	241	2.58
42	2.46	92	2.49	142	2.6	192	2.51	242	2.56
43	2.56	93	2.43	143	2.56	193	2.43	243	2.44
44	2.51	94	2.55	144	2.49	194	2.48	244	2.47
45	2.44	95	2.63	145	2.49	195	2.57	245	2.54
46	2.55	96	2.49	146	2.53	196	2.45	246	2.48
47	2.54	97	2.41	147	2.54	197	2.54	247	2.52
48	2.51	98	2.48	148	2.53	198	2.43	248	2.51
49	2.55	99	2.51	149	2.54	199	2.51	249	2.58
50	2.44	100	2.52	150	2.47	200	2.42	250	2.57

**Table B.3** Raw gramload data of HGAs without tack tail on Up tab.

**Raw Flexure Dn**

NO	Gram	NO	Gram	NO	Gram	NO	Gram	NO	Gram
1	2.59	51	2.41	101	2.36	151	2.58	201	2.46
2	2.4	52	2.51	102	2.48	152	2.47	202	2.41
3	2.45	53	2.49	103	2.38	153	2.48	203	2.5
4	2.52	54	2.42	104	2.51	154	2.48	204	2.54
5	2.46	55	2.46	105	2.49	155	2.47	205	2.47
6	2.59	56	2.59	106	2.47	156	2.57	206	2.53
7	2.43	57	2.42	107	2.42	157	2.47	207	2.51
8	2.6	58	2.48	108	2.55	158	2.39	208	2.51
9	2.47	59	2.52	109	2.52	159	2.49	209	2.49
10	2.46	60	2.45	110	2.62	160	2.51	210	2.52
11	2.5	61	2.47	111	2.52	161	2.47	211	2.57
12	2.52	62	2.47	112	2.63	162	2.56	212	2.44
13	2.56	63	2.53	113	2.51	163	2.52	213	2.47
14	2.62	64	2.57	114	2.38	164	2.51	214	2.46
15	2.56	65	2.46	115	2.52	165	2.5	215	2.51
16	2.41	66	2.5	116	2.4	166	2.45	216	2.55
17	2.47	67	2.59	117	2.56	167	2.52	217	2.5
18	2.61	68	2.38	118	2.56	168	2.54	218	2.43
19	2.52	69	2.52	119	2.42	169	2.56	219	2.51
20	2.52	70	2.49	120	2.52	170	2.48	220	2.47
21	2.54	71	2.58	121	2.51	171	2.45	221	2.43
22	2.47	72	2.56	122	2.46	172	2.46	222	2.58
23	2.47	73	2.51	123	2.55	173	2.53	223	2.6
24	2.41	74	2.5	124	2.52	174	2.47	224	2.53
25	2.51	75	2.55	125	2.45	175	2.5	225	2.61
26	2.47	76	2.5	126	2.39	176	2.51	226	2.55
27	2.59	77	2.53	127	2.59	177	2.45	227	2.53
28	2.54	78	2.42	128	2.64	178	2.47	228	2.52
29	2.43	79	2.56	129	2.52	179	2.48	229	2.48
30	2.58	80	2.5	130	2.44	180	2.43	230	2.52
31	2.47	81	2.55	131	2.52	181	2.52	231	2.52
32	2.56	82	2.52	132	2.51	182	2.5	232	2.47
33	2.48	83	2.49	133	2.48	183	2.5	233	2.46
34	2.58	84	2.55	134	2.57	184	2.47	234	2.51
35	2.45	85	2.44	135	2.44	185	2.44	235	2.57
36	2.41	86	2.53	136	2.49	186	2.48	236	2.51
37	2.5	87	2.55	137	2.54	187	2.57	237	2.62
38	2.44	88	2.57	138	2.47	188	2.53	238	2.54
39	2.57	89	2.59	139	2.47	189	2.41	239	2.52
40	2.5	90	2.49	140	2.49	190	2.49	240	2.48
41	2.46	91	2.43	141	2.51	191	2.46	241	2.53
42	2.45	92	2.45	142	2.47	192	2.55	242	2.54
43	2.5	93	2.5	143	2.58	193	2.5	243	2.42
44	2.56	94	2.49	144	2.48	194	2.44	244	2.58
45	2.53	95	2.53	145	2.48	195	2.45	245	2.36
46	2.52	96	2.56	146	2.49	196	2.51	246	2.41
47	2.48	97	2.54	147	2.56	197	2.43	247	2.52
48	2.56	98	2.61	148	2.59	198	2.56	248	2.53
49	2.42	99	2.5	149	2.5	199	2.5	249	2.52
50	2.52	100	2.49	150	2.46	200	2.52	250	2.45

