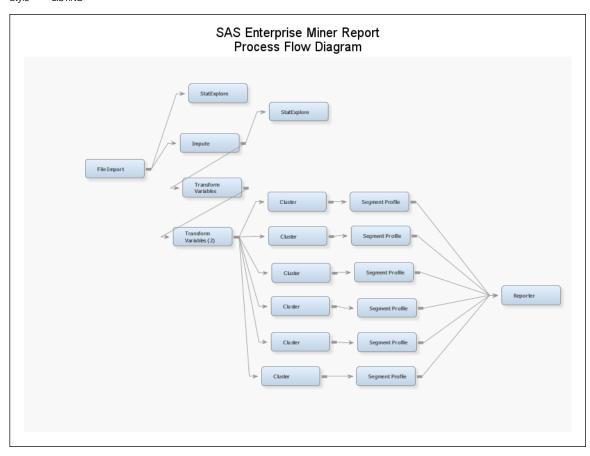
User = u63340697
Date = 18:33:28 09 September 2023
Project = Assignment1_cluster
Diagram = a1_1

Start Node = Report Node label = Reporter Nodes = PATH Showall = N

Format = PDF Style = LISTING



Node=File Import Summary

Node id = FIMPORT Node label = File Import Meta path = FIMPORT Notes =

Node=File Import Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	FileImport		GuessRows	500		NameRow	Υ	
AccessTable	NoTableName		IFileName	D:\2023s2\Unsupervised_learning\Assignment1\assign1-data.csv		Password	NoPassword	
AdvancedAdvisor	N		ImportType	Local	LOCAL	Role	TRAIN	
Delimiter	,		MaxCols	10000		SkipRows	0	
FileType	csv	XLS	MaxRows	1000000		Summarize	N	

Node=File Import Data Attributes

Attribute	Value	Attribute	Value	Attribute	Value
Data Name	FIMPORT_DATA	Date Created	09/09/2023 16:44:47	Data Size	132096
Data Type	DATA	Date Modified	09/09/2023 16:44:47	Role	TRAIN
Data Label		Number Rows	699	Segment	
Engine	V9	Number Columns	10	Data Library	EMWS2

Node=File Import Variables List

Name	Label	Role	Level	Туре	Length	Format	Creator
Bare_Nuclei		INPUT	INTERVAL	N	8	BEST12.0	
Bland_Chromatin		INPUT	INTERVAL	N	8	BEST12.0	
Clump_Thickness		INPUT	INTERVAL	N	8	BEST12.0	
ID_number	ID number	ID	NOMINAL	N	8	BEST12.0	
Marginal_Adhesion		INPUT	INTERVAL	N	8	BEST12.0	
Mitoses		INPUT	INTERVAL	N	8	BEST12.0	
Normal_Nucleoli		INPUT	INTERVAL	N	8	BEST12.0	
S_E_Cell_Size		INPUT	INTERVAL	N	8	BEST12.0	
Uniformity_Cell_Shape		INPUT	INTERVAL	N	8	BEST12.0	
Uniformity_Cell_Size		INPUT	INTERVAL	N	8	BEST12.0	

Node=File Import Created Variables List

Node=Impute Summary

Node id = Impt Node label = Impute Meta path = FIMPORT => Impt Notes =

Node=Impute Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Impute		IndicatorRole	REJECTED		MinCatSize	5	
ABWTuning	9		IndicatorSource	IMPUTED		Normalize	Υ	
AHUBERTuning	1.5		LeafSize	5		Nrules	5	
AWAVETuning	6.2831853072		MaxPctMissing	50		Nsurrs	2	
DefaultChar			Maxbranch	2		RandomSeed	12345	
DefaultNum			Maxdepth	6		ReplaceVariable	N	
DistributionMissing	N		MethodClass	COUNT		SpacingProportion	90	
HideVariable	Υ		MethodInterval	DISTRIBUTION	MEAN	Splitsize		
ImputeNoMissing	N		MethodTargetClass	NONE		ValidateTestMissing	N	
Indicator	NONE		MethodTargetInterval	DISTRIBUTION	NONE			

Node=Impute Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL	2	Bare_Nuclei Uniformity_Cell_Size

Node=Impute Imputation Summary

Variable Name	Impute Method	Imputed Variable	Impute Value	Role	Measurement Level	Label	Number of Missing for TRAIN
Bare_Nuclei	DISTRIBUTION	IMP_Bare_Nuclei		INPUT	INTERVAL		16

Node=Transform Variables Summary

Node id = Trans Node label = Transform Variables Meta path = FIMPORT => Impt => Trans Notes =

Node=Transform Variables Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Transform		EmSampleSize	DEFAULT		MissingValue	USEINSEARCH	
DefaultClassMethod	NONE		GroupCutoff	0.1		NumberofBins	VARIABLES	
DefaultClassTargetMethod	NONE		GroupMissing	N		Offset	1	
DefaultMethod	NONE		HideVariable	Υ		RejectVariable	Υ	
DefaultTargetMethod	NONE		MaxOptimalBins	4		SummaryStatistics	Υ	
EmRandomSeed	12345		MinOffset	Υ		SummaryVariables	TRANSFORMED	
EmSampleMethod	FIRSTN		MissingAsLevel	N		UseMetaTransform	Υ	

Node=Transform Variables Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	Bland_Chromatin Clump_Thickness IMP_Bare_Nuclei Marginal_Adhesion Mitoses Normal_Nucleoli S_E_Cell_Size Uniformity_Cell_Shape Uniformity_Cell_Size

Node=Transform Variables Transformations Statistics

Source	Method	Variable Name	Formula	Number of Levels	Non Missing	Missing
Input	Original	Bland_Chromatin			699	0
Input	Original	Clump_Thickness			699	0
Input	Original	IMP_Bare_Nuclei			699	0
Input	Original	Marginal_Adhesion			699	0
Input	Original	Mitoses			699	0
Input	Original	Normal_Nucleoli			699	0
Input	Original	S_E_Cell_Size			699	0
Input	Original	Uniformity_Cell_Shape			699	0
Input	Original	Uniformity_Cell_Size			699	0
Output	Formula	Т	Clump_thickness+Uniformity_cell_size+Uniformity_cell_shape+Marginal_adhesion+S_e_cell_size+IMP_Bare_nuclei+Bland_chromatin+Normal_nucleoli+Mitoses		699	0

Minimum	Maximum	Mean	Standard Deviation	Skewness	Kurtosis	Label
1	10	3.4378	2.4384	1.09997	0.1846	
1	10	4.4177	2.8157	0.59286	-0.6237	
1	10	3.5494	3.6382	0.98634	-0.8020	Imputed Bare_Nuclei
1	10	2.8069	2.8554	1.52447	0.9879	
1	10	1.5894	1.7151	3.56066	12.6579	
1	10	2.8670	3.0536	1.42226	0.4743	
1	10	3.2160	2.2143	1.71217	2.1691	
1	10	3.2074	2.9719	1.16186	0.0070	
1	10	3.1345	3.0515	1.23314	0.0988	
9	84	28.2260	20.1727	0.95519	-0.4872	

Node=Transform Variables (2) Summary

Node id = Trans2 Node label = Transform Variables (2) Meta path = FIMPORT => Impt => Trans => Trans2 Notes =

Node=Transform Variables (2) Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Transform		EmSampleSize	DEFAULT		MissingValue	USEINSEARCH	
DefaultClassMethod	NONE		GroupCutoff	0.1		NumberofBins	VARIABLES	
DefaultClassTargetMethod	NONE		GroupMissing	N		Offset	1	
DefaultMethod	NONE		HideVariable	Υ		RejectVariable	Υ	
DefaultTargetMethod	NONE		MaxOptimalBins	4		SummaryStatistics	Υ	
EmRandomSeed	12345		MinOffset	Υ		SummaryVariables	TRANSFORMED	
EmSampleMethod	FIRSTN		MissingAsLevel	N		UseMetaTransform	Υ	

Node=Transform Variables (2) Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL	10	Bland_Chromatin Clump_Thickness IMP_Bare_Nuclei Marginal_Adhesion Mitoses Normal_Nucleoli S_E_Cell_Size T Uniformity_Cell_Shape Uniformity_Cell_Size

Node=Transform Variables (2) Transformations Statistics

Source	Method	Variable Name	Formula	Number of Levels
Input	Original	Bland_Chromatin		
Input	Original	Clump_Thickness		
Input	Original	IMP_Bare_Nuclei		
Input	Original	Marginal_Adhesion		
Input	Original	Mitoses		
Input	Original	Normal_Nucleoli		
Input	Original	S_E_Cell_Size		
Input	Original	Т		
Input	Original	Uniformity_Cell_Shape		
Input	Original	Uniformity_Cell_Size		
Output	Formula	lgt_Bare_nuclei	log(IMP_Bare_nuclei/(t-IMP_Bare_nuclei))	
Output	Formula	lgt_Bland_chromatin	log(Bland_chromatin/(t-Bland_chromatin))	
Output	Formula	lgt_Clump_thickness	log(Clump_thickness/(t-Clump_thickness))	
Output	Formula	lgt_Marginal_adhesion	log(Marginal_adhesion/(t-Marginal_adhesion))	
Output	Formula	lgt_Mitoses	log(Mitoses/(t-Mitoses))	
Output	Formula	lgt_Normal_nucleoli	log(Normal_nucleoli/(t-Normal_nucleoli))	
Output	Formula	lgt_S_e_cell_size	log(S_e_cell_size/(t-S_e_cell_size))	
Output	Formula	lgt_Uniformity_cell_shape	log(Uniformity_cell_shape/(t-Uniformity_cell_shape))	
Output	Formula	lgt_Uniformity_cell_size	log(Uniformity_cell_size/(t-Uniformity_cell_size))	

