

Data visualization using GANNO, GMAP and GREMOVE to map data onto the human body

Rui Huang, Jennifer McGinniss, and Toshio Kimura, Regeneron Pharmaceuticals, Inc.

ABSTRACT

In many therapeutic areas, symptom severity is captured separately for different body regions. Reporting these data through traditional summary tables by body regions and symptoms will be difficult for readers to understand and interpret. In contrast, data visualization tools can communicate complex information in an easily digestible format. This paper demonstrates two visualization methods in SAS to map data onto the human body where colors and symbols represent severity and symptoms in different body regions.

The first approach uses the SAS GANNO function on a background image of the human body to overlay symbols on impacted body regions via X, Y coordinates with Unicode symbols indicating symptoms, size representing proportion of patients and color representing severity. The second approach handles the human body as geographic regions. This method requires a map dataset of the body regions which can be generated in SAS JMP through the Custom Map Creator add-on. SAS geographical map functions such as GREMOVE can be used to further customize the map by combining body regions, and the GMAP function is used to display data onto those regions as colors based on their value (such as symptom severity). Various applications and alternative forms can be used to highlight treatment effect including splitting the body into half where one side is placebo and the other side is the active treatment or one side is baseline and the other side is the final visit. Figure examples will be provided to demonstrate how the methods compare.

INTRODUCTION

In many therapeutic areas, symptom severity is captured for different body regions. For example, patient-reported outcomes may report moderate (severity) pain (symptom) in the right arm (location) while reporting mild in the lower extremities. Traditional summary tables by symptom and location results in numerous, long tables that may span multiple pages making it difficult for readers to understand and interpret. Separately reporting each symptom and region makes detecting overall patterns very challenging, and, therefore, the reviewer may fail to see the entire picture. In contrast, visualization tools can overcome these challenges by transforming complex data into an easily digestible format. Through simulated examples from existing clinical study data, specifically patient-reported flare-ups in patients living with fibrodysplasia ossificans progressiva (FOP) and symptom severity score in patients experiencing atopic dermatitis, we will demonstrate two data visualization methods for displaying these types of outcomes.

METHOD 1

Through simulated examples from patient-reported flare-ups in patients living with FOP, the first method displays patient-reported flare-ups as coordinates with each reported symptom represented by a different symbol, severity represented by color, and incidence represented by size. The traditional method of reporting this type of information using a standard table may look like the following as shown in Table 1:

Table 1. Example table of symptom severity score and frequency by body region for Method 1

Body Region	Symptom	Placebo		Study Drug	
		Frequency	Severity	Frequency	Severity
Head	Pain	25	3	5	1
	Warmth	25	3	0	N/A
	Decrease in Movement	0	N/A	0	N/A
	Swelling	25	4	5	2
Arm	Pain	0	N/A	15	1
	Warmth	25	4	0	N/A
	Decrease in Movement	15	4	5	2
	Swelling	15	3	0	N/A
Trunk	Pain	25	3	15	1
	Warmth	0	N/A	0	N/A
	Decrease in Movement	15	4	5	2
	Swelling	15	4	5	2
Leg	Pain	25	4	0	N/A
	Warmth	25	4	15	1
	Decrease in Movement	25	3	0	N/A
	Swelling	25	3	0	N/A

In contrast to the traditional table, a figure displaying the same information as the table would be an easier way of reviewing all of the information in a more easily interpretable fashion. The first method of displaying symbols onto the body are detailed below.

PREPARE THE ANALYSIS RESULTS DATASET

Since the analysis can vary by different use, the steps to generate the analysis results dataset are not shown. In this example, each of the 4 body regions contain 4 symptoms with 2 analysis results (severity score and number of patients with the symptom). In this example, the results have been categorized in order to simplify downstream processing, since the focus of the paper is on data visualization. Therefore, the analysis results dataset (METHOD1_RESULTS) looks like the following as shown in Table 2:

Table 2. Analysis Results Dataset for Method 1 (METHOD1_RESULTS)

	Treatment	Region	Symptom	Frequency	Frequency_CAT	Severity_CAT
1	Placebo	Head	Swelling	25	3	4
2	Placebo	Head	Pain	25	3	3
3	Placebo	Head	Warmth	25	3	3
4	Placebo	Arm	Decrease in movement	15	2	4
5	Placebo	Arm	Warmth	25	3	4
6	Placebo	Arm	Swelling	15	2	3
7	Placebo	Trunk	Decrease in movement	15	2	4
8	Placebo	Trunk	Pain	25	3	3
9	Placebo	Trunk	Swelling	15	2	4
10	Placebo	Leg	Decrease in movement	25	3	3
11	Placebo	Leg	Pain	25	3	4
12	Placebo	Leg	Swelling	25	3	3
13	Placebo	Leg	Warmth	25	3	4
14	Study Drug	Head	Pain	5	1	1
15	Study Drug	Head	Swelling	5	1	2
16	Study Drug	Arm	Pain	15	2	1
17	Study Drug	Arm	Decrease in movement	5	1	2
18	Study Drug	Trunk	Swelling	5	1	2
19	Study Drug	Leg	Warmth	15	2	1

