decision rule

2020-03-19

For the model:

$$Y_{ji} = S_{ji}(\beta_j + b_{ji} + \Gamma_j(\alpha' x_{ji})) + \epsilon_{ji},\ j \in \{1, 2\}$$

Parameter settings

I have tried different parameter settings.

Setting 1:

The fixed effect β:

	intercept	slope	concavity
Drug	18.6	-2.3	0.17
Placebo	18.6	-1.9	0.14

The fixed effect Γ:

	intercept	slope	concavity
Drug	0	1	0
Placebo	0	$\cos(\theta)$	$\sin(\theta)$

The random effect's covariance matrix:

	Drug				Placebo		
	intercept	slope	concavity		intercept	slope	concavity
intercept	8.869	2.766	-0.359	intercept	9.507	1.012	-0.093
slope	2.766	1.016	-0.104	slope	1.012	3.856	-0.395
concavity	-0.359	-0.104	1.5	concavity	-0.093	-0.395	1.5

Setting 2:

EMBARC's parameter

The random effect's covariance matrix:

	Drug				Placebo		
	intercept	slope	concavity		intercept	slope	concavity
intercept	8.869	2.766	-0.359	intercept	9.507	1.012	-0.093
slope	2.766	1.016	-0.104	slope	1.012	3.856	-0.395
concavity	-0.359	-0.104	0.015	concavity	-0.093	-0.395	0.045

Setting 3:

Make the intercept smaller

The fixed effect β:

	intercept	slope	concavity
Drug	1	-2.3	1.5
Placebo	1.1	-1.9	1

The fixed effect Γ:

	intercept	slope	concavity
Drug	0	1	0
Placebo	0	$\cos(\theta)$	$\sin(\theta)$

The random effect's covariance matrix:

	Drug				Placebo		
	intercept	slope	concavity		intercept	slope	concavity
intercept	4	0	0	intercept	4	1.732	1
slope	0	9	0	slope	1.732	1.75	0.433
concavity	0	0	1	concavity	1	0.433	1.25

Concordance proportion calculation

For the training dataset, we simulate $n = 100$ in each treatment group (200 subjects in total). The covariates are generated from $X \sim MVN(0, \Sigma)$, where

$$\Sigma_x = \begin{pmatrix} 1 & \rho & ... & \rho \\ \rho & 1 & ... & \rho \\ ... & ... & ... & ... \\ \rho & ... & \rho & 1 \end{pmatrix}_{p \times p}$$

The outcome Y is then generated from the model

$$Y_{ji} = S_{ji}(\beta_j + b_{ji} + \Gamma_j(\alpha' x_{ji})) + \epsilon_{ji}, \ j \in \{1, 2\}$$

For the testing dataset, $N = 1000$ subjects are generated. For each subjects, the outcome if he or she get treatment and the outcome if he or she get placebo are both generated.

For the testing dataset, since we have both outcomes, we know the treatment group assignment for each subject.

$$\text{group assignment} = \begin{cases} \text{Drug group} & \Delta Y_{pbo} > \Delta Y_{drg} \\ \text{Placebo group} & \Delta Y_{pbo} \leq \Delta Y_{drg} \end{cases}$$

To estimated the treatment assigment for the testing data, we tried two methods, longitudinal average slope methods and change score methods.

For the longitudinal average slope method, we used the ullback-Leibler divergence method to estimated $\hat{\alpha}$ and $\hat{\beta}_{drg}, \hat{\Gamma}_{drg}, \hat{\beta}_{pbo}, \hat{\Gamma}_{pbo}$. The the estimated fixed effects Z can be calculated as:

$$\hat{z}_{i,drg} = S[\hat{\beta}_{drg} + \hat{\Gamma}_{drg}\hat{\alpha}' x_i]$$

$$\hat{z}_{i,pbo} = S[\hat{\beta}_{pbo} + \hat{\Gamma}_{pbo}\hat{\alpha}' x_i]$$

Given that, the estimated group assignment can be calculated as

$$\text{estimated group assignment} = \begin{cases} \text{Drug group} & \Delta\hat{z}_{i,pbo} > \Delta\hat{z}_{i,drg} \\ \text{Placebo group} & \Delta\hat{z}_{i,pbo} \leq \Delta\hat{z}_{i,drg} \end{cases}$$

The concordance proportion is then calculated as

$$\frac{\sum_{i=1}^{N} I(\text{estimated group assignment} = \text{true group assignment})}{N}$$

p.s. previous I used $\hat{z}_{i,drg} = S[\beta_{drg} + \Gamma_{drg}\alpha' x_i]$ and $\Delta Y = \hat{z}_{7,drg} - \hat{z}_{1,drg}$ as the true group assignment rule for the longitudinal method, instead of the true ΔY in the testing dataset.

