

# Visualizing Essential Metrics for Assessing Disease Dynamics in Hematologic Oncology Trials: A SAS Graphic Approach

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## ABSTRACT

Chronic Lymphocytic Leukemia (CLL) and Small Lymphocytic Lymphoma (SLL) are different manifestations of the same disease. Patients with CLL and SLL can exhibit lymph node involvement, leading to lymphadenopathy due to the accumulation of abnormal lymphocytes. Absolute Lymphocyte Count (ALC) and Sum of Products of Diameters (SPD) for target lesions are both important metrics for assessing disease dynamics in CLL and SLL. These measures are essential for indicating disease progression, evaluating treatment responses, and guiding clinical decision-making. To enhance the understanding of these data, trends in ALC and SPD over time are monitored using dual-axis plots. This paper presents a comprehensive approach utilizing SAS graphics to illustrate the trends of ALC and SPD, detailing the processes of data collection and data visualization. Ultimately, this work aims to contribute to improved insights in hematologic oncology trials.

## INTRODUCTION

CLL and SLL are different manifestations of the same disease and are managed in the same way. CLL primarily affects the blood and bone marrow, while SLL predominantly involves the lymph nodes. Both conditions are characterized by the slow growth of white blood cells known as lymphocytes. Lymphocytes are a subtype of white blood cell that play a crucial role in the immune system, primarily taking part in the body's response to infections and diseases. In CLL/SLL, ALC refers to the total number of lymphocytes present in a specific volume of blood. Monitoring changes in ALC over time can assess how well a patient is responding to treatment. SPD is a method used to quantify tumor burden in tissues based on imaging. It is calculated by measuring the diameters of multiple tumors or lymph nodes in a patient and summing the products of these diameters for predefined target lesions per lymphoma response criteria. Monitoring changes in SPD can provide a measure of how treatment impacts tumor burden.

A dual-axis plot provides a more integrated view of tracking ALC and SPD over time, enabling simultaneous visualization on a single graph. This can help identify correlations that might be missed when these metrics are viewed in separate plots. By viewing ALC and SPD together, researchers can learn better how changes in lymphocyte counts relate to tumor burden, obtaining a more comprehensive view of the patient's response to treatment. Additionally, a dual-axis plot condenses information into a single visual representation, making it easier to present and interpret data without requiring multiple separate plots.

The remainder of the paper is organized into three sections: First, derivation of ALC and SPD from source SDTM datasets; Second, generation of analysis values (AVAL) for customized ADaM datasets with examples; Third, creation of dual-axis plots in SAS 9.4 using the SGPLOT procedure and the Graph Template Language (GTL).

## RETRIEVING DATA FROM SDTM DOMAIN

Within the Study Data Tabulation Model (SDTM), ALC data are typically captured in the Laboratory Test Results (LB) domain, while SPD measurements are generally derived from the Tumor Results (TR) domain.

- The LB domain captures essential information related to laboratory tests conducted during clinical trials. The ALC is included in the LB domain when LBTESTCD is equal to "LYM" (see Figure 1).

|                     |                               |
|---------------------|-------------------------------|
| Absolute Lymphocyte | LBORRES when LBTESTCD = 'LYM' |
| LBTEST              | Unit:                         |
|                     | LBORRESU                      |

Figure 1: eCRF for LYM Collection

- The TR domain includes measurements and/or assessments of the tumors and lesions identified in the Tumor/Lesion Identification (TU) domain. The calculation of SPD is based on the measurements of the longest diameter (LDi) and the shortest diameter (SDi) (see Figure 2) obtained from the TR domain.

|                  |        |                                 |          |          |
|------------------|--------|---------------------------------|----------|----------|
| Longest Diameter | TRTEST | TRORRES when TRTESTCD = 'LDIAM' | TRSTRESC | TRSTRESN |
| Short Axis       | TRTEST | TRORRES when TRTESTCD = 'LPERP' | TRSTRESC | TRSTRESN |

Figure 2: eCRF for LDi and SDi Collection

## GENERATING ANALYSIS VALUE FOR ADAM

To generate plots showing ALC and SPD over time, we developed customized ADaM dataset: ADLYM (Analysis Dataset of Lymphocyte, derived from SDTM LB domain) and ADTL (Analysis Dataset of Target Lesions, derived from SDTM TR domain). Both datasets follow the Basic Data Structure (BDS), which consists of one or more observations for each subject, analysis parameter, and analysis time point.