PREPARE THE ANNOTATION DATASET

Method 1 will use the analysis results dataset as shown in Table 2 and plot the values onto a background image. The plotting of the data will be done through PROC GANNO; therefore, the annotation dataset must be generated. The following steps were taken to generate the annotation dataset:

- 1) Generate the X-Y coordinates metadata: We first generated a X-Y coordinate metadata which will serve as the location for each symbol in the figure. In this example, the X-Y coordinate position metadata was generated for each body region, symptom and treatment group. This figure will be split in half with placebo on the left half and study drug on the right half; therefore, the X-axis will be adjusted accordingly.
- 2) Merge the X-Y coordinate metadata with the analysis results dataset: The analysis results dataset (METHOD1_RESULTS) was merged with the X-Y coordinate metadata. Each value will now have the associated coordinate position.
- 3) Create the annotation dataset for the analysis results: The dataset generated by Step 2 will be used as the basis for the annotation dataset. Symbols will be defined for each symptom, and colors associated with each severity score. Size of the symbol will vary as a function of frequency. For the purposes of this example, the frequency has been categorized so that that categorized frequency variable (Frequency_CAT) can be used as the value for the symbol size.

The symbols are defined by using Unicode characters. Using Unicode will open up the types of symbols available to use to depict different symptoms. There may be different ways in which Unicode characters can be used in

SAS as well as some limits as to which Unicode characters are available for use. In this example, the text has been set to the Unicode characters as shown below coupled with the style of "Albany AMT/unicode". When SAS reads the Unicode coding coupled with the appropriately defined style, SAS will convert the code to another set of characters which will appear in the text variable of the table as shown in Table 3; however, when this is rendered in generating the figure, the correct symbol will appear in the figure. The code to implement this is as follows:

```

data ANNO_RESULTS;
set input;
length function color $8 text $100;
retain function 'symbol' xsys ysys '1' when 'a' position '3' style 'Albany AMT/unicode';

if Symptom = 'Pain' then text='21AF'x ;
else if Symptom = 'Warmth' then text='2668'x ;
else if Symptom = 'Swelling' then text='273A'x ;
else if Symptom = 'Decrease in movement' then text='219D'x ;

if Severity_CAT = 4 then color='red' ;
else if Severity_CAT = 3 then color='orange' ;
else if Severity_CAT = 2 then color='green' ;
else if Severity_CAT = 1 then color='blue' ;

size = Frequency_CAT;

run;

```

- 4) Create the annotation dataset for treatment labels and legend: In addition to the annotation dataset for the analysis results, another annotation dataset (ANNO_LABELS) will be generated for the treatment labels and the line between the left and right halves to clearly separate the two sides. The legend will also be added through this annotation dataset.
- 5) Merge the 2 annotation datasets into a single final annotation dataset (ANNO_METHOD1): The 2 annotation datasets generated in Step 3 and 4 are set together to create a single final annotation dataset. The final dataset is shown below in Table 3 where records 1 through 19 are for the analysis results, 20 through 24 are for the treatment labels and the line separator, and 25 through 48 are for the legend. One thing to note is that the text column as displayed below in Table 3 is for illustration purposes only. The handling of Unicode across different applications has some peculiarities and appeared differently when copying the contents into Word; therefore, the text column in Table 3 mimics what is displayed when opening the dataset in SAS.

Table 3. Annotation Dataset for Method 1 (ANNO_METHOD1)