**Table B.4** Raw gramload data of incoming flexure on Dn tab.

**Current Process Dn**

NO	Gram	NO	Gram	NO	Gram	NO	Gram	NO	Gram
1	2.63	51	2.57	101	2.58	151	2.57	201	2.65
2	2.55	52	2.62	102	2.75	152	2.65	202	2.63
3	2.62	53	2.61	103	2.68	153	2.56	203	2.58
4	2.59	54	2.41	104	2.57	154	2.51	204	2.7
5	2.55	55	2.53	105	2.63	155	2.77	205	2.65
6	2.59	56	2.63	106	2.5	156	2.59	206	2.58
7	2.59	57	2.51	107	2.67	157	2.62	207	2.56
8	2.56	58	2.68	108	2.64	158	2.7	208	2.55
9	2.57	59	2.64	109	2.57	159	2.53	209	2.68
10	2.64	60	2.56	110	2.56	160	2.51	210	2.6
11	2.56	61	2.59	111	2.54	161	2.73	211	2.54
12	2.6	62	2.58	112	2.58	162	2.6	212	2.61
13	2.58	63	2.62	113	2.6	163	2.63	213	2.59
14	2.56	64	2.53	114	2.52	164	2.43	214	2.71
15	2.68	65	2.57	115	2.71	165	2.57	215	2.74
16	2.64	66	2.74	116	2.52	166	2.71	216	2.49
17	2.48	67	2.63	117	2.61	167	2.69	217	2.61
18	2.55	68	2.65	118	2.72	168	2.58	218	2.6
19	2.58	69	2.47	119	2.59	169	2.67	219	2.7
20	2.58	70	2.59	120	2.58	170	2.59	220	2.62
21	2.48	71	2.61	121	2.6	171	2.56	221	2.71
22	2.56	72	2.58	122	2.62	172	2.61	222	2.57
23	2.49	73	2.67	123	2.64	173	2.46	223	2.59
24	2.57	74	2.65	124	2.52	174	2.56	224	2.53
25	2.68	75	2.54	125	2.69	175	2.59	225	2.63
26	2.35	76	2.56	126	2.53	176	2.53	226	2.64
27	2.6	77	2.59	127	2.69	177	2.47	227	2.51
28	2.66	78	2.59	128	2.54	178	2.62	228	2.63
29	2.66	79	2.58	129	2.66	179	2.7	229	2.56
30	2.62	80	2.6	130	2.48	180	2.84	230	2.56
31	2.5	81	2.6	131	2.71	181	2.52	231	2.55
32	2.64	82	2.63	132	2.68	182	2.51	232	2.72
33	2.58	83	2.74	133	2.71	183	2.61	233	2.61
34	2.66	84	2.58	134	2.62	184	2.67	234	2.66
35	2.79	85	2.64	135	2.64	185	2.57	235	2.56
36	2.63	86	2.64	136	2.65	186	2.72	236	2.73
37	2.57	87	2.59	137	2.55	187	2.55	237	2.72
38	2.47	88	2.67	138	2.68	188	2.47	238	2.75
39	2.59	89	2.53	139	2.7	189	2.68	239	2.67
40	2.58	90	2.69	140	2.64	190	2.62	240	2.61
41	2.57	91	2.47	141	2.57	191	2.77	241	2.59
42	2.57	92	2.62	142	2.61	192	2.76	242	2.66
43	2.65	93	2.64	143	2.52	193	2.63	243	2.61
44	2.53	94	2.62	144	2.61	194	2.7	244	2.5
45	2.63	95	2.59	145	2.56	195	2.75	245	2.65
46	2.66	96	2.66	146	2.59	196	2.62	246	2.62
47	2.62	97	2.62	147	2.58	197	2.66	247	2.63
48	2.63	98	2.49	148	2.55	198	2.65	248	2.6
49	2.62	99	2.62	149	2.76	199	2.54	249	2.66
50	2.49	100	2.72	150	2.42	200	2.68	250	2.64