Non Missing	Missing	Minimum	Maximum	Mean	Standard Deviation	Skewness	Kurtosis	Label
699	0	1.00000	10.0000	3.4378	2.4384	1.09997	0.1846	
699	0	1.00000	10.0000	4.4177	2.8157	0.59286	-0.6237	
699	0	1.00000	10.0000	3.5494	3.6382	0.98634	-0.8020	Imputed Bare_Nuclei
699	0	1.00000	10.0000	2.8069	2.8554	1.52447	0.9879	
699	0	1.00000	10.0000	1.5894	1.7151	3.56066	12.6579	
699	0	1.00000	10.0000	2.8670	3.0536	1.42226	0.4743	
699	0	1.00000	10.0000	3.2160	2.2143	1.71217	2.1691	
699	0	9.00000	84.0000	28.2260	20.1727	0.95519	-0.4872	
699	0	1.00000	10.0000	3.2074	2.9719	1.16186	0.0070	
699	0	1.00000	10.0000	3.1345	3.0515	1.23314	0.0988	
699	0	-4.30407	0.1178	-2.2279	0.6093	0.27428	0.8707	
699	0	-3.76120	-0.4520	-1.9687	0.4981	-0.09743	-0.2965	
699	0	-4.00733	-0.2877	-1.6724	0.6282	-0.21598	-0.5222	
699	0	-4.07754	-0.7419	-2.3763	0.5262	-0.15310	0.9023	
699	0	-4.36945	-0.1178	-2.8116	0.6232	-0.49217	0.5414	
699	0	-4.23411	-0.7538	-2.4014	0.5389	-0.38806	1.3456	
699	0	-3.29584	0.2231	-1.9771	0.4348	-0.28981	0.7097	
699	0	-3.52636	-0.9163	-2.2275	0.4211	0.41510	-0.0715	
699	0	-3.85015	-1.2238	-2.2801	0.3939	0.28168	0.0385	

Node=Cluster Summary

Node id = Clus6 Node label = Cluster Meta path = FIMPORT => Impt => Trans => Trans2 => Clus6 Notes =

Node=Cluster Properties

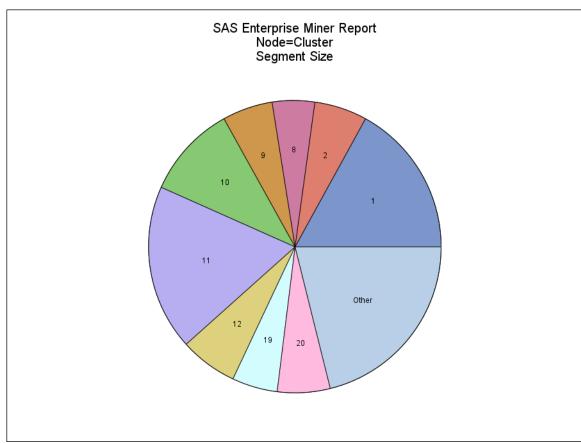
Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Cluster		FinalMaxNum	20		MissingNominal	DEFAULT	
AutomaticMaxNum	50		HideVariable	Υ		MissingOrdinal	DEFAULT	
AutomaticMethod	WARD		ImputationMethod	NONE		NominalEncoding	GLM	
AutomaticMinNum	2		Initial	DEFAULT		NumberClusterMethod	AUTOMATIC	
Bins	100		Learn			OrdinalEncoding	RANK	
CCCCutOff	3		LeamFinal	0.02		Radius	0	
ClusterGraphs	Υ		LearnInitial	0.5		Stdize	STD	
Clusvar	_SEGMENT_		LearnSteps	1000		Summary	N	
ClusvarLabel	Segment Variable		MaxC	2	10	TrainDefaults	Υ	
ClusvarRole	SEGMENT		MaxIter	10		TreeProfile	Υ	
DistancePlot	Υ		MaxSteps	1200		XConv	0.0001	
Drift	N		MissingInterval	DEFAULT				

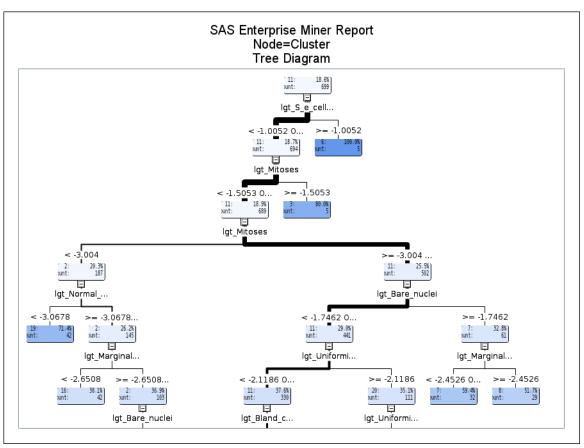
Node=Cluster Variable Summary

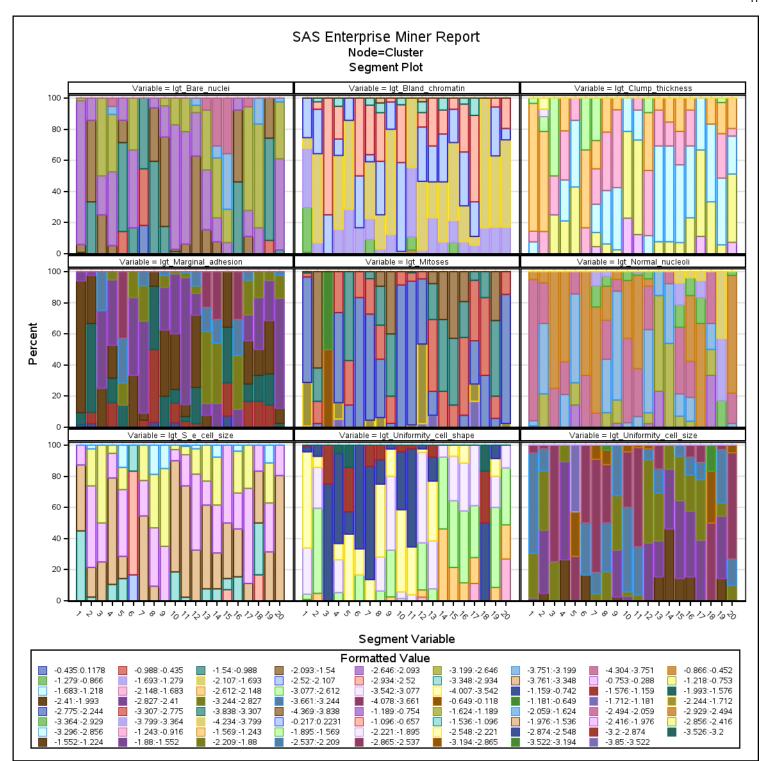
Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size

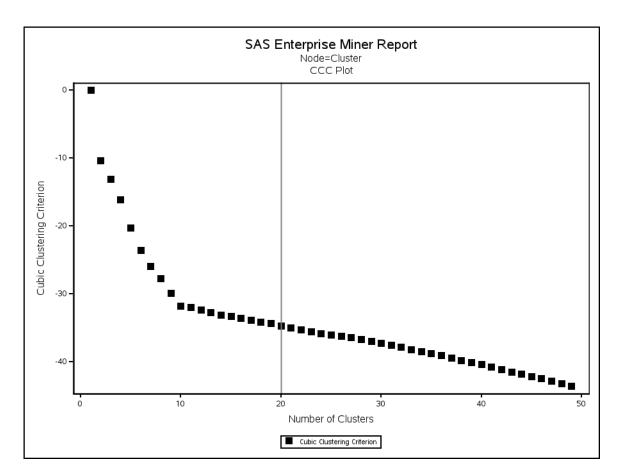
Variable	Segment 1	Segment 2	Segment 3	Segment 4	Segment 5	Segment 6	Segment 7	Segment 8	Segment 9
Clustering Criterion	0.623	0.6232	0.6232	0.6232	0.62315	0.62315	0.6232	0.6232	0.6232
Maximum Relative Change in Cluster Seeds	0.063	0.0634	0.0634	0.0634	0.06339	0.06339	0.0634	0.0634	0.0634
Improvement in Clustering Criterion									
Frequency of Cluster	118.000	42.0000	4.0000	19.0000	7.00000	6.00000	22.0000	32.0000	40.0000
Root-Mean-Square Standard Deviation	0.491	0.6559	0.8679	0.7448	0.95780	0.83908	0.7835	0.7820	0.6033
Maximum Distance from Cluster Seed	3.474	3.1184	3.0058	3.0978	3.32329	3.05840	3.8672	3.9606	2.4688
Nearest Cluster	12.000	9.0000	10.0000	12.0000	7.00000	1.00000	8.0000	9.0000	2.0000
Distance to Nearest Cluster	2.235	1.7861	4.0968	2.3375	3.17403	2.81889	2.8843	2.6201	1.7861
lgt_Bare_nuclei	-2.302	-1.7288	-2.4847	-2.7709	-1.40368	-2.36335	-0.8702	-1.4920	-1.8584
lgt_Bland_chromatin	-1.573	-2.0564	-2.6035	-2.0791	-1.86062	-2.36550	-2.0786	-2.3838	-1.9346
lgt_Clump_thickness	-2.242	-2.5442	-2.1356	-1.6891	-1.41493	-2.44727	-2.0297	-1.7891	-1.7459
lgt_Marginal_adhesion	-2.252	-1.8726	-2.7822	-2.2013	-3.30763	-2.57429	-2.7073	-1.6352	-2.3227
lgt_Mitoses	-2.349	-3.7883	-0.5819	-2.5401	-3.31348	-2.57429	-2.7246	-3.0229	-3.6607
lgt_Normal_nucleoli	-2.302	-1.9479	-2.6824	-2.4167	-1.70023	-2.57429	-2.7914	-2.2503	-1.8034
lgt_S_e_cell_size	-1.621	-2.2366	-2.3012	-1.8412	-2.25206	-0.70903	-2.0731	-2.4538	-2.5461
lgt_Uniformity_cell_shape	-2.297	-1.9237	-2.7907	-2.5080	-2.73128	-2.44288	-2.6868	-2.3933	-1.9990
lgt_Uniformity_cell_size	-2.320	-1.9359	-2.6035	-1.6543	-3.14961	-2.36734	-2.6384	-2.5043	-2.0514