The analysis parameter "ALC for CLL/SLL" is included in the ADLYM dataset. To derive the analysis value for this parameter and obtain non-missing laboratory values, LB.LBSTRESN is mapped to AVAL for records where LB.LBTESTCD has a data value of "LYM". Baseline and post-baseline observations are both included.

In this example, lesion diameter measurements are provided by the investigator. The parameter "Sum of Diameter of Target Lesions per Investigator" is included as an analysis parameter in ADTL dataset. To derive this parameter, the SPD for target lesions is calculated based on investigator assessments recorded in the TR domain, using the longest and shortest diameters for each target lesion per visit. The per-visit SPD is obtained by summing the products of the longest and shortest diameters across predefined target lesions.

All example data in this paper are dummy and do not reflect observations from study subjects.

## CALCULATION OF SPD FOR TARGET LESION

- Step 1: Identification of target lesions for SPD calculation

Target lesions included in the SPD parameter were identified using the TU domain. Lesion designations in TU were linked to corresponding measurements in TR domain via the unique lesion identifiers TULNKID/TRLNKID, ensuring consistent mapping between identification and assessment records. In the illustrative example (Table 1), the subject (USUBJID = 1111) had two target lesions TN1 (Liver) and TN2 (Mediastinal Lymph Node) which were classified within the LSNHM group for the CLL/SLL cohorts and included in the SPD computation.

| DOMAIN | USUBJID | TUGRPID | TUSPID | TULNKID | TUTEST               | TUSTRESC | TULOC                  | TUMETHOD | TUEVAL       |
|--------|---------|---------|--------|---------|----------------------|----------|------------------------|----------|--------------|
| TU     | 1111    | LSNHM   | 1      | TN1     | Tumor Identification | TARGET   | LIVER                  | CT SCAN  | INVESTIGATOR |
| TU     | 1111    | LSNHM   | 2      | TN2     | Tumor Identification | TARGET   | MEDIASTINAL LYMPH NODE | CT SCAN  | INVESTIGATOR |

Table 1: TU Domain Example for TUTEST = "Tumor Identification" and TUSTRESC = "TARGET"

- Step 2: Measurement of diameters and calculation of lesion-wise products

For each target lesion, the longest diameter (LDi) and shortest diameter (SDi) were recorded, typically in millimeters (mm). In the data collection shown in Table 2, "Longest Perpendicular" corresponds to the shortest diameter. As illustrated, the LDi and SDi measurements at each time point for all target lesions for the subject (USUBJID = 1111) depicted in Table 1 are captured in the TR domain. For each time point and each lesion, the product of diameters was computed as LDi × SDi, forming the lesion-level inputs for subsequent SPD aggregation.