	X	Y	FUNCTION	COLOR	TEXT	style	SIZE	XSYS	YSYS	WHEN	POSITION	LINE
1	19	55	symbol	red	!	Albany AMT/unicode	2	1	1	a	3	
2	21	55	symbol	red	&h	Albany AMT/unicode	3	1	1	a	3	
3	19	57	symbol	orange	:	Albany AMT/unicode	2	1	1	a	3	
4	31	84	symbol	red	:	Albany AMT/unicode	3	1	1	a	3	
5	33	84	symbol	orange	!	Albany AMT/unicode	3	1	1	a	3	
6	31	86	symbol	orange	&h	Albany AMT/unicode	3	1	1	a	3	
7	31	24	symbol	orange	!	Albany AMT/unicode	3	1	1	a	3	
8	33	24	symbol	red	!	Albany AMT/unicode	3	1	1	a	3	
9	31	27	symbol	orange	:	Albany AMT/unicode	3	1	1	a	3	
10	33	27	symbol	red	&h	Albany AMT/unicode	3	1	1	a	3	
11	31	55	symbol	red	!	Albany AMT/unicode	2	1	1	a	3	
12	33	55	symbol	orange	!	Albany AMT/unicode	3	1	1	a	3	
13	31	57	symbol	red	:	Albany AMT/unicode	2	1	1	a	3	
14	53	55	symbol	blue	!	Albany AMT/unicode	2	1	1	a	3	
15	53	55	symbol	green	!	Albany AMT/unicode	1	1	1	a	3	
16	40	84	symbol	blue	!	Albany AMT/unicode	1	1	1	a	3	
17	42	84	symbol	green	:	Albany AMT/unicode	1	1	1	a	3	
18	40	24	symbol	blue	&h	Albany AMT/unicode	2	1	1	a	3	
19	40	55	symbol	green	:	Albany AMT/unicode	1	1	1	a	3	
20	36.3	5	move					1	1	a	3	
21	36.3	96	draw	black			0.5	1	1	a	3	3
22	0	95	label	black	Patient-reported Flare-ups in Placebo Arm		1	1	1	a	3	3
23	42	95	label	black	Patient-reported Flare-ups in Study Drug Arm		1	1	1	a	3	3
24	64	28	label	black	Number of Patients with Symptoms		1.1	1	1	a	3	3
25	65	26	symbol	black	dot		3	1	1	a	3	3
26	72	25	label	black	25		1	1	1	a	3	3

	X	Y	FUNCTION	COLOR	TEXT	style	SIZE	XSYS	YSYS	WHEN	POSITION	LINE
27	65	22	symbol	black	dot		2	1	1	a	3	3
28	72	21	label	black	15		1	1	1	a	3	3
29	65	18	symbol	black	dot		1	1	1	a	3	3
30	72	17	label	black	5		1	1	1	a	3	3
31	64	50	label	black	Symptom		1.1	1	1	a	3	3
32	65	48	symbol	black	!	Albany AMT/unicode	2	1	1	a	3	3
33	72	47	label	black	Pain	NONE	1	1	1	a	3	3
34	65	44	symbol	black	&h	Albany AMT/unicode	2	1	1	a	3	3
35	72	43	label	black	Warmth	NONE	1	1	1	a	3	3
36	65	40	symbol	black	!	Albany AMT/unicode	2	1	1	a	3	3
37	72	39	label	black	Decrease in movement	NONE	1	1	1	a	3	3
38	65	36	symbol	black	;	Albany AMT/unicode	2	1	1	a	3	3
39	72	35	label	black	Swelling	NONE	1	1	1	a	3	3
40	64	72	label	black	Average Severity	NONE	1.1	1	1	a	3	3
41	65	70	symbol	red	dot	NONE	1	1	1	a	3	3
42	72	69	label	black	4	NONE	1	1	1	a	3	3
43	65	66	symbol	orange	dot	NONE	1	1	1	a	3	3
44	72	65	label	black	3	NONE	1	1	1	a	3	3
45	65	62	symbol	green	dot	NONE	1	1	1	a	3	3
46	72	61	label	black	2	NONE	1	1	1	a	3	3
47	65	58	symbol	blue	dot	NONE	1	1	1	a	3	3
48	72	57	label	black	1	NONE	1	1	1	a	3	3

CREATE THE FIGURE USING PROC GANNO

To incorporate a background image into the figure, GOPTIONS will be used to define the file name and location that will be used as the background image. The image being used in this example is BODY_OUTLINE.png (note that a directory path may be required in the iback argument) and the code to set this file as the background is provided below:

```
goptions reset=all device=png iback="BODY_OUTLINE.png" imagestyle=fit;
```

Once the annotation dataset is generated, plotting the annotation dataset using PROC GANNO only requires a few lines of code as shown below along with final output in Figure 1:

```
proc ganno annotate=ANNO_METHOD1 datasys;
run;
quit;
```