Segment 10	Segment 11	Segment 12	Segment 13	Segment 14	Segment 15	Segment 16	Segment 17	Segment 18	Segment 19	Segment 20
0.6232	0.623	0.6232	0.6232	0.6232	0.6232	0.6232	0.6232	0.6232	0.6232	0.6232
0.0634	0.063	0.0634	0.0634	0.0634	0.0634	0.0634	0.0634	0.0634	0.0634	0.0634
70.0000	130.000	43.0000	13.0000	13.0000	14.0000	26.0000	18.0000	6.0000	35.0000	41.0000
0.5069	0.461	0.6975	0.8520	0.7942	0.8581	0.8023	0.8291	0.7642	0.7829	0.6130
3.4531	3.974	3.6323	3.6802	2.9354	3.4066	3.4247	3.7924	2.8674	3.8327	3.0310
11.0000	10.000	1.0000	14.0000	13.0000	4.0000	9.0000	20.0000	11.0000	16.0000	17.0000
2.0324	2.032	2.2346	2.4339	2.4339	2.9056	2.8549	2.3278	2.5965	3.2252	2.3278
-2.5005	-2.549	-2.1619	-2.6285	-3.1369	-3.4333	-1.5505	-2.7110	-2.9203	-1.3859	-2.6260
-2.4864	-1.564	-2.2311	-2.1585	-2.1630	-1.9753	-2.3330	-2.5977	-1.8454	-2.0049	-1.9978
-0.9844	-1.090	-2.1782	-1.6386	-1.6343	-1.7549	-1.5734	-1.1189	-1.4796	-1.7815	-1.3897
-2.2154	-2.528	-2.3041	-3.2490	-3.2774	-1.7882	-3.3356	-2.3110	-2.2616	-2.1917	-2.6592
-2.5294	-2.605	-2.2519	-3.1144	-3.5632	-3.7072	-3.3340	-2.5500	-2.9203	-3.6309	-2.6418
-2.4903	-2.558	-2.0440	-1.3422	-1.6450	-2.5750	-2.5462	-2.9646	-1.5944	-3.7035	-2.6161
-1.7360	-1.918	-2.1224	-1.9603	-2.2580	-1.9567	-2.1287	-2.2940	-1.6080	-2.2674	-1.8678
-2.4863	-2.575	-1.9173	-2.3529	-1.6162	-1.8015	-1.8561	-1.7052	-2.9203	-1.9519	-1.5644
-2.4754	-2.573	-1.9717	-1.9846	-1.6190	-1.7862	-1.8489	-2.0411	-2.9203	-1.9519	-2.5713









Node=Cluster Summary

Node id = Clus5 Node label = Cluster Meta path = FIMPORT => Impt => Trans => Trans2 => Clus5 Notes =

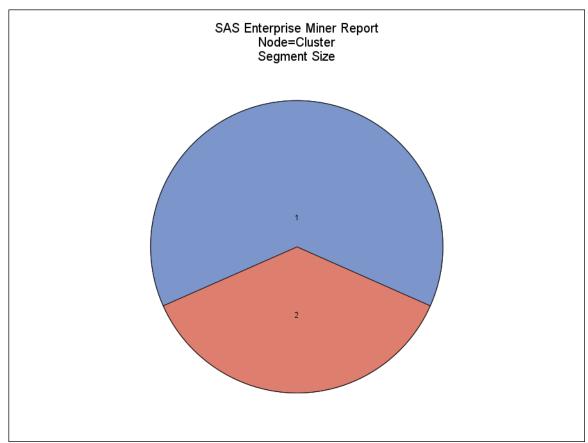
Node=Cluster Properties

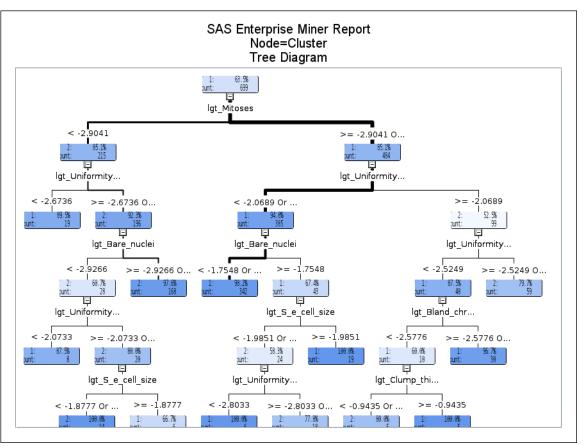
Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Cluster		FinalMaxNum	20		MissingNominal	DEFAULT	
AutomaticMaxNum	50		HideVariable	Υ		MissingOrdinal	DEFAULT	
AutomaticMethod	WARD		ImputationMethod	NONE		NominalEncoding	GLM	
AutomaticMinNum	2		Initial	DEFAULT		NumberClusterMethod	USER	AUTOMATIC
Bins	100		Learn			OrdinalEncoding	RANK	
CCCCutOff	3		LeamFinal	0.02		Radius	0	
ClusterGraphs	Υ		LearnInitial	0.5		Stdize	STD	
Clusvar	_SEGMENT_		LearnSteps	1000		Summary	N	
ClusvarLabel	Segment Variable		MaxC	2	10	TrainDefaults	Υ	
ClusvarRole	SEGMENT		MaxIter	10		TreeProfile	Υ	
DistancePlot	Υ		MaxSteps	1200		XConv	0.0001	
Drift	N		MissingInterval	DEFAULT				

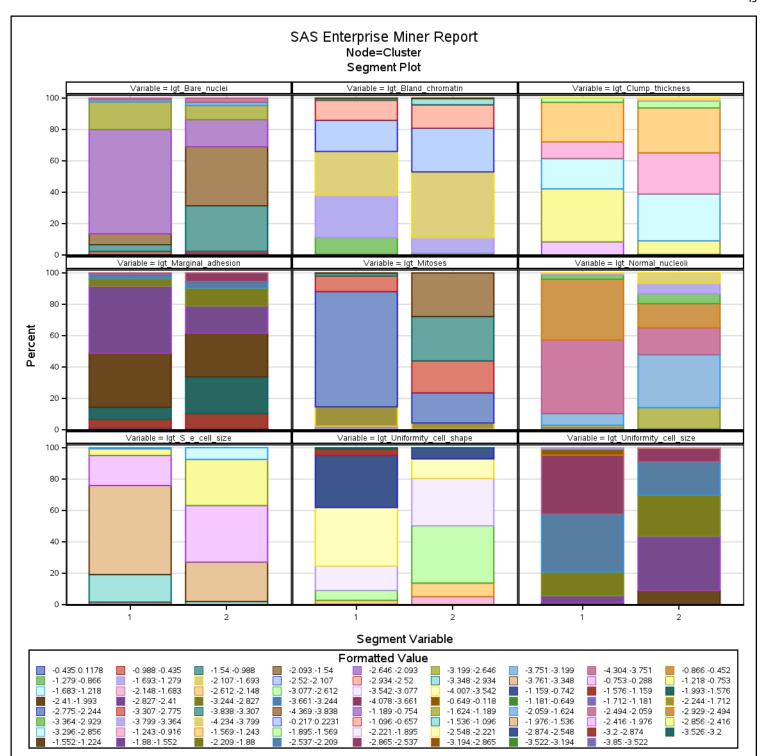
Node=Cluster Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL		lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size
ID	NOMINAL	1	ID_number