At Screening, the diameter (TN1) = LDi \* SDi = 43 \* 32 = 1376 mm

At Cycle 4, the diameter (TN1) = LDi \* SDi = 38 \* 28 = 1064 mm

At Cycle 6, the diameter (TN1) = LDi \* SDi = 33 \* 29 = 957 mm

At Screening, the diameter (TN2) = LDi \* SDi = 49 \* 39 = 1911 mm

At Cycle 4, the diameter (TN2) = LDi \* SDi = 48 \* 32 = 1536 mm

At Cycle 6, the diameter (TN2) = LDi \* SDi = 35 \* 26 = 910 mm

| DOMAIN | USUBJID | TRGRPID | TRSPID | TRLNKID | TRTEST                | TRCAT  | TRSTRESN | TRSTRESU | TRMETHOD | VISIT     |
|--------|---------|---------|--------|---------|-----------------------|--------|----------|----------|----------|-----------|
| TR     | 1111    | LSNHM   | 1      | TN1     | Longest Diameter      | TARGET | 43       | mm       | CT SCAN  | Screening |
| TR     | 1111    | LSNHM   | 1      | TN1     | Longest Perpendicular | TARGET | 32       | mm       | CT SCAN  | Screening |
| TR     | 1111    | LSNHM   | 1      | TN1     | Longest Diameter      | TARGET | 38       | mm       | CT SCAN  | Cycle 4   |
| TR     | 1111    | LSNHM   | 1      | TN1     | Longest Perpendicular | TARGET | 28       | mm       | CT SCAN  | Cycle 4   |
| TR     | 1111    | LSNHM   | 1      | TN1     | Longest Diameter      | TARGET | 33       | mm       | CT SCAN  | Cycle 6   |
| TR     | 1111    | LSNHM   | 1      | TN1     | Longest Perpendicular | TARGET | 29       | mm       | CT SCAN  | Cycle 6   |
| TR     | 1111    | LSNHM   | 2      | TN2     | Longest Diameter      | TARGET | 49       | mm       | CT SCAN  | Screening |
| TR     | 1111    | LSNHM   | 2      | TN2     | Longest Perpendicular | TARGET | 39       | mm       | CT SCAN  | Screening |
| TR     | 1111    | LSNHM   | 2      | TN2     | Longest Diameter      | TARGET | 48       | mm       | CT SCAN  | Cycle 4   |
| TR     | 1111    | LSNHM   | 2      | TN2     | Longest Perpendicular | TARGET | 32       | mm       | CT SCAN  | Cycle 4   |
| TR     | 1111    | LSNHM   | 2      | TN2     | Longest Diameter      | TARGET | 35       | mm       | CT SCAN  | Cycle 6   |
| TR     | 1111    | LSNHM   | 2      | TN2     | Longest Perpendicular | TARGET | 26       | mm       | CT SCAN  | Cycle 6   |

**Table 2: TR Domain Example for TRTEST in (“Longest Diameter” and “Longest Perpendicular”) Where TRCAT = “TARGET”**

- Step 3: Aggregation of lesion-wise products to derive SPD

At each assessment time point, the sum of the lesion-wise products ( $LDi \times SDi$ ) across all predefined target lesions was computed to obtain the SPD.

At Screening,  $TN1 + TN2 = 1376 + 1911 = 3287$  mm

At Cycle 4,  $TN1 + TN2 = 1064 + 1536 = 2600$  mm

At Cycle 6,  $TN1 + TN2 = 957 + 910 = 1867$  mm

| USUBJID | PARAMCD | BASE | AVAL | CHG   | PCHG         | TRDTC      | NNTLINV | ADT        | ADY | ABLFL | ANL01FL |
|---------|---------|------|------|-------|--------------|------------|---------|------------|-----|-------|---------|
| 1111    | SPDINV  | 3287 | 3287 | .     | .            | 2022-09-27 | 2       | 2022-09-27 | -24 | Y     |         |
| 1111    | SPDINV  | 3287 | 2600 | -687  | -20.90051719 | 2023-01-24 | 2       | 2023-01-24 | 96  |       | Y       |
| 1111    | SPDINV  | 3287 | 1867 | -1420 | -43.20048677 | 2023-04-04 | 2       | 2023-04-04 | 166 |       | Y       |

**Table 3: Example for SPDINV in ADTL for the Subject Corresponding to Table 2**

- Step 4: Selection of observations for inclusion in the analysis

Verify that the Total Number of Target Lesions (NNTLINV) assessed at each post-baseline visit matches the baseline Total Number of Target Lesions. In this example, subjects with fewer post-baseline target lesions than at baseline are excluded from the analysis. For example (Table 4), a subject (USUBJID = 2222) with six target lesions at baseline but only with two lesions (TN3 and TN4) assessed at Cycle 2 would be excluded, as the reduced count reflects non-evaluable lesions rather than true lesion shrinkage. Accordingly, the analysis flag (ANL01FL) for the associated post-baseline records is set to “N”, indicating exclusion (see Table 5). Note: In other studies, subjects with fewer post-baseline target lesions than at baseline may be included if the reduction reflects completed resolution of lesions (i.e., no longer evaluable). That scenario is not addressed in this example.