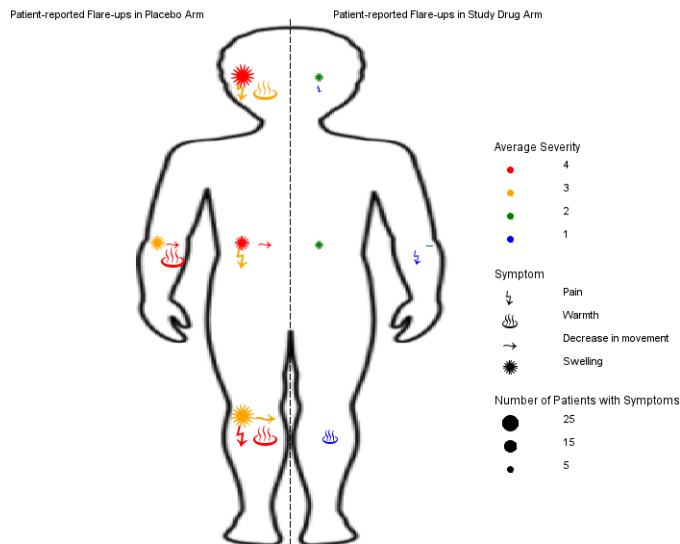


Figure 1. Final Figure using Method 1

METHOD 2

The second method treats body regions in a similar manner as geographic regions and uses SAS mapping functions to display values expressed through different colors onto different body regions. Table 4 below shows the typical table that displays the analysis results for different body regions over multiple time points using simulated clinical data for symptom severity score in patients with atopic dermatitis where larger values in the symptom score represents worse severity. A typical figure corresponding to this analysis may be a line plot showing each body region as a separate figure or perhaps many lines overlaid on top of each other in a single figure. Since the data are collected for each body region, a figure showing the results on those impacted body regions would be an alternative and more effective figure type which will be discussed in further detail in this section.

Table 4. Example table of symptom severity score over time for Method 2

Endpoint	Visit	Body Region	Placebo	Study Drug
Symptom Severity Score	Visit 1	Head	29.5	29.0
		Arm	28.5	28.0
		Trunk	27.5	27.0
		Leg	26.5	26.0
	Visit 2	Head	27.2	11.3
		Arm	25.5	9.1
		Trunk	23.8	8.0
		Leg	22.2	6.3
	Visit 3	Head	24.2	9.0
		Arm	22.5	8.0
		Trunk	20.8	7.0
		Leg	19.2	6.0
	Visit 4	Head	23.5	1.0
		Arm	22.5	1.0
		Trunk	21.5	1.0
		Leg	20.5	1.0

CREATE THE MAP DATASETS OF THE BODY REGIONS

In order to use map functions, the body regions must be available as a map dataset. If a map dataset is not available, the map dataset can be generated in SAS JMP through the Custom Map Creator JMP add-in. Steps to create the map dataset were detailed in the blog post by Conners^[1]. Using the JMP Custom Map Creator, an uploaded image can be traced to generate the map dataset. The Custom Map Creator will then export the x-y coordinate and shape datasets as SAS datasets. Figure 2 shows a screenshot of the Custom Map Creator after outlining the body figure. Tables 5 and 6 show the structure of the exported datasets. In this example, the datasets are named BODY_XY and BODY_REGION. While the BODY_REGION dataset is created and used as a reference in relating the Shape_ID to a label, the BODY_REGION dataset will not be used directly in further data processing. The body regions have been split in half to the left and right sides, since the data visualization in this example will display the results for placebo on the left and for study drug on the right.

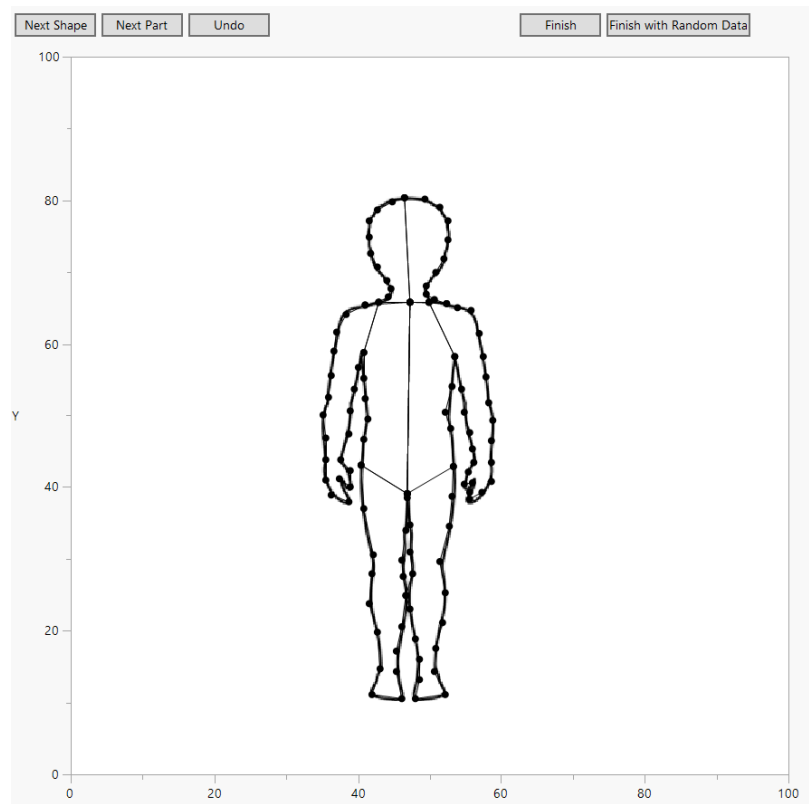


Figure 2. Outline the body figure

Table 5. Exported x-y coordinates dataset (BODY_XY)