For the change score method, the change in outcome Y can be fitted with a linear regression with covariates X, i.e.

$$\Delta\hat{Y} = \hat{\gamma}_1 x_1 + ... + \hat{\gamma}_p x_p$$

where $\hat{\gamma}_i$ is estimated with the same model in training dataset. Then

$$\text{estimated group assignment} = \begin{cases} \text{Drug group} & \Delta\hat{Y}^{cs}_{pbo} > \Delta\hat{Y}^{cs}_{drg} \\ \text{Placebo group} & \Delta\hat{Y}^{cs}_{pbo} \leq \Delta\hat{Y}^{cs}_{drg} \end{cases}$$

The concordance proportion is then calculated as

$$\frac{\sum_{i=1}^{N} I(\text{estimated group assignment} = \text{true group assignment})}{N}$$

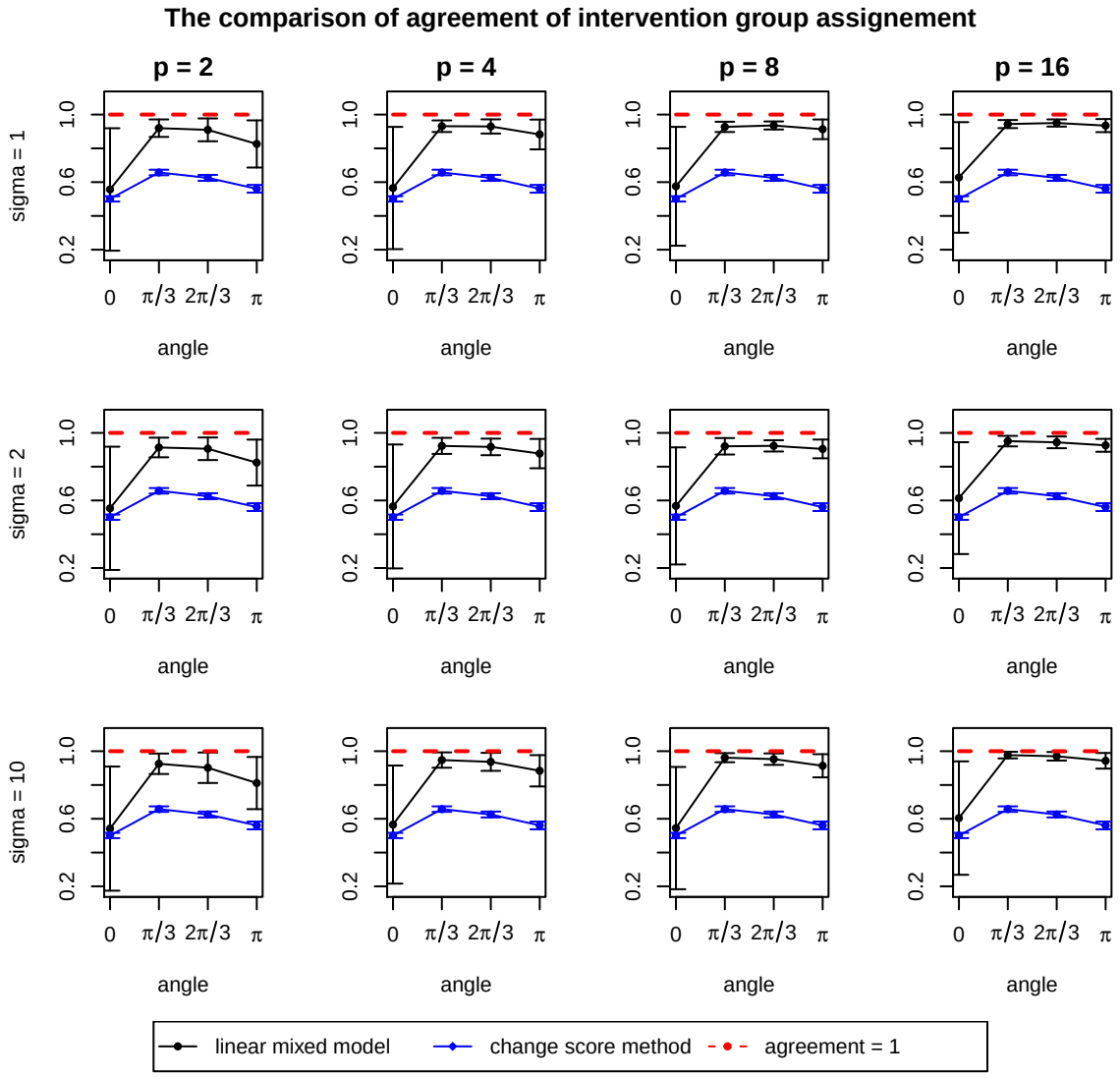
We would like to compare which method can achieve a higher concordance proportion.