| DOMAIN | USUBJID | TRSPID | TRLNKID | TRTESTCD | TRCAT | TRSTRESN | TRSTRESU | TRMETHOD | VISIT   | TRSTAT    | TRREASND | TRDTC      |
|--------|---------|--------|---------|----------|-------|----------|----------|----------|---------|-----------|----------|------------|
| TR     | 2222    |        | 1       | TN1      | LDIAM | TARGET   | 24       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 1       | TN1      | LPERP | TARGET   | 20       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 1       | TN1      | LPERP | TARGET   | .        |          | CT SCAN | Cycle 2   | NOT DONE | 2023-06-07 |
| TR     | 2222    |        | 2       | TN2      | LDIAM | TARGET   | 25       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 2       | TN2      | LPERP | TARGET   | 23       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 2       | TN2      | LPERP | TARGET   | .        |          | CT SCAN | Cycle 2   | NOT DONE | 2023-06-07 |
| TR     | 2222    |        | 3       | TN3      | LDIAM | TARGET   | 54       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 3       | TN3      | LPERP | TARGET   | 31       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 3       | TN3      | LDIAM | TARGET   | 43       | mm       | CT SCAN | Cycle 2   |          | 2023-06-07 |
| TR     | 2222    |        | 3       | TN3      | LPERP | TARGET   | 27       | mm       | CT SCAN | Cycle 2   |          | 2023-06-07 |
| TR     | 2222    |        | 4       | TN4      | LDIAM | TARGET   | 64       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 4       | TN4      | LPERP | TARGET   | 21       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 4       | TN4      | LDIAM | TARGET   | 97       | mm       | CT SCAN | Cycle 2   |          | 2023-06-07 |
| TR     | 2222    |        | 4       | TN4      | LPERP | TARGET   | 32       | mm       | CT SCAN | Cycle 2   |          | 2023-06-07 |
| TR     | 2222    |        | 5       | TN5      | LDIAM | TARGET   | 70       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 5       | TN5      | LPERP | TARGET   | 36       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 5       | TN5      | LPERP | TARGET   | .        |          | CT SCAN | Cycle 2   | NOT DONE | 2023-06-07 |
| TR     | 2222    |        | 6       | TN6      | LPERP | TARGET   | 69       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 6       | TN6      | LPERP | TARGET   | 40       | mm       | CT SCAN | Screening |          | 2023-04-18 |
| TR     | 2222    |        | 6       | TN6      | LPERP | TARGET   | .        |          | CT SCAN | Cycle 2   | NOT DONE | 2023-06-07 |

**Table 4: TR Domain Example for Non-evaluable Target Lesion**

| USUBJID | PARAMCD | PARCAT1 | BASE | AVAL | CHG   | PCHG      | NNTLINV | VISIT     | ADY | ANL01FL |
|---------|---------|---------|------|------|-------|-----------|---------|-----------|-----|---------|
| 2222    | SPDINV  | INV     | 9353 | 9353 | .     | .         | 6       | Screening | -7  |         |
| 2222    | SPDINV  | INV     | 9353 | 4265 | -5088 | -54.39966 | 2       | Cycle 2   | 47  | N       |

**Table 5: Example for SPDINV in ADTL for a Subject (USUBJID = 2222) Corresponding to Table 4**

## DATA DYNAMIC VISUALIZATION

### KEY CHECKS BEFORE PLOTTING

- Standardize a common visit structure across both data endpoints  
Because ALC and SPD may follow different visit schedules (with laboratory assessments typically more frequently), data should be preprocessed to align observations by analysis day (ADY) or mapped to a common visit grid defined by the study design. In this example, 'Month' was derived as their analysis visit. (see Table 6)
- Selection of appropriate dual-axis scales to represent trends accurately  
Because ALC and SPD typically span different numeric ranges, plotting both on a single scale can obscure one or both series. Therefore, it is important to review the data and select appropriate dual-axis scales that accurately represent the trends for both datasets.
- Selection of appropriate statistical procedure for graphical display  
In this example, median change was used to analyze ALC and SPD rather than mean change. Clinical datasets often contain outliers arising from measurement error or atypical patient responses, which can disproportionately influence the mean. The median is more robust to extreme values and better reflects the central tendency. In addition, the analysis focuses on the central trend of the data, which is often more relevant in clinical settings where the goal is to understand the typical patient response. Note: Scatter plot points reflect the median, with upper and lower error bars showing the 75<sup>th</sup> and 25<sup>th</sup> percentiles, respectively.