	Shape_ID	X	Y
1	1	41.78	68.62
2	1	42.34	79.58
3	1	42.53	77.69
4	1	42.72	75.43
5	1	43.48	81.85
6	1	43.86	73.72
7	1	44.05	69.19
8	1	44.99	72.21
9	1	45.18	69.94
10	1	45.75	71.27
11	1	45.75	83.36
12	1	47.64	83.93
13	1	47.64	83.93
14	1	47.83	68.81
15	2	47.64	83.93
16	2	47.83	68.81
17	2	49.91	83.55
18	2	50.09	71.46
19	2	50.28	70.32
20	2	51.23	72.40
21	2	51.42	69.57
22	2	51.80	82.42
23	2	52.36	73.72
24	2	53.12	75.43
25	2	53.12	80.53
26	2	53.31	69.00
27	2	53.50	77.88
28	2	54.44	68.81
..

Table 6. Exported shape dataset (BODY_REGION)

	Shape_ID	Name
1	1	Left_Head
2	2	Right_Head
3	3	Left_Arm
4	4	Right_Arm
5	5	Left_Trunk
6	6	Right_Trunk
7	7	Left_Leg
8	8	Right_Leg

Once the BODY_XY dataset is created and imported into SAS, the map dataset can be further customized using the GREMOVE procedure. One notable function is to combine multiple neighboring regions into a larger region. This would, therefore, allow for a granular body region dataset to be developed and stored after which the granular regions can be combined together based on project needs. The GREMOVE procedure will process the input dataset and eliminate points along the border of adjoining regions thus creating a new contiguous region. Although this example does not use combined body regions, the code to combine multiple shapes into newly assigned shapes is nevertheless shown below. The example below joins the left and right head region by eliminating 3 points (records 13, 15, 16 from the pre-GREMOVE dataset highlighted in pink) that lie on the border of the original Shape_ID's 1 and 2. The dataset before PROC GREMOVE is shown in Table 7 showing the NewShape_ID column, and the dataset after PROC GREMOVE is shown in Table 8 with 3 less records.

```
proc gremove data=BODY_XY out=BODY_XY_COMBINED_SHAPES;
  by newshape_id;
  id shape_id;
run;
```

Table 7. Dataset before PROC GREMOVE

	NewShape_ID	Shape_ID	X	Y
1	1	1	41.78	68.62
2	1	1	42.34	79.58
3	1	1	42.53	77.69
4	1	1	42.72	75.43
5	1	1	43.48	81.85
6	1	1	43.86	73.72
7	1	1	44.05	69.19
8	1	1	44.99	72.21
9	1	1	45.18	69.94
10	1	1	45.75	71.27
11	1	1	45.75	83.36
12	1	1	47.64	83.93
13	1	1	47.64	83.93
14	1	1	47.83	68.81
15	1	2	47.64	83.93
16	1	2	47.83	68.81
17	1	2	49.91	83.55
18	1	2	50.09	71.46
19	1	2	50.28	70.32
20	1	2	51.23	72.40
21	1	2	51.42	69.57
22	1	2	51.80	82.42
23	1	2	52.36	73.72
24	1	2	53.12	75.43
25	1	2	53.12	80.53
26	1	2	53.31	69.00
27	1	2	53.50	77.88
28	1	2	54.44	68.81
...

Table 8. Dataset after PROC GREMOVE

	Segment	NewShape_ID	X	Y
1	1	1	41.78	68.62
2	1	1	42.34	79.58
3	1	1	42.53	77.69
4	1	1	42.72	75.43
5	1	1	43.48	81.85
6	1	1	43.86	73.72
7	1	1	44.05	69.19
8	1	1	44.99	72.21
9	1	1	45.18	69.94
10	1	1	45.75	71.27
11	1	1	45.75	83.36
12	1	1	47.64	83.93
13	1	1	47.83	68.81
14	1	1	49.91	83.55
15	1	1	50.09	71.46
16	1	1	50.28	70.32
17	1	1	51.23	72.40
18	1	1	51.42	69.57
19	1	1	51.80	82.42
20	1	1	52.36	73.72
21	1	1	53.12	75.43
22	1	1	53.12	80.53
23	1	1	53.31	69.00
24	1	1	53.50	77.88
25	1	1	54.44	68.81
...

PREPARE THE ANALYSIS RESULTS DATASET

As noted earlier, the example scenario will compare the analysis results of placebo and study drug for the symptom severity score for each body region. To facilitate review of the results, the body image will be split in half where the left side represents placebo and the right side represents study drug. The analysis results which are assumed to have already been computed using the appropriate analysis method. In this example, the mean has already been calculated and associated to the Shape_ID based on both the body region and treatment (procedure not shown). Table 9 shows the resulting dataset, BODY_ANALYSIS, which includes the computed mean symptom severity score for each body region by treatment.