Variable	Segment 1	Segment 2
Clustering Criterion	0.904	0.904
Maximum Relative Change in Cluster Seeds	0.000	0.000
Improvement in Clustering Criterion	0.000	0.000
Frequency of Cluster	444.000	255.000
Root-Mean-Square Standard Deviation	0.824	1.033
Maximum Distance from Cluster Seed	5.882	5.580
Nearest Cluster	2.000	1.000
Distance to Nearest Cluster	2.650	2.650
lgt_Bare_nuclei	-2.407	-1.916
lgt_Bland_chromatin	-1.875	-2.131
lgt_Clump_thickness	-1.525	-1.928
lgt_Marginal_adhesion	-2.401	-2.334
lgt_Mitoses	-2.507	-3.341
lgt_Normal_nucleoli	-2.436	-2.341
lgt_S_e_cell_size	-1.805	-2.277
lgt_Uniformity_cell_shape	-2.408	-1.912
lgt_Uniformity_cell_size	-2.444	-1.996







Node=Cluster Summary

Node id = Clus4 Node label = Cluster Meta path = FIMPORT => Impt => Trans => Trans2 => Clus4 Notes =

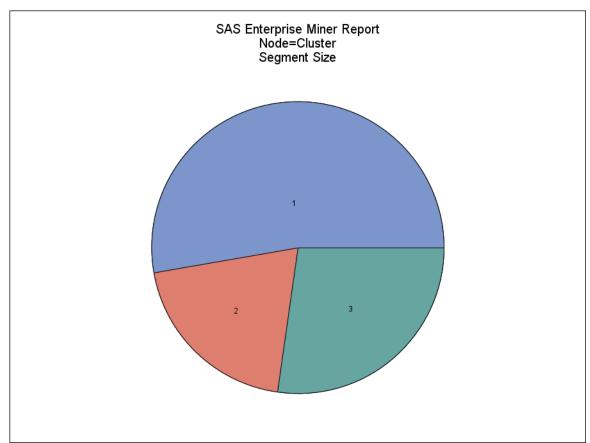
Node=Cluster Properties

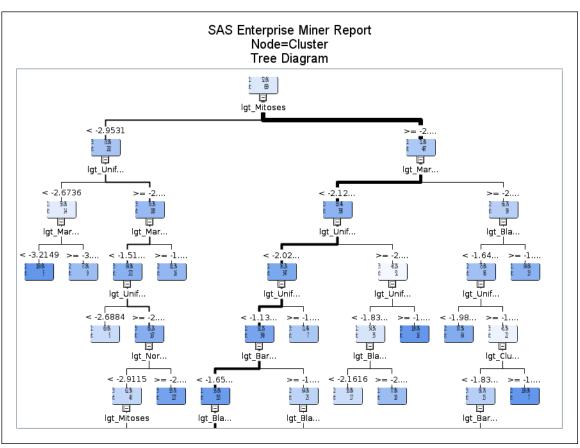
Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Cluster		FinalMaxNum	20		MissingNominal	DEFAULT	
AutomaticMaxNum	50		HideVariable	Υ		MissingOrdinal	DEFAULT	
AutomaticMethod	WARD		ImputationMethod	NONE		NominalEncoding	GLM	
AutomaticMinNum	2		Initial	DEFAULT		NumberClusterMethod	USER	AUTOMATIC
Bins	100		Learn			OrdinalEncoding	RANK	
CCCCutOff	3		LeamFinal	0.02		Radius	0	
ClusterGraphs	Υ		LearnInitial	0.5		Stdize	STD	
Clusvar	_SEGMENT_		LeamSteps	1000		Summary	N	
ClusvarLabel	Segment Variable		MaxC	3	10	TrainDefaults	Υ	
ClusvarRole	SEGMENT		MaxIter	10		TreeProfile	Υ	
DistancePlot	Υ		MaxSteps	1200		XConv	0.0001	
Drift	N		MissingInterval	DEFAULT				

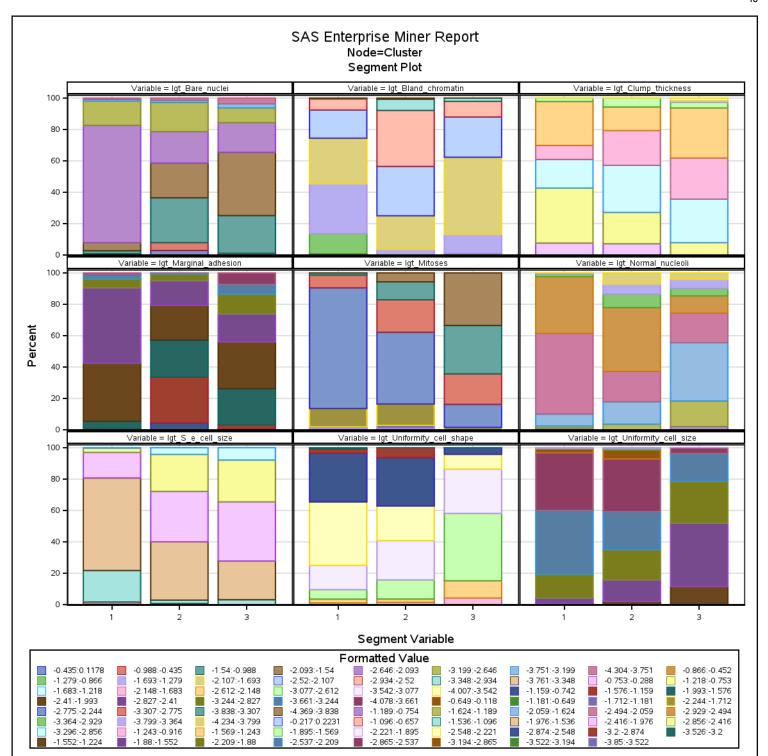
Node=Cluster Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL		lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size
ID	NOMINAL	1	ID_number

Variable	Segment 1	Segment 2	Segment 3
Clustering Criterion	0.873	0.873	0.873
Maximum Relative Change in Cluster Seeds	0.008	0.008	0.008
Improvement in Clustering Criterion			
Frequency of Cluster	368.000	140.000	191.000
Root-Mean-Square Standard Deviation	0.744	1.017	0.989
Maximum Distance from Cluster Seed	5.914	5.319	5.274
Nearest Cluster	2.000	1.000	2.000
Distance to Nearest Cluster	2.200	2.200	2.555
lgt_Bare_nuclei	-2.454	-1.934	-2.007
lgt_Bland_chromatin	-1.761	-2.402	-2.051
lgt_Clump_thickness	-1.532	-1.623	-1.978
lgt_Marginal_adhesion	-2.503	-1.918	-2.468
lgt_Mitoses	-2.495	-2.752	-3.465
lgt_Normal_nucleoli	-2.416	-2.643	-2.195
lgt_S_e_cell_size	-1.761	-2.145	-2.269
lgt_Uniformity_cell_shape	-2.385	-2.324	-1.853
lgt_Uniformity_cell_size	-2.442	-2.356	-1.912







Node=Cluster Summary

Node id = Clus3 Node label = Cluster Meta path = FIMPORT => Impt => Trans => Trans2 => Clus3 Notes =

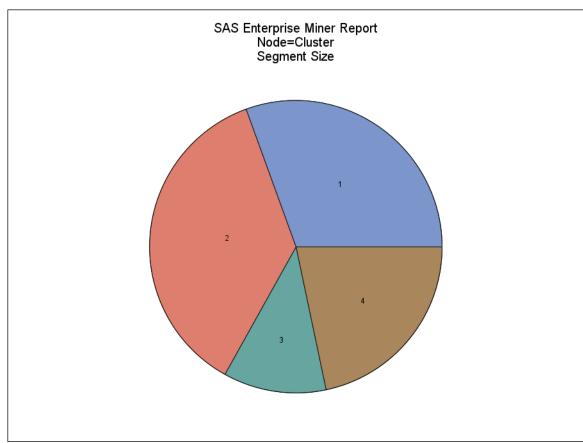
Node=Cluster Properties

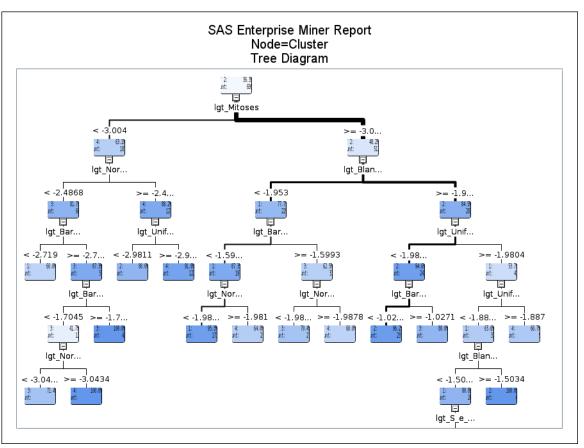
Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Cluster		FinalMaxNum	20		MissingNominal	DEFAULT	
AutomaticMaxNum	50		HideVariable	Υ		MissingOrdinal	DEFAULT	
AutomaticMethod	WARD		ImputationMethod	NONE		NominalEncoding	GLM	
AutomaticMinNum	2		Initial	DEFAULT		NumberClusterMethod	USER	AUTOMATIC
Bins	100		Learn			OrdinalEncoding	RANK	
CCCCutOff	3		LeamFinal	0.02		Radius	0	
ClusterGraphs	Υ		LearnInitial	0.5		Stdize	STD	
Clusvar	_SEGMENT_		LeamSteps	1000		Summary	N	
ClusvarLabel	Segment Variable		MaxC	4	10	TrainDefaults	Υ	
ClusvarRole	SEGMENT		MaxIter	10		TreeProfile	Υ	
DistancePlot	Υ		MaxSteps	1200		XConv	0.0001	
Drift	N		MissingInterval	DEFAULT				