### GRAPH APPROACH

Both the SAS SGPLOT and GTL procedures can produce dual-axis plot. SGPLOT is designed for straightforward, typically single-cell plots (one graph per output), while GTL offers flexible and powerful capabilities for constructing complex multi-cell layouts with multiple plots arranged in rows/columns. Table 6 represents an example of the input dataset used to generate the dual-axis plot with the SGPLOT and GTL procedures.

| AVISITC | AVISIT  | N1 | MEDIAN1  | P251     | P751     | N2 | MEDIAN2  | P252     | P752     | GROUPCD | GROUPCD | COUNT1 | COUNT2 |
|---------|---------|----|----------|----------|----------|----|----------|----------|----------|---------|---------|--------|--------|
| BL      | BL      | 92 | 0        | 0        | 0        | 91 | 0        | 0        | 0        | ALC     | SPD     | 92     | 91     |
| 1       | Month 1 | 87 | 97.3513  | -25.2703 | 275.0418 | 6  | -29.2636 | -79.8576 | -12.5062 | ALC     | SPD     | 87     | 6      |
| 2       | Month 2 | 81 | 214.2961 | 71.71748 | 329.4458 | 3  | 52.54443 | -93.2917 | 58.28468 | ALC     | SPD     | 81     | 3      |
| 3       | Month 3 | 75 | 182.2604 | 15.71703 | 331.7468 | 69 | 9.488875 | -67.7971 | 53.17379 | ALC     | SPD     | 75     | 69     |
| 4       | Month 4 | 69 | 240.471  | 83.55525 | 336.6376 | 7  | -19.969  | -52.584  | 25.91491 | ALC     | SPD     | 69     | 7      |
| 5       | Month 5 | 62 | 242.5988 | 63.79369 | 352.4564 | 21 | -30.0867 | -54.5043 | 22.45496 | ALC     | SPD     | 62     | 21     |
| 6       | Month 6 | 55 | 136.8807 | -5.8317  | 286.8924 | 41 | -7.18848 | -47.4888 | 48.8586  | ALC     | SPD     | 55     | 41     |

Table 6: Example Input Dataset for Creating the Graph

### EXAMPLE 1: THE SGPLOT PROCEDURE

The SGPLOT procedure generates the dual-axis graph illustrated in Figure 3. This graph is a single-cell plot featuring dual y-axis: the primary (left) y-axis is ALC data (median1), while the secondary (right) y-axis corresponds to SPD data (median2). Within this single-cell layout, scatter plots with square-filled markers and associated error bars are overlaid with series lines for both ALC and SPD data. Additionally, two x-axis tables are positioned aligned below the plot area, aligned with the x-axis, displaying subject counts for ALC and SPD, respectively. Both the graphical elements and the x-axis tables are combined within the same single-cell layout.

Median Change in ALC and SPD in CLL/SLL Patients  
(APaT Population)