While the GMAP CHORO statement that is used to generate the figure can handle continuous values, pre-processing the analysis results dataset by categorizing and formatting the continuous value into a categorical variable (MEAN_CAT and the format MEAN_CAT_FMT.) may make the formatting of the output easier to control. There are options such as MIDPOINT and RANGE within the PROC GMAP CHORO statement that can be used to generate similar displays although they are not used in this example.

Table 9. Example of an analysis results dataset (BODY_ANALYSIS)

	AVISITN	AVISIT	TRTN	TRT	Shape_ID	Region	PARAMCD	PARAM	MEAN	MEAN_CAT
1	1	Visit 1	1	Placebo	1	Left_Head	SYMPSEV	Symptom Severity Score	29.5	> 25
2	1	Visit 1	1	Placebo	3	Left_Arm	SYMPSEV	Symptom Severity Score	28.5	> 25
3	1	Visit 1	1	Placebo	5	Left_Trunk	SYMPSEV	Symptom Severity Score	27.5	> 25
4	1	Visit 1	1	Placebo	7	Left_Leg	SYMPSEV	Symptom Severity Score	26.5	> 25
5	1	Visit 1	2	Study Drug	2	Right_Head	SYMPSEV	Symptom Severity Score	29.0	> 25
6	1	Visit 1	2	Study Drug	4	Right_Arm	SYMPSEV	Symptom Severity Score	28.0	> 25
7	1	Visit 1	2	Study Drug	6	Right_Trunk	SYMPSEV	Symptom Severity Score	27.0	> 25
8	1	Visit 1	2	Study Drug	8	Right_Leg	SYMPSEV	Symptom Severity Score	26.0	> 25
9	2	Visit 2	1	Placebo	1	Left_Head	SYMPSEV	Symptom Severity Score	27.2	> 25
10	2	Visit 2	1	Placebo	3	Left_Arm	SYMPSEV	Symptom Severity Score	25.5	> 25
11	2	Visit 2	1	Placebo	5	Left_Trunk	SYMPSEV	Symptom Severity Score	23.8	20 to 25
12	2	Visit 2	1	Placebo	7	Left_Leg	SYMPSEV	Symptom Severity Score	22.2	20 to 25
13	2	Visit 2	2	Study Drug	2	Right_Head	SYMPSEV	Symptom Severity Score	11.3	10 to 15
14	2	Visit 2	2	Study Drug	4	Right_Arm	SYMPSEV	Symptom Severity Score	9.1	5 to 10
15	2	Visit 2	2	Study Drug	6	Right_Trunk	SYMPSEV	Symptom Severity Score	8.0	5 to 10
16	2	Visit 2	2	Study Drug	8	Right_Leg	SYMPSEV	Symptom Severity Score	6.3	5 to 10
...

PREPARE THE ANNOTATION DATASET

In addition to the map dataset (BODY_XY) and the analysis results dataset (BODY_ANALYSIS), the annotation dataset (BODY_ANN) must also be generated. The annotation dataset is used to draw the black dotted line to differentiate the left and right halves of the body. Additionally, the treatment labels are drawn onto the figure through the annotation dataset. The code used to generate the annotation dataset along with the resulting dataset is shown below in Table 10:

```

data BODY_ANN;
  length function color $8 position $1 text $20;
  retain xsys ysys '2' hsys '3' when 'a' position '5';

  /** Draw the left-right separator ***/
  function='move';   x=48;       y=12; output;
  function='draw';   line=3;     size=0.5;      color='black'; x=48; y=100; output;

  /** Draw the Placebo label ***/
  function='label';  size=1.5;   color='black'; style='Arial Black'; x=39; y=82;
  text='Placebo';   output;

  /** Draw the Treatment label ***/
  function='label';  size=1.5;   color='black'; style='Arial Black'; x=56; y=82;
  text='Study Drug'; output;
run;

```

Table 10. Example the annotation dataset (BODY_ANN)

	FUNCTION	COLOR	POSITION	TEXT	XSYS	YSYS	HSYS	WHEN	X	Y	LINE	SIZE	STYLE
1	move		5		2	2	3	a	48	12			
2	draw	black	5		2	2	3	a	48	100	3	0.5	
3	label	black	5	Placebo	2	2	3	a	39	82	3	1.5	Arial Black
4	label	black	5	Study Drug	2	2	3	a	56	82	3	1.5	Arial Black
...