Results

Setting 1

			Purity		Cosine similarity		Agreement	
Dimension	Sigma	Angle	Mean	SD	Mean	SD	Mean	SD
2	1	0	0.4941	0.2182	0.8520	0.2066	0.5566	0.3624
		60	1.5468	0.4369	0.9706	0.0465	0.9196	0.0517
		120	4.5609	1.0666	0.9857	0.0206	0.9096	0.0675
		180	7.4982	1.6440	0.9921	0.0120	0.8261	0.1396
	2	0	0.9088	1.0308	0.8660	0.1958	0.5534	0.3649
		60	2.5074	5.0316	0.9520	0.0889	0.9136	0.0581
		120	6.7709	12.5737	0.9744	0.0377	0.9060	0.0668
		180	10.6863	17.6086	0.9840	0.0228	0.8241	0.1362
	10	0	1020.8285	3945.5138	0.9550	0.1401	0.5417	0.3675
		60	1954.7484	9010.6063	0.9779	0.0839	0.9256	0.0605
		120	1817.5259	7761.0103	0.9652	0.1273	0.9020	0.0901
		180	3080.9066	11341.4179	0.9529	0.1168	0.8115	0.1544
4	1	0	0.5908	0.2283	0.8101	0.1722	0.5653	0.3618
		60	2.3377	0.5761	0.9303	0.0636	0.9312	0.0343
		120	7.5200	1.6407	0.9609	0.0323	0.9298	0.0419
		180	12.5537	2.5724	0.9766	0.0200	0.8822	0.0882
	2	0	1.5461	2.8809	0.8137	0.1863	0.5646	0.3668
		60	3.4636	3.0137	0.9041	0.1148	0.9230	0.0475
		120	12.0052	15.5890	0.9219	0.0907	0.9170	0.0490
		180	19.7302	28.1132	0.9546	0.0411	0.8775	0.0868
	10	0	545.7065	2666.8060	0.9899	0.0556	0.5656	0.3495
		60	1142.0264	7640.9531	0.9798	0.0733	0.9476	0.0455