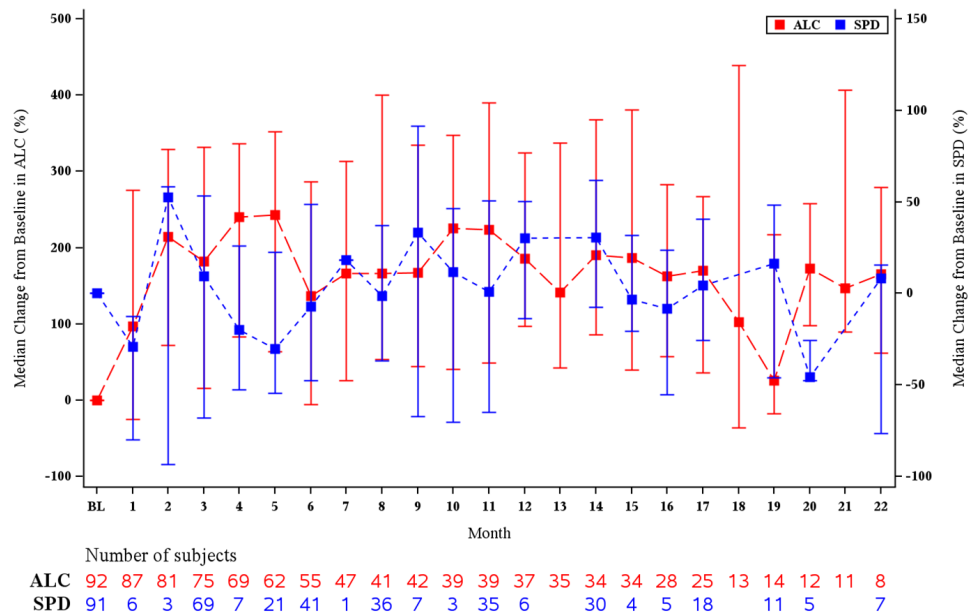


Figure 3: SGPLOT Dual-axis Graph for ALC and SPD

SGPLOT CODE :

```
proc sgplot data=for_graph;
  yaxis label="Median Change from Baseline in ALC (%)"
    values=(-100 to 500 by 100);
  y2axis label="Median Change from Baseline in SPD (%)"
    values=(-100 to 150 by 50);
  xaxis label="Month" type=discrete;
  scatter x=avisitc y=median1/yerrorlower=p251 yerrorupper=p751
    errorbarattrs=(color=red pattern=solid)
    markerattrs=(symbol=squarefilled color=red)
    legendlabel="ALC" name="s1";
  series x=avisitc y=median1/lineattrs=(pattern=mediumdash color=red);
  scatter x=avisitc y=median2/y2axis yerrorlower=p252 yerrorupper=p752
    errorbarattrs=(color=blue pattern=solid)
    markerattrs=(symbol=squarefilled color=blue)
    legendlabel="SPD" name="s2";
  series x=avisitc y=median2/y2axis
    lineattrs=(pattern=shortdash color=blue);
  keylegend "s1" "s2"/location=inside position=topright across=2;
  xaxistable count1/labelattrs=(weight = bold size = 10) label="ALC"
    valueattrs=(color=red size=10)
    title = "Number of subjects" titleattrs=(size=10);
  xaxistable count2/labelattrs=(weight = bold size = 10) label="SPD"
    valueattrs=(color=blue size=10);
run;
```

Note:

- The **yaxis** and **y2axis** statements define the primary (left) and secondary (right) y-axis corresponding to the ALC and SPD data, respectively. The **xaxis** statement specifies the x-axis of the plot. These statements control various plot features, for

example, label option customizes the text displayed on each axis, while the min and max options displayed data range along each axis.

- **/y2axis** option indicates that the y-value (median2) should be plotted against the secondary y-axis (the right-side y-axis).
- The attributes options in SPGLOT help to control the visual properties of specific plot element (see Table 7).

| Attribute     | Controls              | Common Options                    |
|---------------|-----------------------|-----------------------------------|
| errorbarattrs | error bars            | color, pattern, thickness         |
| markerattrs   | markers (points)      | color, symbol, size, transparency |
| lineattrs     | lines                 | color, pattern, thickness         |
| labelattrs    | axis labels           | color, size, weight, family       |
| valueattrs    | axis tick value       | color, size, weight               |
| titleattrs    | titles (tables, axes) | color, size, weight               |

Table 7: Common Attribute Options

- The option **legendlabel="ALC"** in the scatter plot specifies the text "ALC" that appears in the legend for this plot element. The option **name="s1"** assigns the name "s1" to this scatter plot, which can be referenced later in the keylegend statement.
- The statement **keylegend "s1" "s2"** displays a legend for the plot elements named "s1" and "s2", which correspond to the **name=** option assigned earlier.

#### EXAMPLE 2: MULTI-CELL DUAL-AXIS GRAPH USING GRAPH TEMPLATE LANGUAGE

The GTL procedure, used in conjunction with the SGRENDER procedure, produces the dual-axis graph shown in Figure 4. The graph is a multi-cell plot comprising three distinct cells. The first cell displays series plots for ALC and SPD, along with scatter plots including error bars for both variables. The second cell presents the text "Number of Subjects" and a table summarizing the monthly ALC number of subjects. The third cell provides a corresponding table for monthly SPD number of subjects.