CREATE THE BODY MAP FIGURE VIA PROC GMAP IN SAS

With the three datasets prepared (BODY_XY, BODY_ANALYSIS and BODY_ANNO), the GMAP procedure can now be used to generate the figure. Within the GMAP procedure, the MAP argument defines the map dataset used to generate the map; in this example, the BODY_XY dataset contains the map dataset. The DATA argument defines the analysis results which in this example is the BODY_ANALYSIS dataset containing the analysis value in the MEAN_CAT variable. The records in MAP and DATA are linked through the variables defined in the ID statement. The Shape_ID variable links the two datasets. The ID statement can take on more than one variable, and those variables may be numeric or character variables; this feature can be used when creating the figure across multiple visits. The CHORO statement adds the color to the regions based on a value in the BODY_ANALYSIS dataset. The variable to be used is the MEAN_CAT variable. The format for MEAN_CAT is MEAN_CAT_FMT. which is defined in the FORMAT statement. The ANNOTATE argument defines the dataset used for annotations which in this example is the BODY_ANNO dataset. In addition, there are several options that are also defined. The ALL option is used to ensure that all regions in the map dataset will be used. The COUTLINE option of white defines the color of the shape border.

Lastly, the color and pattern that is used by PROC GMAP are defined in the PATTERN statements. For this example, the following PATTERN statements were used:

```
pattern1 value=solid color='Teal';  
pattern2 value=solid color='LightSeaGreen';  
pattern3 value=solid color='Pink';  
pattern4 value=solid color='LightCoral';  
pattern5 value=solid color='Crimson';
```

The code to generate the body map along with the output are shown below in Figure 3:

```
proc gmap map=BODY_XY data=BODY_ANALYSIS all;  
  id shape_id;  
  format mean_cat mean_cat_fmt.;  
  choro mean_cat / coutline=white annotate=BODY_ANNO;  
run;  
quit;
```

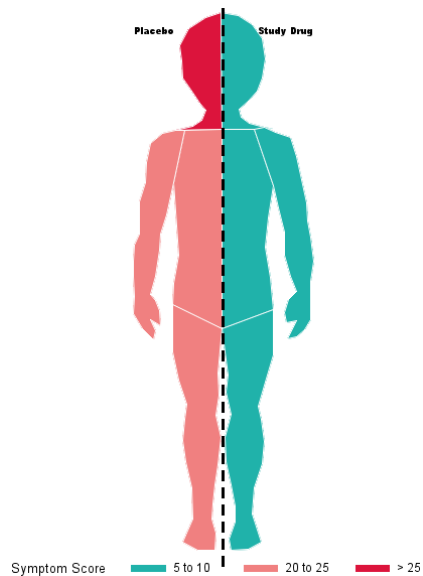


Figure 3. Sample output from GMAP

CREATE THE BODY MAP FIGURE OVER TIME

Assessing symptom severity over time is a common analysis which the human body map figure can be modified to accommodate. The body figure would be repeated over multiple visits; therefore, the shape would have to be duplicated and the x-axis for the x-y coordinates need be adjusted accordingly for each visit in the BODY_XY dataset. Similarly, the additional records and the x-axis adjustments must also be made in the BODY_ANNO dataset to create the left-right separator and the treatment labels for each visit. The visit label will also be added to the annotation dataset.

The example code below is a small macro that will create the BODY_XY_VISIT and BODY_ANNO_VISIT datasets to create the body map shapes for each visit:

```
%macro map_by_visit_data;

proc sql noprint;
  /** Count the number of visits ***/
  select count(distinct avisit)
         into: n_visit separated by " "
  from   BODY_ANALYSIS
  ;
  /** Store the visit name for each visit ***/
  select distinct avisit
         into: u_visit separated by ","
  from   BODY_ANALYSIS
  ;
quit;

/** Loop through each visit to duplicate the body shape for each visit ***/
%do i=1 %to &n_visit.;

  %let visit = %scan(%bquote(&u_visit.), &i., %str(,));
  data map&i.;
    set BODY_XY;
    avisit = "&visit.";
    /** Adjust the x-axis to shift the shape to the right ***/
    x = x + %eval( 27 * ( &i - 1 ) );
  run;

%end;

/** Set all of the newly created map datasets together ***/
data BODY_XY_VISIT;
  set map:;
run;

/** Create the BODY_ANNO_VISIT dataset ***/
data BODY_ANNO_VISIT;
  length function color $8 position $1 text $20;
  retain xsys ysys '2' hsys '3' when 'a' position '5';

  /** Loop through each visit ***/
  %do i=1 %to &n_visit.;

    /** Draw the left-right separator ***/
    function='move';   x=48 + %eval(27*(&i-1)); y=14; output;
    function='draw';   line=3;   size=0.5; color='black'; x=48 + %eval(27*(&i-1)); y=85; output;

    /** Draw the Placebo label ***/
    function='label';  size=1.5; color='black'; style='Arial Black'; x=39 + %eval(27*(&i-1)); y=82;
    text='Placebo';   output;

    /** Draw the Treatment label ***/
    function='label';  size=1.5; color='black'; style='Arial Black'; x=56 + %eval(27*(&i-1)); y=82;
    text='Study Drug'; output;

    /** Draw the Visit label ***/
    %let visit = %scan(%bquote(&u_visit.), &i., %str(,));
    function='label';  size=1.5; color='black'; style='Arial Black'; x=48 + %eval(27*(&i-1)); y=12;
    text="&visit.";   output;

  %end;

run;
```

```
%mend;
```