**Table B.5** Raw gramload data of HGAs with tack tail on Dn tab.



**No tack tail Dn**

NO	Gram	NO	Gram	NO	Gram	NO	Gram	NO	Gram
1	2.54	51	2.47	101	2.55	151	2.51	201	2.47
2	2.5	52	2.49	102	2.56	152	2.56	202	2.42
3	2.51	53	2.59	103	2.42	153	2.51	203	2.53
4	2.48	54	2.41	104	2.52	154	2.59	204	2.42
5	2.54	55	2.47	105	2.54	155	2.37	205	2.43
6	2.43	56	2.43	106	2.44	156	2.64	206	2.49
7	2.52	57	2.6	107	2.47	157	2.53	207	2.56
8	2.5	58	2.49	108	2.45	158	2.51	208	2.37
9	2.51	59	2.47	109	2.47	159	2.5	209	2.57
10	2.39	60	2.49	110	2.51	160	2.44	210	2.55
11	2.48	61	2.5	111	2.55	161	2.61	211	2.49
12	2.48	62	2.43	112	2.36	162	2.49	212	2.59
13	2.53	63	2.49	113	2.53	163	2.51	213	2.62
14	2.56	64	2.56	114	2.52	164	2.52	214	2.46
15	2.43	65	2.52	115	2.47	165	2.43	215	2.49
16	2.51	66	2.623	116	2.45	166	2.43	216	2.51
17	2.52	67	2.45	117	2.47	167	2.61	217	2.45
18	2.55	68	2.48	118	2.49	168	2.56	218	2.56
19	2.44	69	2.5	119	2.46	169	2.41	219	2.44
20	2.38	70	2.44	120	2.43	170	2.45	220	2.53
21	2.48	71	2.47	121	2.46	171	2.49	221	2.46
22	2.56	72	2.53	122	2.48	172	2.46	222	2.55
23	2.43	73	2.44	123	2.44	173	2.56	223	2.65
24	2.39	74	2.57	124	2.5	174	2.48	224	2.45
25	2.4	75	2.44	125	2.44	175	2.58	225	2.41
26	2.47	76	2.42	126	2.44	176	2.55	226	2.43
27	2.45	77	2.66	127	2.49	177	2.55	227	2.5
28	2.45	78	2.54	128	2.49	178	2.44	228	2.54
29	2.59	79	2.49	129	2.51	179	2.35	229	2.45
30	2.49	80	2.58	130	2.53	180	2.47	230	2.46
31	2.53	81	2.5	131	2.5	181	2.49	231	2.51
32	2.46	82	2.64	132	2.42	182	2.55	232	2.49
33	2.49	83	2.55	133	2.43	183	2.47	233	2.5
34	2.56	84	2.54	134	2.53	184	2.5	234	2.51
35	2.59	85	2.56	135	2.54	185	2.44	235	2.6
36	2.58	86	2.51	136	2.5	186	2.43	236	2.41
37	2.53	87	2.41	137	2.39	187	2.48	237	2.46
38	2.43	88	2.51	138	2.62	188	2.5	238	2.54
39	2.45	89	2.54	139	2.56	189	2.48	239	2.44
40	2.53	90	2.59	140	2.48	190	2.47	240	2.55
41	2.51	91	2.49	141	2.53	191	2.47	241	2.52
42	2.53	92	2.5	142	2.42	192	2.57	242	2.5
43	2.48	93	2.48	143	2.49	193	2.51	243	2.5
44	2.59	94	2.58	144	2.47	194	2.41	244	2.51
45	2.55	95	2.43	145	2.46	195	2.61	245	2.48
46	2.53	96	2.41	146	2.52	196	2.41	246	2.49
47	2.45	97	2.52	147	2.5	197	2.58	247	2.6
48	2.56	98	2.55	148	2.52	198	2.52	248	2.54
49	2.5	99	2.58	149	2.42	199	2.43	249	2.54
50	2.55	100	2.48	150	2.49	200	2.48	250	2.58

**Table B.6** Raw gramload data of HGAs without tack tail on Dn tab.

Gramload data are analyzed through Homogeneity of variance in Minitab Software. This analysis is to know there is a significant differences of populations' variances among raw flexure, HGA with tack tail, and HGA without tack tail.