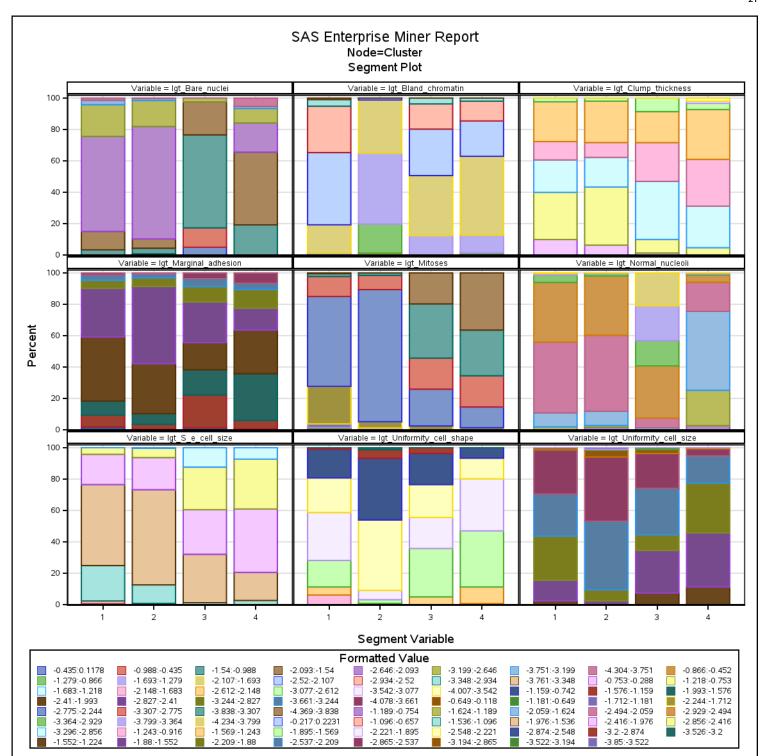
Node=Cluster Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL		lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size
ID	NOMINAL	1	ID_number

Variable	Segment 1	Segment 2	Segment 3	Segment 4
Clustering Criterion	0.825	0.825	0.8252	0.825
Maximum Relative Change in Cluster Seeds	0.020	0.020	0.0204	0.020
Improvement in Clustering Criterion				
Frequency of Cluster	213.000	254.000	81.0000	151.000
Root-Mean-Square Standard Deviation	0.847	0.687	0.9994	0.910
Maximum Distance from Cluster Seed	5.737	5.646	4.6073	5.337
Nearest Cluster	2.000	1.000	4.0000	1.000
Distance to Nearest Cluster	2.070	2.070	2.9055	2.833
lgt_Bare_nuclei	-2.446	-2.449	-1.2884	-2.052
lgt_Bland_chromatin	-2.380	-1.519	-2.1408	-2.052
lgt_Clump_thickness	-1.528	-1.535	-1.8248	-2.026
lgt_Marginal_adhesion	-2.322	-2.468	-2.2737	-2.353
lgt_Mitoses	-2.457	-2.542	-3.3086	-3.499
lgt_Normal_nucleoli	-2.453	-2.418	-3.1992	-1.873
lgt_S_e_cell_size	-1.757	-1.858	-2.2870	-2.322
lgt_Uniformity_cell_shape	-2.126	-2.504	-2.1579	-1.942
lgt_Uniformity_cell_size	-2.283	-2.510	-2.1641	-1.952







Node=Cluster Summary

Node id = Clus2 Node label = Cluster Meta path = FIMPORT => Impt => Trans => Trans2 => Clus2 Notes =

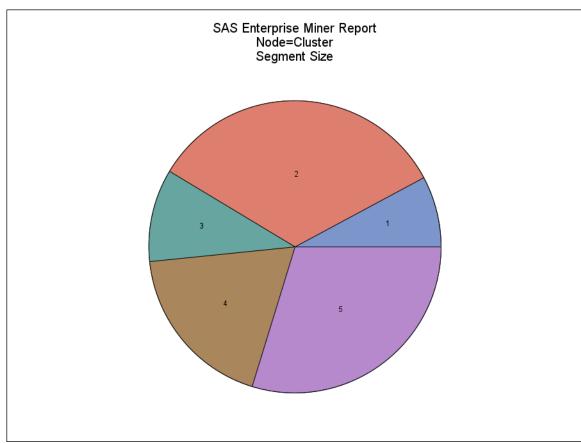
Node=Cluster Properties

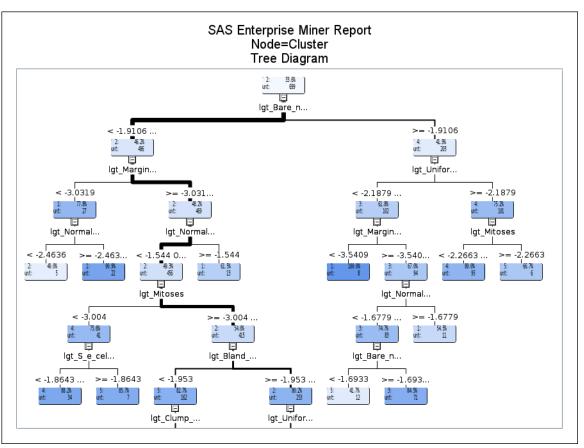
Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Cluster		FinalMaxNum	20		MissingNominal	DEFAULT	
AutomaticMaxNum	50		HideVariable	Υ		MissingOrdinal	DEFAULT	
AutomaticMethod	WARD		ImputationMethod	NONE		NominalEncoding	GLM	
AutomaticMinNum	2		Initial	DEFAULT		NumberClusterMethod	USER	AUTOMATIC
Bins	100		Learn			OrdinalEncoding	RANK	
CCCCutOff	3		LearnFinal	0.02		Radius	0	
ClusterGraphs	Υ		LearnInitial	0.5		Stdize	STD	
Clusvar	_SEGMENT_		LearnSteps	1000		Summary	N	
ClusvarLabel	Segment Variable		MaxC	5	10	TrainDefaults	Υ	
ClusvarRole	SEGMENT		MaxIter	10		TreeProfile	Υ	
DistancePlot	Υ		MaxSteps	1200		XConv	0.0001	
Drift	N		MissingInterval	DEFAULT				

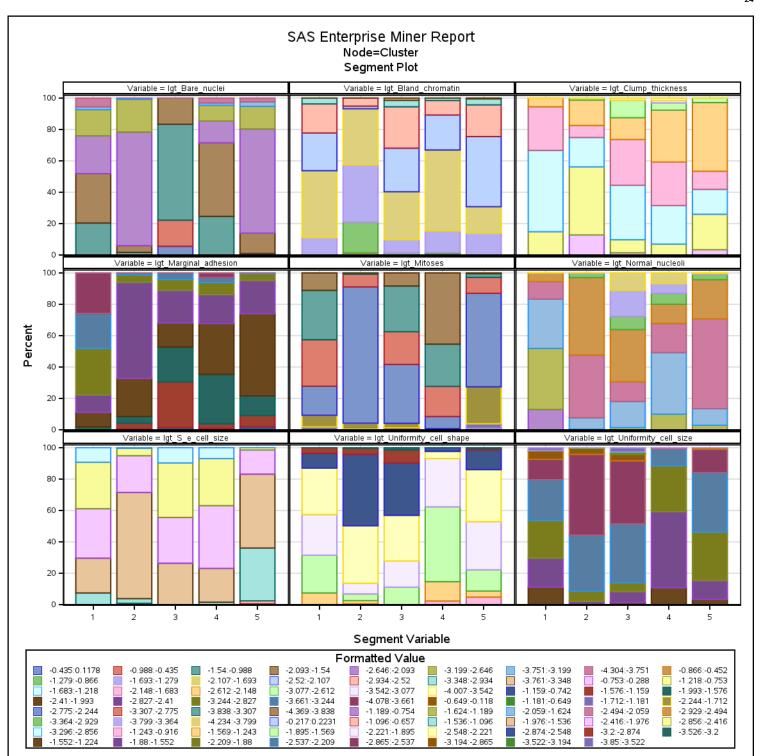
Node=Cluster Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL		lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size
ID	NOMINAL	1	ID_number