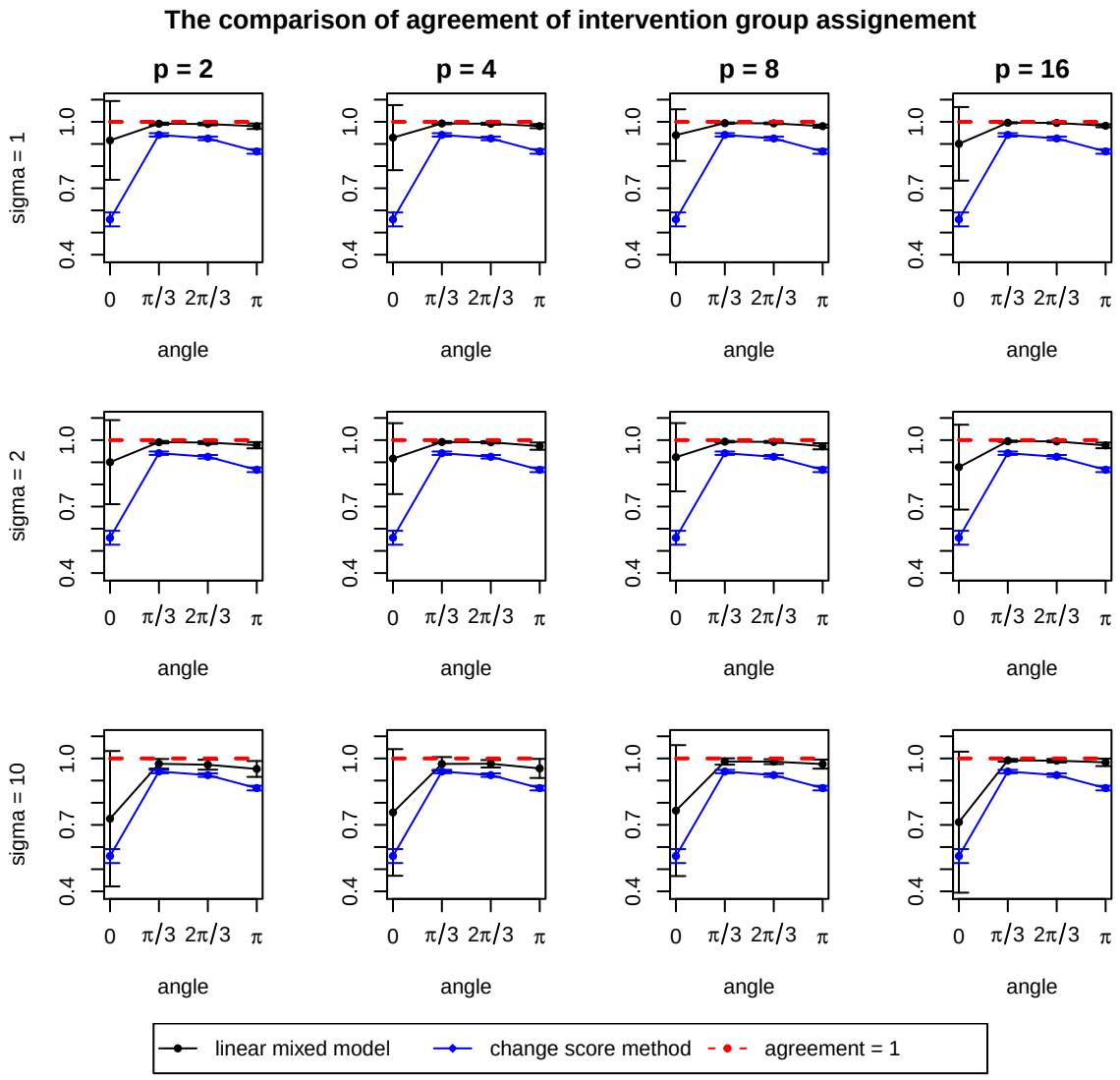
		120	2872.3701	11314.6790	0.9840	0.0663	0.9370	0.0533
		180	2046.5676	7963.4221	0.9824	0.0681	0.8841	0.0926
8	1	0	0.7183	0.3380	0.7003	0.1497	0.5754	0.3518
		60	3.6919	0.8491	0.8559	0.1040	0.9273	0.0304
		120	12.8547	3.1406	0.9146	0.0550	0.9356	0.0238
		180	22.4677	6.1550	0.9479	0.0287	0.9128	0.0582
	2	0	7.0189	51.6329	0.7575	0.1402	0.5678	0.3466
		60	10.3262	51.8376	0.8294	0.1548	0.9206	0.0487
		120	31.2540	130.1463	0.8571	0.1116	0.9231	0.0334
		180	421.0805	3841.9870	0.9085	0.0585	0.9050	0.0555
	10	0	1163.4518	5294.3756	0.9989	0.0055	0.5448	0.3619
		60	1369.4918	4853.7169	0.9930	0.0401	0.9616	0.0269
		120	4112.5607	13736.4404	0.9937	0.0405	0.9531	0.0339
		180	1732.4927	7971.6727	0.9959	0.0349	0.9138	0.0686
16	1	0	0.8735	0.3864	0.6842	0.1698	0.6279	0.3273
		60	6.9310	1.4942	0.8280	0.1028	0.9438	0.0239
		120	24.9727	5.2131	0.8904	0.0644	0.9502	0.0213
		180	44.4030	10.1076	0.9174	0.0457	0.9347	0.0386
	2	0	2.4095	3.9985	0.7778	0.1795	0.6137	0.3310
		60	8.8935	5.6064	0.8682	0.1402	0.9513	0.0311
		120	38.6863	33.9093	0.8640	0.1474	0.9441	0.0347
		180	77.4618	96.0817	0.8716	0.0911	0.9264	0.0381
	10	0	422.5353	1924.9107	0.9998	0.0002	0.6041	0.3358
		60	773.8957	3814.6546	0.9998	0.0002	0.9770	0.0196
		120	2098.7287	9566.4763	0.9998	0.0002	0.9700	0.0253
		180	1491.9371	8049.9292	0.9998	0.0002	0.9432	0.0463