This graph is constructed by combining the LAYOUT LATTICE and LATOUT OVERLAY statements. The LAYOUT LATTICE statement defines the multi-cell structure, while three nested LATOUT OVERLAY statements specify the plot within each cell. Both LAYOUT LATTICE and LATOUT OVERLAY blocks are terminated with the ENDLAYOUT statement.

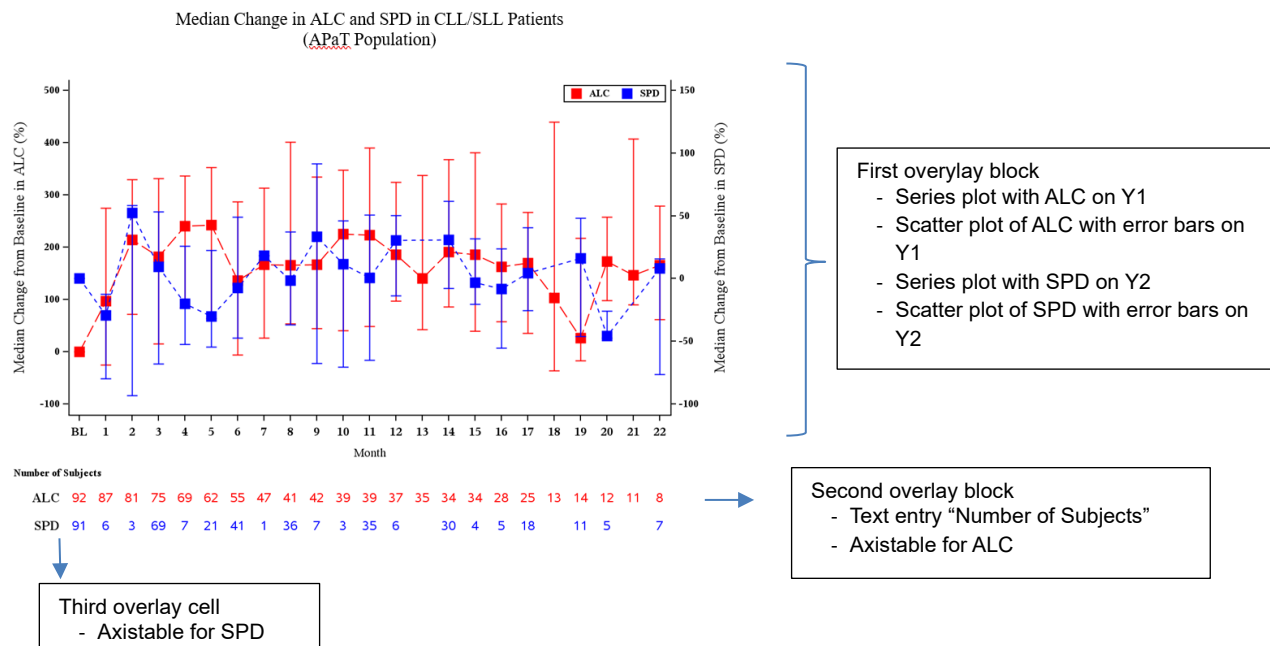


Figure 4: Dual-axis Graph for ALC and SPD by Using GTL

#### GTL CODE :

```
proc template;
  define statgraph overtime;
    begingraph;
      layout lattice/columns=1 rows=3 rowweights=(0.86 0.09 0.05) rowgutter=5pt;
```

```

***First layout block***;
layout overlay /xaxisopts=(Label="Month" type=discrete
    discreteopts=(tickvaluefitpolicy=splitrotate )
    tickvalueattrs=(size=8pt))
    yaxisopts=(label="Median Change from Baseline in
    ALC (%)" labelattrs=(size=10pt)
    type=linear linearopts=(tickvaluelist=(-100 0 100
    200 300 400 500)
    viewmin=-100 viewmax=500))
    y2axisopts=(label="Median Change from Baseline in
    SPD (%)" labelattrs=(size=10pt) type=linear
    linearopts=(tickvaluelist=(-100 -50 0 50 100 150)
    viewmin=-100 viewmax=150) );

scatterplot x=avisitc y=median1/yaxis=y
    yerrorupper=p751
    yerrorlower=p251
    errorbarattrs=(color=red
    pattern=solid)
    legendlabel="ALC"
    name="s1"
    markerattrs=(symbol=squarefilled
    color=red size=8pt);

seriesplot x=avisitc y=median1/yaxis=y
    lineattrs=(pattern=mediumdash
    thickness=1 color=red);

scatterplot x=avisitc y=median2/yaxis=y2
    yerrorupper=p752
    yerrorlower=p252
    errorbarattrs=(color=blue
    pattern=solid)
    legendlabel="SPD" name="s2"
    markerattrs=(symbol=squarefilled
    color=blue size=8pt);

seriesplot x=avisitc y=median2/yaxis=y2
    lineattrs=(pattern=shortdash
    thickness=1 color=blue);

discretelegend "s1" "s2"/
    location=inside across=2
    valign=top border=true;

endlayout;

***Second layout block***;
layout overlay/xaxisopts=(display=none);
    entry valign=left "Number of Subjects"/location=outside
    valign=top;
    axistable value=count1 x=avisitc/label="ALC"
    valueattrs=(size=9pt color=red)
    labelattrs=(weight=bold size=9pt)
    display=(label values);

endlayout;

***Third layout block***;
layout overlay/xaxisopts=(display=none);
    axistable value=count2 x=avisitc/label="SPD"
    valueattrs=(size=9pt color=blue)
    labelattrs=(weight=bold size=9pt)
    display=(label values);

```

```

endlayout;

endlayout;

endgraph;
end;
run;

proc sgrender data=for_graph template=overtime;
run;

```

Note:

- The **xaxisopts**, **yaxisopts**, **y2axisopts** options are specified inside a layout overlay block. Each layout overlay defines a single plot area with its own axes, so axis options apply specifically to that overlay.