Variable	Segment 1	Segment 2	Segment 3	Segment 4	Segment 5
Clustering Criterion	0.8149	0.815	0.8149	0.815	0.815
Maximum Relative Change in Cluster Seeds	0.0407	0.041	0.0407	0.041	0.041
Improvement in Clustering Criterion					
Frequency of Cluster	54.0000	235.000	72.0000	130.000	208.000
Root-Mean-Square Standard Deviation	0.9733	0.648	1.0069	0.922	0.800
Maximum Distance from Cluster Seed	5.0432	5.172	5.4385	5.171	5.590
Nearest Cluster	4.0000	5.000	4.0000	1.000	2.000
Distance to Nearest Cluster	2.6402	2.008	2.8577	2.640	2.008
lgt_Bare_nuclei	-2.1776	-2.519	-1.2048	-1.950	-2.440
lgt_Bland_chromatin	-2.1466	-1.583	-2.2364	-2.016	-2.236
lgt_Clump_thickness	-1.5974	-1.335	-1.8615	-2.015	-1.793
lgt_Marginal_adhesion	-3.1850	-2.483	-2.0654	-2.276	-2.216
lgt_Mitoses	-3.1356	-2.569	-3.0492	-3.611	-2.419
lgt_Normal_nucleoli	-1.6366	-2.505	-2.8197	-2.343	-2.375
lgt_S_e_cell_size	-2.2390	-1.885	-2.3178	-2.315	-1.684
lgt_Uniformity_cell_shape	-2.1145	-2.477	-2.4358	-1.825	-2.155
lgt_Uniformity_cell_size	-2.1408	-2.531	-2.4837	-1.854	-2.228







Node=Cluster Summary

Node id = Clus Node label = Cluster Meta path = FIMPORT => Impt => Trans => Trans2 => Clus Notes =

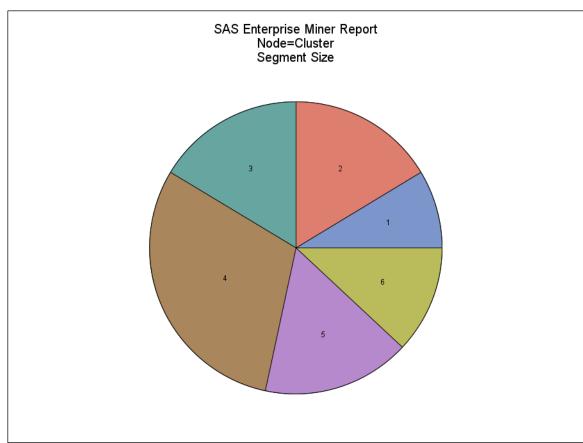
Node=Cluster Properties

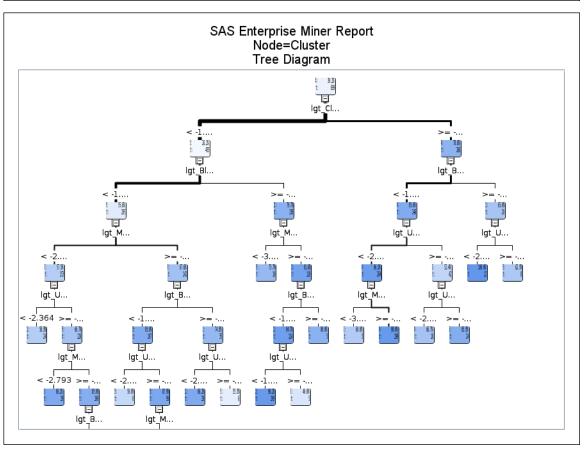
Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Cluster		FinalMaxNum	20		MissingNominal	DEFAULT	
AutomaticMaxNum	50		HideVariable	Υ		MissingOrdinal	DEFAULT	
AutomaticMethod	WARD		ImputationMethod	NONE		NominalEncoding	GLM	
AutomaticMinNum	2		Initial	DEFAULT		NumberClusterMethod	USER	AUTOMATIC
Bins	100		Learn			OrdinalEncoding	RANK	
CCCCutOff	3		LeamFinal	0.02		Radius	0	
ClusterGraphs	Υ		LearnInitial	0.5		Stdize	STD	
Clusvar	_SEGMENT_		LearnSteps	1000		Summary	N	
ClusvarLabel	Segment Variable		MaxC	6	10	TrainDefaults	Υ	
ClusvarRole	SEGMENT		MaxIter	10		TreeProfile	Υ	
DistancePlot	Υ		MaxSteps	1200		XConv	0.0001	
Drift	N		MissingInterval	DEFAULT				

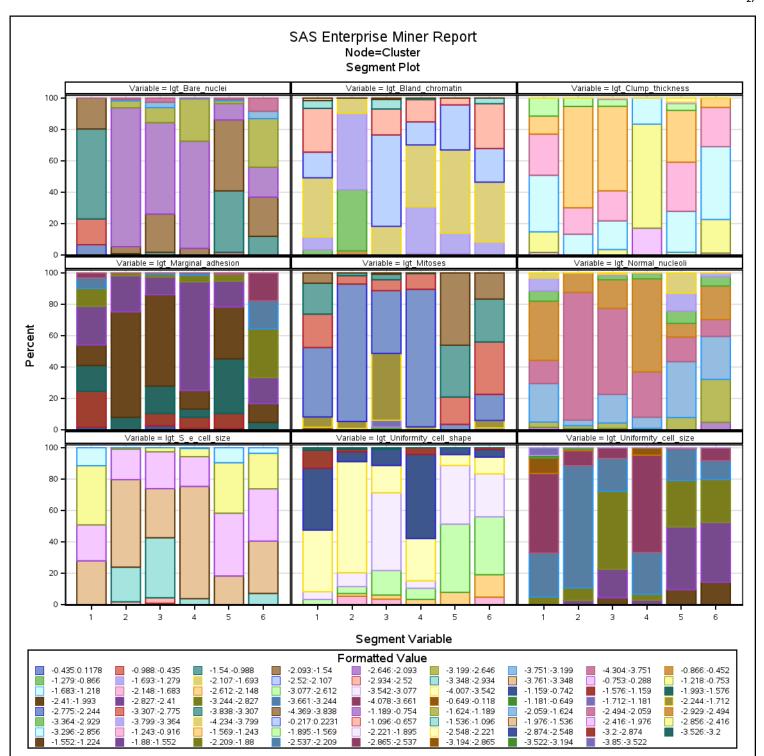
Node=Cluster Variable Summary

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size
ID	NOMINAL	1	ID_number

Variable	Segment 1	Segment 2	Segment 3	Segment 4	Segment 5	Segment 6
Clustering Criterion	0.7677	0.768	0.768	0.768	0.768	0.7677
Maximum Relative Change in Cluster Seeds	0.0214	0.021	0.021	0.021	0.021	0.0214
Improvement in Clustering Criterion						
Frequency of Cluster	61.0000	113.000	115.000	211.000	115.000	84.0000
Root-Mean-Square Standard Deviation	0.9904	0.568	0.777	0.613	0.885	0.9813
Maximum Distance from Cluster Seed	4.7433	5.240	5.670	4.157	4.843	4.4994
Nearest Cluster	4.0000	3.000	2.000	2.000	6.000	5.0000
Distance to Nearest Cluster	2.9147	2.209	2.209	2.416	2.736	2.7359
lgt_Bare_nuclei	-1.2098	-2.395	-2.331	-2.582	-1.691	-2.4459
lgt_Bland_chromatin	-2.2014	-1.344	-2.332	-1.917	-1.990	-2.2438
lgt_Clump_thickness	-1.7829	-2.184	-2.086	-0.989	-2.057	-1.5265
lgt_Marginal_adhesion	-2.2686	-2.345	-2.118	-2.457	-2.094	-3.0339
lgt_Mitoses	-2.8955	-2.445	-2.329	-2.611	-3.693	-3.2000
lgt_Normal_nucleoli	-2.4928	-2.349	-2.282	-2.537	-2.543	-2.0363
lgt_S_e_cell_size	-2.3385	-1.733	-1.689	-1.889	-2.358	-2.1360
lgt_Uniformity_cell_shape	-2.5615	-2.278	-2.114	-2.478	-1.919	-1.8643
lgt_Uniformity_cell_size	-2.6515	-2.385	-2.103	-2.564	-1.913	-1.9024