### Homogeneity of Variance

Response	Gram_up			
Factors	OPTN_Up			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
5.28E-02	5.85E-02	6.54E-02	250	No_tack
4.91E-02	5.44E-02	6.09E-02	250	Raw
6.59E-02	7.30E-02	8.17E-02	250	Tack

Bartlett's Test (normal distribution)

Test Statistic: 24.119

P-Value : 0.000

Response	Gram_Dn			
Factors	OPTN_Dn			
ConfLvl	95.0000			
Lower	Sigma	Upper	N	Factor Levels
5.30E-02	5.87E-02	6.57E-02	250	No_tack
4.97E-02	5.51E-02	6.16E-02	250	Raw
6.66E-02	7.38E-02	8.26E-02	250	Tack

Bartlett's Test (normal distribution)

Test Statistic: 24.381

P-Value : 0.000

Gramload data are, further, analyzed through ANOVA in Minitab Software. This analysis is to study difference in mean and standard deviation among raw flexure, HGA with tack tail, and HGA without tack tail.

### One-way Analysis of Variance (ANOVA)

#### Analysis of Variance for Gram up

Source	DF	SS	MS	F	P
OPTN_Up	2	2.12779	1.06390	272.78	0.000
Error	747	2.91347	0.00390		
Total	749	5.04126			

#### Individual 95% CIs For Mean

#### Based on Pooled StDev

Level	N	Mean	StDev	-----+-----+-----+-----
No_tack	250	2.4976	0.0585	(-*-)
Raw	250	2.5017	0.0544	(-*-)
Tack	250	2.6126	0.0730	(-*-)
				-----+-----+-----+-----
Pooled StDev = 0.0625				2.520 2.560 2.600

**Analysis of Variance for Gram Dn**

Source	DF	SS	MS	F	P
OPTN_Dn	2	1.90929	0.95464	240.20	0.000
Error	747	2.96888	0.00397		
Total	749	4.87817			

Individual 95% CIs For Mean

Based on Pooled StDev

Level	N	Mean	StDev	
No_tack	250	2.4983	0.0587	(-*-)
Raw	250	2.5016	0.0551	(-*-)
Tack	250	2.6070	0.0738	(-*-)

Pooled StDev = 0.0630

-----+-----+-----+-----  
2.520 2.555 2.590

From ANOVA, Gramload show the result in same pattern. Analysis of Variance by considering P-Value of each test, the result shows that all P-Value are below 0.05. That means standard deviations of three groups are not equal. ***There is at least one group that its standard deviation does not equal to others.***

Considering individual 95% CIs for Mean, the results show that ***mean of control group (Including Tack tail) is significantly higher than other two groups.*** And its standard deviation is also significantly higher than other two groups. While Mean and standard deviation of Evaluation group shows no significantly different from raw flexure.

Gramload of Evaluation group was compared to gramload target that is set at 2.5 grams with T<sub>test</sub> of the mean in Minitab Software.

**T-Test of the Mean of Up tab**

Test of mu = 2.50000 vs mu not = 2.50000

Variable	N	Mean	StDev	SE Mean	T	P
New_Up	250	2.49757	0.05847	0.00370	-0.66	0.51

**T-Test of the Mean of Dn tab**

Test of mu = 2.50000 vs mu not = 2.50000

Variable	N	Mean	StDev	SE Mean	T	P
New_Dn	250	2.49833	0.05872	0.00371	-0.45	0.65

Consider from P-Value, they show that all P-Value are above 0.05. That is explained that *Gramload Mean of evaluation group is not significantly different from target*. In other word, it can be explain that gramload of evaluation group is in target and they are not needed to adjust many times. And this benefit may leads to sampling autogram.

## VITA

Sarun Tapananont was born on April 27, 1972 in Chantaburi, Thailand. He obtained his Bachelor's Degree in Industrial Engineering from Chulalongkorn University in 1993 academic year. He continued his graduate study in Engineering Management at the Regional Centre for Manufacturing System Engineering at the same University in 1996.

He has been working for Seagate Technology Company since 1994 as a process engineer. He is responsible for process monitoring and improvement.