Setting 2

			Purity		Cosine similarity		Agreement	
Dimension	Sigma	Angle	Mean	SD	Mean	SD	Mean	SD
2	1	0	1.5772	0.5836	0.9702	0.0426	0.9160	0.1778
		60	247.2797	50.7826	0.9995	0.0007	0.9913	0.0053
		120	191.9133	40.8291	0.9995	0.0007	0.9900	0.0060
		180	20.6900	3.2617	0.9976	0.0033	0.9800	0.0123
	2	0	879.4013	6369.8261	0.9638	0.0870	0.9005	0.1898
		60	518.4135	1293.5854	0.9994	0.0007	0.9907	0.0056
		120	616.8250	2544.6347	0.9993	0.0009	0.9891	0.0067
		180	60.8464	256.5212	0.9955	0.0084	0.9771	0.0142

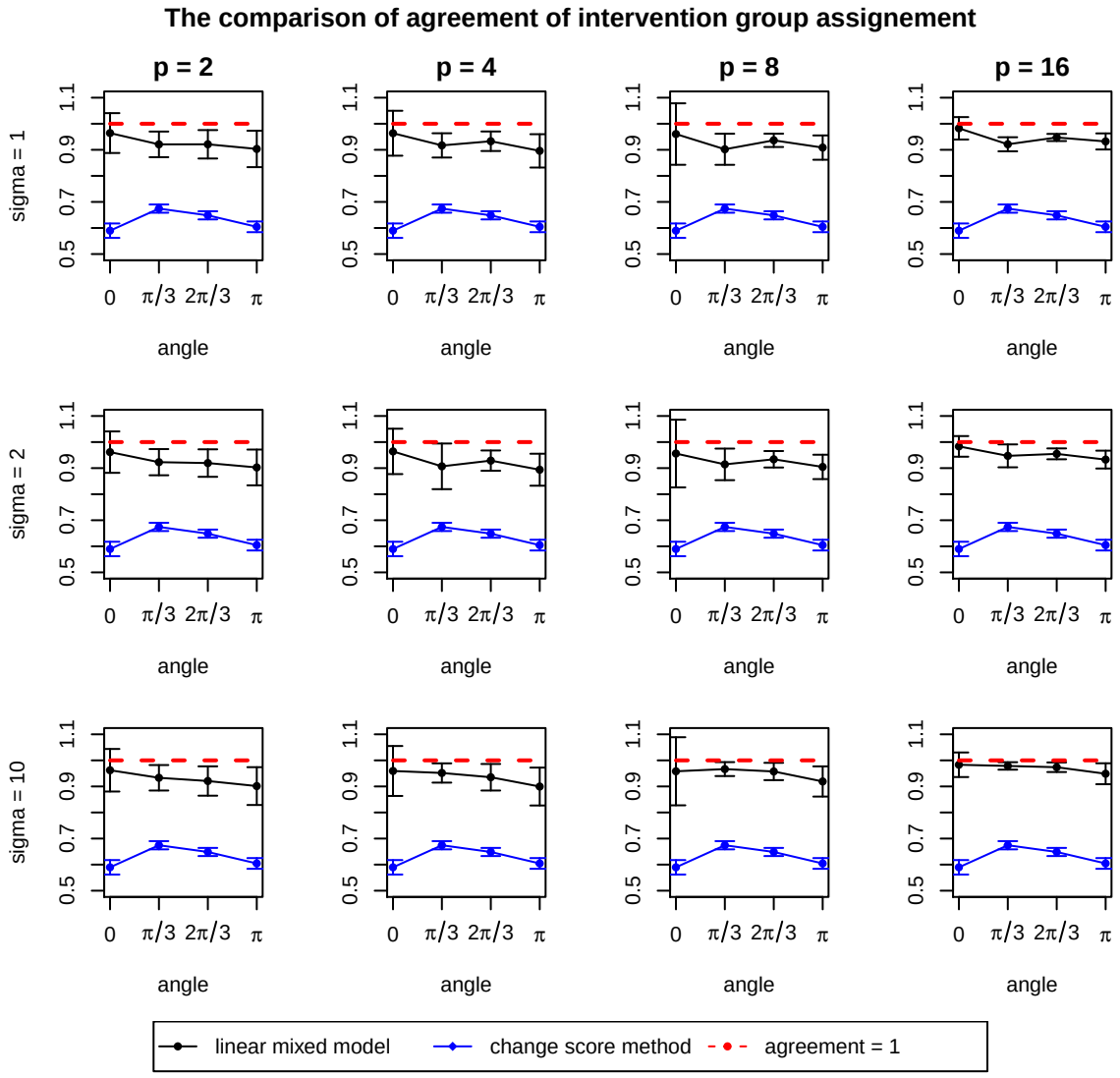
	10	0	4511.1242	15498.8996	0.9672	0.1184	0.7280	0.3057
		60	6811.5626	17095.2600	0.9917	0.0379	0.9759	0.0216
		120	4805.7298	14253.2210	0.9911	0.0382	0.9716	0.0224
		180	2397.9207	10464.8379	0.9843	0.0534	0.9526	0.0358
4	1	0	1.5910	0.5624	0.9243	0.1048	0.9285	0.1469
		60	405.4914	63.5055	0.9991	0.0006	0.9924	0.0036
		120	314.8149	50.2224	0.9990	0.0007	0.9913	0.0047
		180	33.5671	5.4529	0.9925	0.0067	0.9805	0.0093
	2	0	6.8261	29.4817	0.9153	0.1147	0.9164	0.1601
		60	1549.1616	5865.1312	0.9988	0.0010	0.9915	0.0042
		120	752.2896	2915.5866	0.9987	0.0011	0.9904	0.0051
		180	92.9996	321.0636	0.9822	0.0245	0.9729	0.0164
	10	0	7948.4350	20354.1703	0.9713	0.0896	0.7562	0.2859
		60	5621.4665	14339.6538	0.9799	0.0762	0.9753	0.0310
		120	7027.2184	15134.5024	0.9894	0.0250	0.9760	0.0168