However, no changes are necessary in the BODY_ANALYSIS dataset (assuming that the dataset contains the results of all visits) since the ID statement in PROC GMAP can take multiple variables, and the variables can be either numeric or character. Therefore, both Shape_ID and AVISIT will be included in the PROC GMAP ID statement as shown below along with the resulting figure in Figure 4:

```
proc gmap map=BODY_XY_VISIT data=BODY_ANALYSIS all;  
  id shape_id avisit;  
  format mean_cat mean_cat_fmt.;  
  choro mean_cat / outline=white annotate=BODY_ANNO_VISIT;  
run;
```

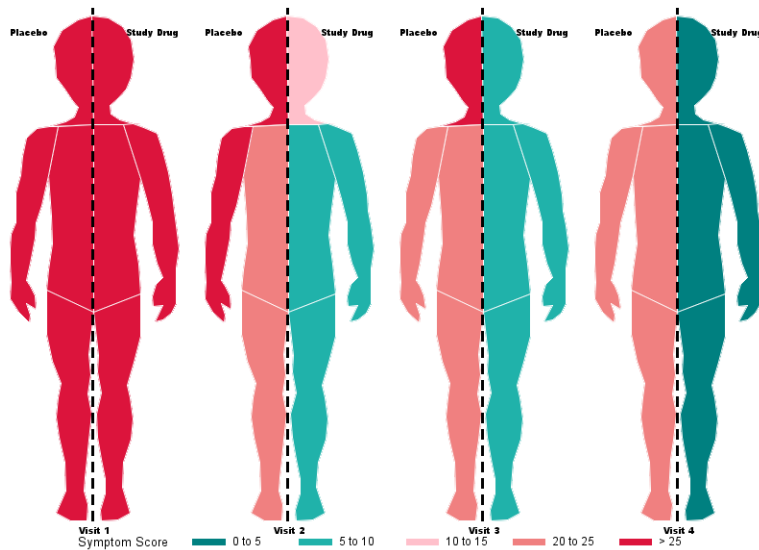


Figure 4. Sample figure of multiple time points

CONCLUSION

Traditional tables displaying the values over time for each body region may result in lengthy displays spanning multiple pages which makes understanding and interpreting the results difficult. Unfortunately, these detailed tables may be unavoidable as they contain more specific and precise information. However, they can be accompanied by figures that are better data visualizations of the same information. Placing data onto the body especially when the information is captured for each body region would place the data into the proper context and allow for a more holistic visualization displaying the results for the entire body in a single glance and allows for easier interpretation.

There is at least one drawback to these figures. The major limitation is that the variability of the results is not displayed. There are no error bars associated with each body region. One potential way to address this is through the exploration of gradient color, perhaps radial gradient coloring.

A recent SAS v9.4 maintenance release has introduced PROC SGMAP. Due to the timing of this paper and the availability of maintenance release version on the company server, PROC GMAP instead of PROC SGMAP was used. Based on reading the documentation for PROC SGMAP, some of the code can be simplified and used with ODS graphics features such as SG PANEL which will allow for greater flexibility and ease of use. Future continued work will involve migrating to the newer SGMAP procedure.

Complementing the traditional tables, these figures are able to contextualize, visualize, and represent results to tell an evocative story about the patient journey. The flexibility of these displays allows the user to simultaneously display multiple dimensions of data (e.g., timepoints, treatment groups, multiple outcomes, outcome attributes) in a single view. Treatment effect over time could be easily distinguished intuitively. These data visualization tools will help audiences digest data effectively and improve communication with non-statistical and non-technical colleagues by presenting the

information in a simple, easily digestible format.

REFERENCES

1. Conners, Shannon. JMP Blog. 2015. "Creating a custom map for my workout data in JMP 12." Posted/updated May 8, 2015. <https://community.jmp.com/t5/JMP-Blog/Creating-a-custom-map-for-my-workout-data-in-JMP-12/ba-p/30559>.

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CONTACT INFORMATION

Your comments and questions are valued and encouraged. Contact the author at:

Rui Huang
Regeneron Pharmaceuticals
777 Old Saw Mill River Rd, Tarrytown, NY 10591
e-mail: rui.huang@regeneron.com

Toshio Kimura
Regeneron Pharmaceuticals
777 Old Saw Mill River Rd, Tarrytown, NY 10591
e-mail: toshio.kimura@regeneron.com

Jennifer McGinniss
Regeneron Pharmaceuticals
777 Old Saw Mill River Rd, Tarrytown, NY 10591
e-mail: jennifer.mcginniss@regeneron.com