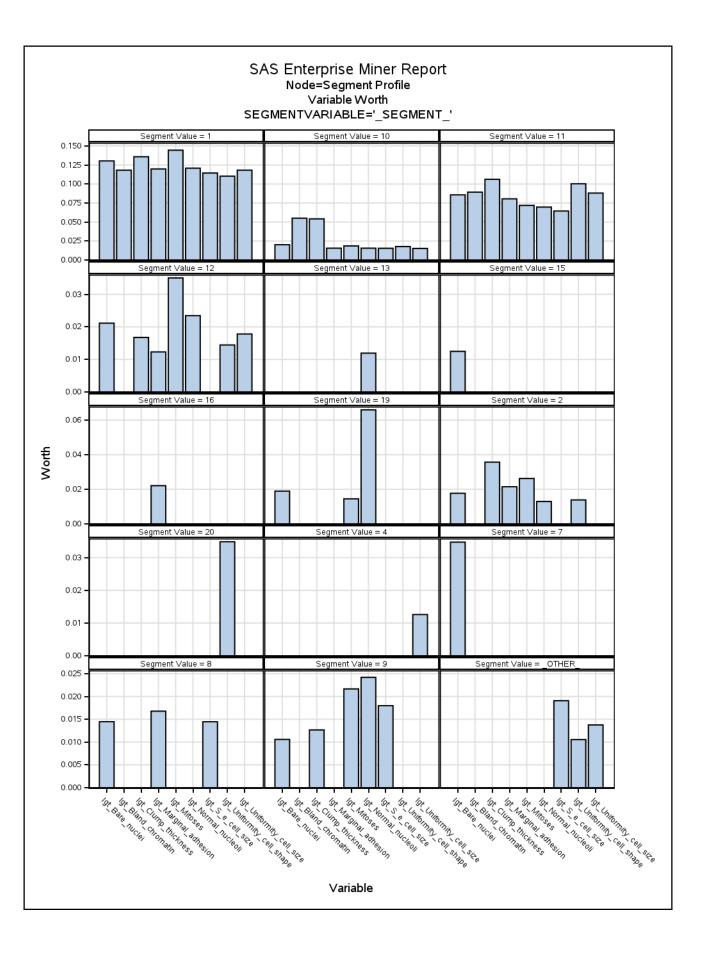
Node=Segment Profile Summary

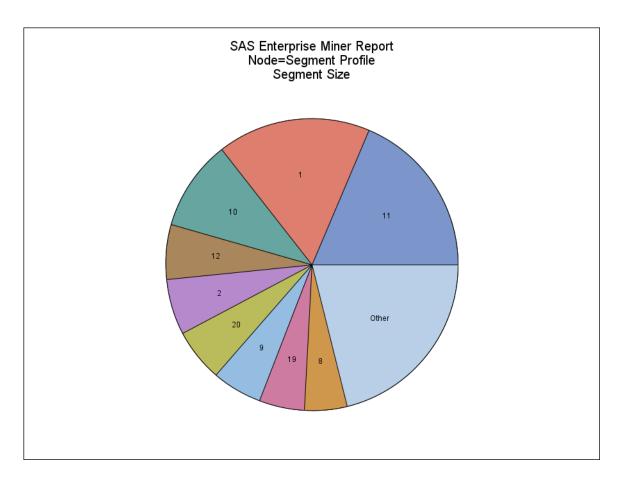
Node id = Prof6 Node label = Segment Profile Meta path = FIMPORT => Impt => Trans => Trans2 => Clus6 => Prof6 Notes =

Node=Segment Profile Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Profile		MinWorth	0.01		ProfileAll	N	
MaxDepth	1		NumHistBars	8		TargetRole	NONE	
MaxNumInput	10		OtherPercentCutOff	95		UseReportVars	Υ	
MaxNumReport	10		PrintWorth	Υ				

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size





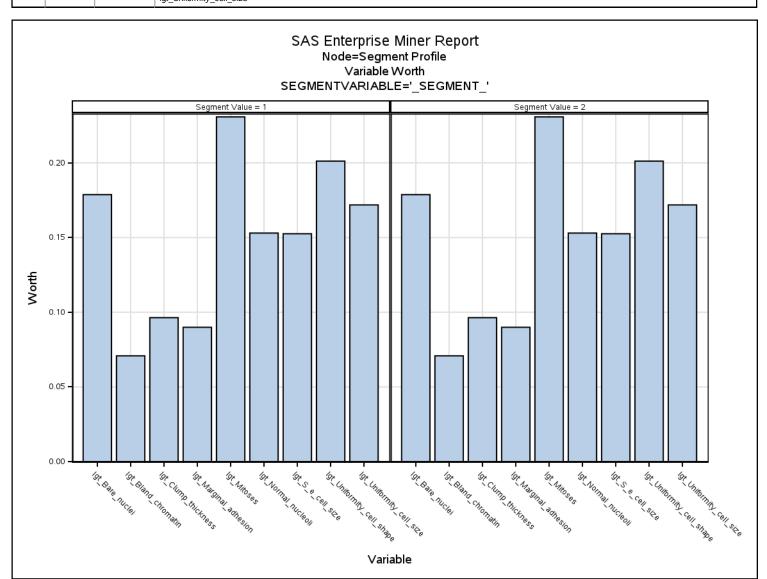
Node=Segment Profile Summary

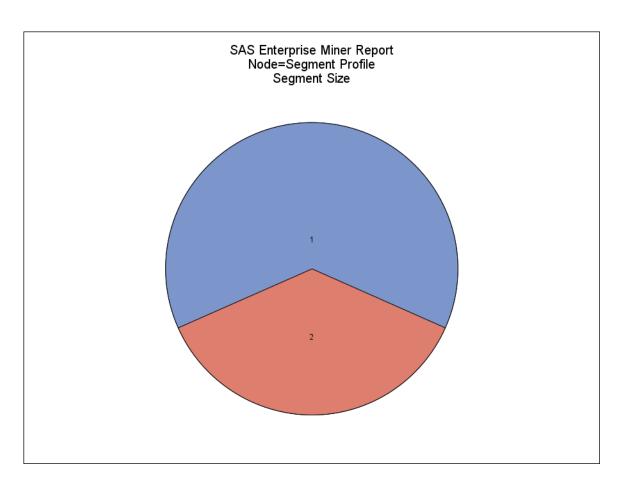
Node id = Prof5 Node label = Segment Profile Meta path = FIMPORT => Impt => Trans => Trans2 => Clus5 => Prof5 Notes =

Node=Segment Profile Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Profile		MinWorth	0.01		ProfileAll	N	
MaxDepth	1		NumHistBars	8		TargetRole	NONE	
MaxNumInput	10		OtherPercentCutOff	95		UseReportVars	Υ	
MaxNumReport	10		PrintWorth	Υ				

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size





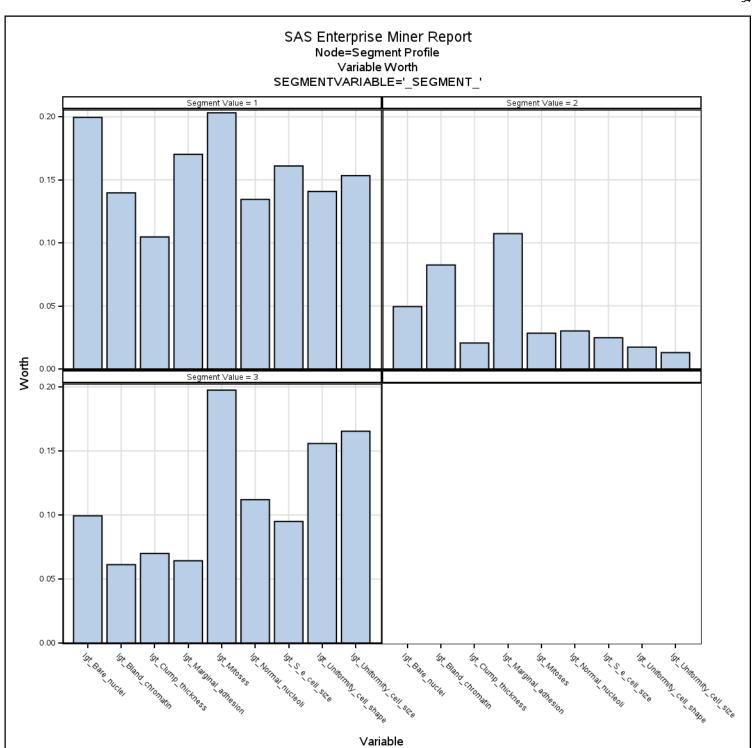
Node=Segment Profile Summary

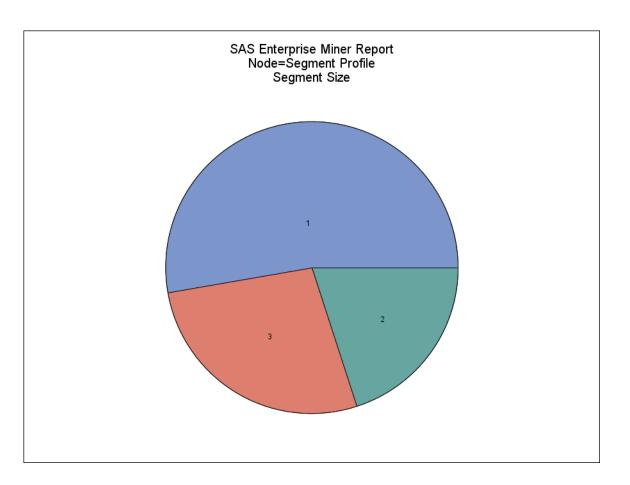
Node id = Prof4 Node label = Segment Profile Meta path = FIMPORT => Impt => Trans => Trans2 => Clus4 => Prof4 Notes =

Node=Segment Profile Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Profile		MinWorth	0.01		ProfileAll	N	
MaxDepth	1		NumHistBars	8		TargetRole	NONE	
MaxNumInput	10		OtherPercentCutOff	95		UseReportVars	Υ	
MaxNumReport	10		PrintWorth	Υ				