		180	3836.7836	11960.5604	0.9657	0.0966	0.9550	0.0431
8	1	0	1.7436	0.6659	0.9046	0.1165	0.9400	0.1165
		60	780.5187	155.9886	0.9988	0.0007	0.9938	0.0033
		120	605.8159	125.4156	0.9987	0.0008	0.9930	0.0038
		180	62.6594	9.8145	0.9841	0.0097	0.9803	0.0070
	2	0	775.8581	7645.3834	0.9168	0.1123	0.9228	0.1540
		60	2206.8778	7694.7257	0.9984	0.0012	0.9931	0.0035
		120	1961.3569	5919.0847	0.9981	0.0013	0.9920	0.0043
		180	1076.1246	6614.0581	0.9670	0.0307	0.9722	0.0139
	10	0	7602.9954	20571.3544	0.9947	0.0344	0.7646	0.2955
		60	8424.6204	15303.8350	0.9913	0.0370	0.9862	0.0144
		120	3872.2562	6287.5508	0.9956	0.0134	0.9857	0.0111
		180	4967.3592	14827.8672	0.9877	0.0454	0.9745	0.0206
16	1	0	1.7547	0.6779	0.9443	0.0830	0.9006	0.1661
		60	1529.9761	297.9284	0.9989	0.0007	0.9956	0.0026
		120	1183.0168	224.7857	0.9986	0.0009	0.9949	0.0031
		180	122.8007	20.5727	0.9764	0.0122	0.9821	0.0068
	2	0	63.2273	528.4508	0.9453	0.0877	0.8780	0.1915
		60	4606.2175	12618.5773	0.9983	0.0013	0.9949	0.0032
		120	2379.9637	2809.5499	0.9977	0.0018	0.9942	0.0037
		180	670.2696	4592.1688	0.9525	0.0438	0.9762	0.0127
	10	0	7361.9942	19862.9779	0.9994	0.0040	0.7124	0.3183
		60	14852.4397	21270.1813	0.9976	0.0063	0.9916	0.0064
		120	11455.9901	19942.0523	0.9971	0.0081	0.9899	0.0080
		180	3835.6653	9336.8916	0.9950	0.0464	0.9824	0.0169