- **/yaxis=y2** shows that the y-value (median2) should be plotted against the secondary y-axis (the right-side y2axis).
- The option **discreteopts=(tickvaluefitpolicy=splitrotate)** controls how tick mark values (the category labels) are displayed on a discrete axis when there is not enough horizontal space.
- The **columns=1 rows=3** from **layout lattice** statement defines a grid layout with 3 rows and 1.
- The option **rowweights** control relative row heights. The option **rowweights=(0.86 0.09 0.05)** specifies the first row takes up 86% of the height, the second 9%, and the third 5%. You can adjust the rowweights values to suit your specific design needs.
- The option **rowgutter** controls spacing between rows. The option **rowgutter=5pt** adds a 5-point gap between each row.
- The statement **discretelegend "s1" "s2"** in the first layout displays a legend for the plot elements named "s1" and "s2", which correspond to the name= option assigned earlier.
- The option **xaxisopts=(display=none)** in the second and the third block specifies hiding the x-axis, so the axis line, tick marks, label, and title are not displayed. Despite the axis being hidden, the coordinate system stays active, allowing other graphical elements to be positioned relative to the x-axis. In these blocks, the **axistable** statement is used to create tables of values aligned with the x-axis categories, providing the subject counts associated with ALC and SPD.

## CONCLUSION

Both the SGPLOT procedure and the Graph Template Language (GTL) effectively produce a dual-axis plot to track ALC and SPD trends over time for assessing disease dynamics in CLL and SLL, and each supports clear visual representation of data. SGPLOT is preferable when its visual styling and spacing meet the requirements and rapid development and execution are priorities. When finer layout control and a standardized, reuseable template are required, GTL is the better choice. In the example above, GTL enables precise control over row heights, spacing, and axis displays, as well as advanced handling of axis tick lists features that are harder to achieve with SGPLOT. Furthermore, when a template is defined with dynamic variables, it can be reused with PROC SGRENDER to apply different datasets without altering the design. Ultimately, prioritizing a thorough understanding of the underlying data and the intended analytical objective will enable more effective use of these tools.

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## ACKNOWLEDGMENTS

The author would like to thank Hong Qi, Yan Xu, Sapan Patel and Mukesh Patel for their review and insightful comments, and the management team at Merck & Co., Inc., Rahway, NJ, USA, for their support.

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