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size





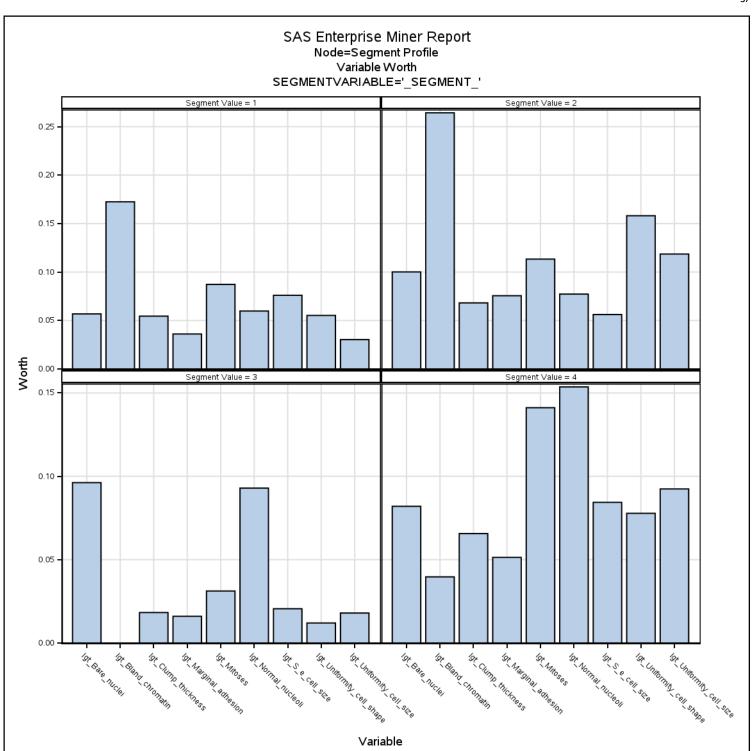
Node=Segment Profile Summary

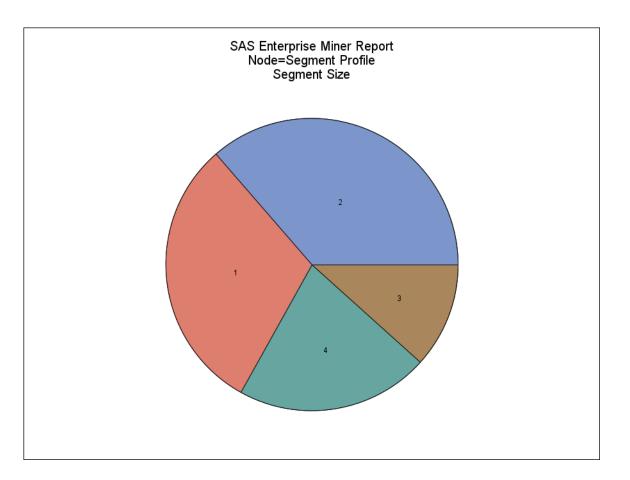
Node id = Prof3 Node label = Segment Profile Meta path = FIMPORT => Impt => Trans => Trans2 => Clus3 => Prof3 Notes =

Node=Segment Profile Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Profile		MinWorth	0.01		ProfileAll	N	
MaxDepth	1		NumHistBars	8		TargetRole	NONE	
MaxNumInput	10		OtherPercentCutOff	95		UseReportVars	Υ	
MaxNumReport	10		PrintWorth	Υ				

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size





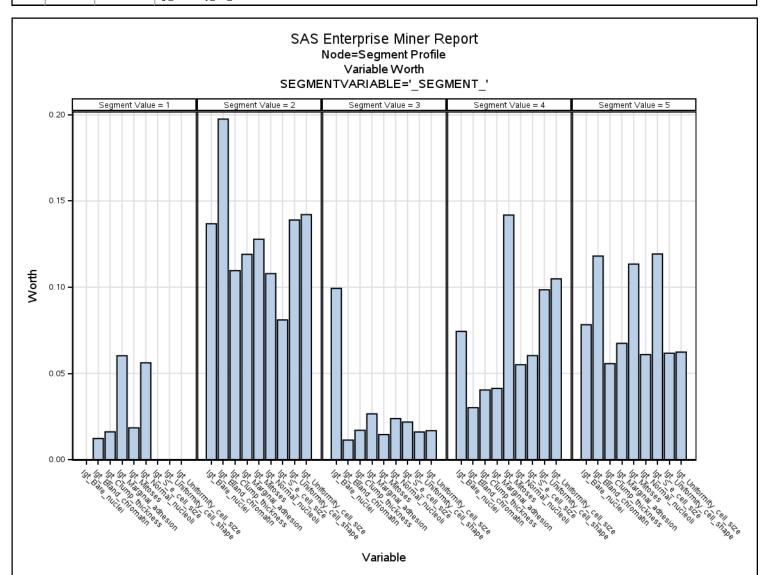
Node=Segment Profile Summary

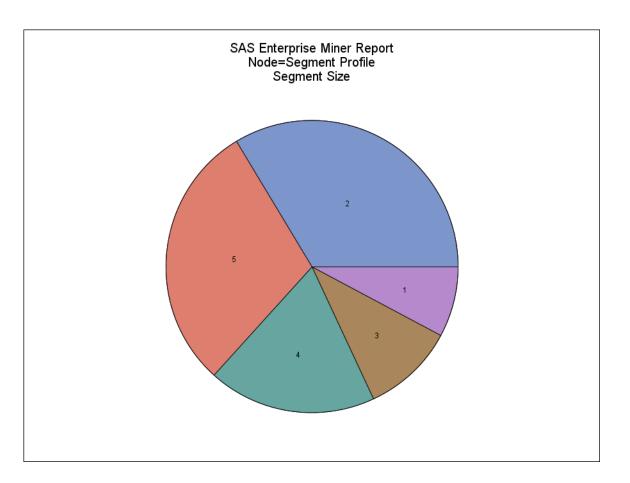
Node id = Prof2 Node label = Segment Profile Meta path = FIMPORT => Impt => Trans => Trans2 => Clus2 => Prof2

Node=Segment Profile Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Profile		MinWorth	0.01		ProfileAll	N	
MaxDepth	1		NumHistBars	8		TargetRole	NONE	
MaxNumInput	10		OtherPercentCutOff	95		UseReportVars	Υ	
MaxNumReport	10		PrintWorth	Υ				

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size





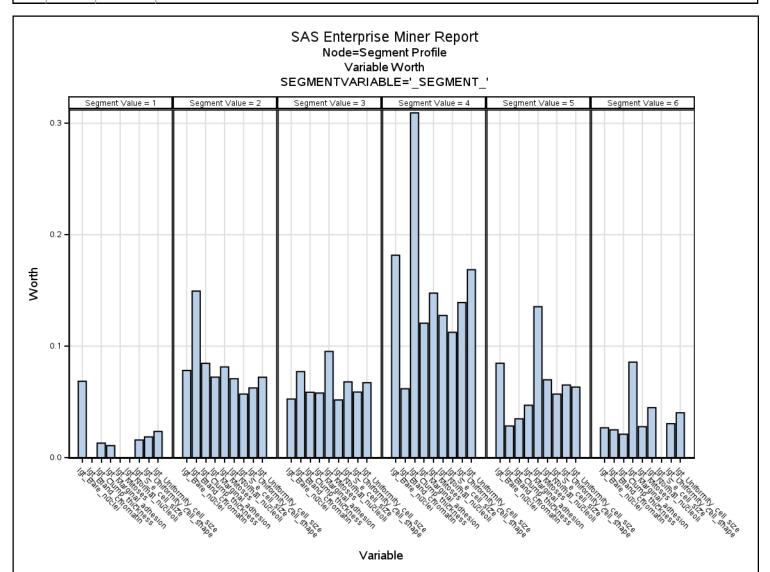
Node=Segment Profile Summary

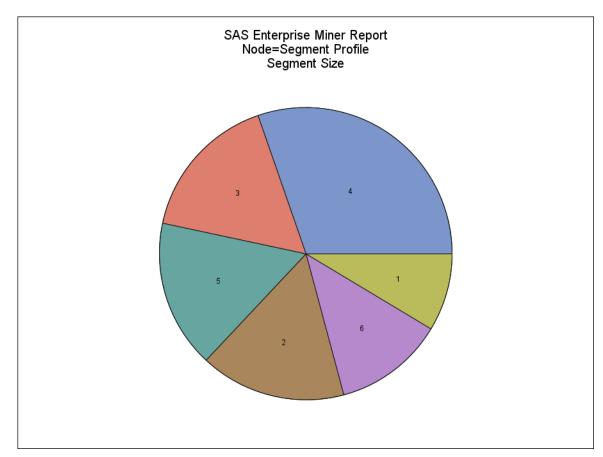
Node id = Prof Node label = Segment Profile Meta path = FIMPORT => Impt => Trans => Trans2 => Clus => Prof Notes =

Node=Segment Profile Properties

Property	Value	Default	Property	Value	Default	Property	Value	Default
Component	Profile		MinWorth	0.01		ProfileAll	N	
MaxDepth	1		NumHistBars	8		TargetRole	NONE	
MaxNumInput	10		OtherPercentCutOff	95		UseReportVars	Υ	
MaxNumReport	10		PrintWorth	Υ				

Role	Level	Frequency Count	Name
INPUT	INTERVAL	9	lgt_Bare_nuclei lgt_Bland_chromatin lgt_Clump_thickness lgt_Marginal_adhesion lgt_Mitoses lgt_Normal_nucleoli lgt_S_e_cell_size lgt_Uniformity_cell_shape lgt_Uniformity_cell_size





End of Report