Setting 3

			Purity		Cosine similarity		Agreement	
Dimension	Sigma	Angle	Mean	SD	Mean	SD	Mean	SD
2	1	0	2.6131	0.9759	0.9629	0.0576	0.9642	0.0764
		60	4.1062	1.2375	0.9489	0.0856	0.9209	0.0492
		120	5.6561	1.6805	0.9849	0.0227	0.9211	0.0545
		180	5.0562	1.6149	0.9810	0.0316	0.9033	0.0698
	2	0	2.9668	2.1767	0.9409	0.0843	0.9614	0.0795
		60	4.4626	2.5513	0.9483	0.0859	0.9228	0.0502
		120	6.1751	3.3962	0.9781	0.0301	0.9194	0.0528
		180	5.5610	3.4237	0.9723	0.0412	0.9026	0.0687

	10	0	490.2517	3997.5421	0.9726	0.0861	0.9621	0.0817
		60	1511.9293	8407.6198	0.9832	0.0648	0.9332	0.0489
		120	1977.4778	10567.2261	0.9909	0.0244	0.9208	0.0563
		180	493.9024	3738.8173	0.9575	0.1220	0.9014	0.0725
4	1	0	3.0034	0.8487	0.9163	0.0706	0.9636	0.0862
		60	5.3294	1.1559	0.8700	0.1275	0.9169	0.0465
		120	8.0522	1.8684	0.9569	0.0331	0.9329	0.0375
		180	7.1907	1.8715	0.9530	0.0334	0.8959	0.0639
	2	0	3.5245	1.5636	0.8857	0.1013	0.9641	0.0871
		60	5.9353	2.1000	0.8506	0.1958	0.9068	0.0876
		120	9.2095	3.4897	0.9388	0.0549	0.9288	0.0389
		180	8.4028	3.7626	0.9300	0.0580	0.8939	0.0614
	10	0	1633.8166	9357.0301	0.9782	0.1078	0.9593	0.0959
		60	1740.0500	9491.5755	0.9909	0.0349	0.9517	0.0370
		120	2118.1459	6382.7453	0.9747	0.0880	0.9353	0.0509
		180	2960.4163	12064.4251	0.9759	0.0861	0.8996	0.0727
8	1	0	3.1261	0.9902	0.8018	0.0955	0.9604	0.1179
		60	7.1522	1.2583	0.7480	0.1743	0.9020	0.0596
		120	12.1406	2.5865	0.8922	0.0573	0.9363	0.0256
		180	10.5602	2.7459	0.8773	0.0596	0.9085	0.0467
	2	0	3.9619	2.1374	0.7835	0.1413	0.9559	0.1299
		60	7.9587	2.8342	0.7974	0.1879	0.9144	0.0606
		120	14.1737	5.3256	0.8792	0.0797	0.9339	0.0316
		180	12.3115	5.8318	0.8518	0.0939	0.9046	0.0468
	10	0	2260.8110	11880.1559	0.9993	0.0012	0.9582	0.1307
		60	4070.6805	15848.5434	0.9937	0.0327	0.9666	0.0268
		120	2489.8110	11910.5039	0.9956	0.0270	0.9574	0.0332
		180	2047.6900	10611.7847	0.9992	0.0033	0.9191	0.0580
16	1	0	3.4416	1.0994	0.7401	0.0690	0.9825	0.0430
		60	11.6418	2.5668	0.7071	0.1176	0.9212	0.0270
		120	21.6146	5.3181	0.8545	0.0519	0.9474	0.0137
		180	18.4528	4.8078	0.8267	0.0584	0.9321	0.0309
	2	0	4.2541	2.6433	0.8035	0.1604	0.9834	0.0396
		60	12.7104	4.4664	0.8410	0.1850	0.9470	0.0439
		120	25.6251	11.4249	0.8903	0.0957	0.9547	0.0208
		180	22.2075	11.7058	0.8465	0.1207	0.9327	0.0342
	10	0	2096.5607	9001.6770	0.9998	0.0001	0.9832	0.0472
		60	781.5405	3072.9190	0.9998	0.0002	0.9787	0.0143
		120	842.9563	2920.3134	0.9998	0.0002	0.9737	0.0184
		180	1179.7116	4456.8136	0.9998	0.0001	0.9487	0.0401


The comparison of agreement of intervention group assignement
p = 2
p = 4
p = 8
p = 16
sigma = 1
sigma = 2
sigma = 10
0.5
0.7
0.9
1.1
0
π/3
2π/3
π
angle
linear mixed model
change score method
agreement = 1