

Confidence Interval Approach for Analytical Similarity Assessment - A Comparison between US FDA and EU EMA Approach

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Citation: Liu Y, Chow S-C. Confidence Interval Approach for Analytical Similarity Assessment - A Comparison between US FDA and EU EMA Approach. Enliven: Biosimilars Bioavailab. 2020; 5(1): 005.

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Received Date: 29th November 2021

Accepted Date: 15th December 2021

Published Date: 26th December 2021

Abstract

For analytical similarity assessment in biosimilar studies, a two one-sided tests (TOST) procedure and a confidence interval (CI) approach are commonly employed to demonstrate biosimilarity between a proposed biosimilar (test) product and an innovative (reference) biological product. TOST is considered an official method for biosimilarity assessment by most regulatory agencies including the United States (US) Food and Drug Administrations (FDA) and the European Medicines Agency (EMA) of the European Union (EU). Since TOST is operationally equivalent to the CI approach, the CI approach is often used for biosimilarity assessment. However, FDA and EMA use the CI approach based on relative change and absolute change in mean response, respectively. This difference may lead to different conclusions regarding biosimilarity between the test product and the reference product, which causes some confusion among sponsors, regulatory agencies, and researchers in academia. This article attempts to clarify the confusion points and compare the FDA and EMA's approach in terms of false positive rate and false negative rate when performing analytical similarity assessment.

Keywords: Equivalence test; Analytical similarity assessment; Sample size calculation

Introduction

It is well-known that the discovery, research, and development of medicine are complex and require a huge investment of time and money. However, once the patent of the original product expires, the approved biosimilar and generic drugs can be manufactured and enter the market. Due to competition, the prices of branded drugs are usually significantly reduced. Consequently, the approval of these drugs becomes particularly important and needs to be taken seriously. Biosimilarity, the active substance in the test drug is similar to the reference medicine in a high degree, is the goal of biosimilar development [1]. According to the Public Health Services Act, FDA [2] would only approve biological products that are demonstrated to be biosimilar on the safety, purity, and potency of the reference product under certain existing scientific knowledge. However, compare with the bioequivalence study on generic drugs, the small-molecule chemical synthesis, the biosimilarity evaluation of biologics are harder due to their large molecular size, complex molecular structure, and difficult manufacturing processes.

In biomedical research, various approaches are used to demonstrate biosimilarity to conduct the comparison of the proposed product and the reference product. Among them, TOST (two one-sided tests) is recommended by both FDA (the United States Food and Drug Administrations) and EMA (European Medicines Agency of European Union) as one of the formal statistical tests of equivalence for the statistical evaluation of analytical similarity and they used confidence interval approach to simultaneously test these two null hypotheses for convenient calculation [3,4]. However, FDA and EMA used a confidence interval approach with different statistical models, measurements, confidence levels, and criteria which have varied statistical properties [5]. Thus, the fundamental difference between the two statistical methods used by the FDA and EMA for similarity evaluation has caused some confusion among sponsors and regulatory agencies when choosing methods [6]. Meanwhile, it is not easy to compare the pros and cons of two methods with different standards and to choose the better one. Therefore, this paper will focus on the comparison between the US FDA approach and the EU EMA approach.

Therefore, the first aim of this article is to study the statistical properties of the confidence interval approach for analytical similarity assessment in biosimilar studies. Second, the purpose of this article is to compare the US FDA approach (based on 90% confidence interval on μ_T / μ_R) and the EU EMA approach (based on 95% confidence interval on $\mu_T - \mu_R$). By simulation, this article proposed a table of the conditional approved probability under the criteria under these two methods of similarity assessment for generic biosimilar products in biomedical research. At the same time, it provides the relationship between the requirement of sample size and desired power. From the article structure aspect, the definition and characteristic of the confidence interval approach of biosimilar testing based on parallel design and standard 2×2 crossover design will be given in the next section. In section 3, a comparison of the US FDA approach and the EU EMA approach will be briefly outlined, whereas the procedures for the calculation of two conditional probabilities will be purposed. Then, statistical properties and justification of the proposed procedure will be studied, which is illustrated applied and verified through a simulation study in section 4. Afterward, the discussion and conclusion remarks will be provided in the last section of this article.

Confidence Interval Approach and Two One-Sided Tests

The confidence interval approach is the method to determine the criterion of the bioequivalence and biosimilarity comparison. Generally, there are two confidence interval approaches, mean difference and geometric mean ratio, which work on two different study designs, crossover design and parallel design.

The confidence interval approach claims the bioequivalence between the reference product and test product when the $(1-2\alpha) \times 100\%$ confidence interval for the mean difference or the ratio of averages totally falls in the bioequivalence or biosimilarity limit. The concept of using confidence intervals to assess bioavailability was first suggested by Westlake [16], who proposed the symmetrical confidence intervals method that modified the conventional confidence interval of the mean difference of two normal populations to symmetric to zero for bioequivalence trials [17]. After discussion and research many scholars [8,9], Westlake modified the confidence interval approach from $(1-\alpha) \times 100\%$ confidence interval into $(1-2\alpha) \times 100\%$ confidence interval to be consistent with the standard of the efficacy testing of FDA [7].

To compare the pharmacokinetic measures of generics and biosimilars, the two one-sided tests procedure was recommended by FDA as the official statistical method for testing interval hypotheses of bioequivalence or biosimilarity since then. The TOST tests procedure was proposed by Schuirmann [10] for the assessment of the equivalence of average bioavailability that separates the interval hypotheses into two one-sided hypotheses. Since the TOST procedure is a size- α test [11], two one-sided tests with α significant level for each side is algebraically equivalent to $(1-2\alpha) \times 100\%$ CI approach in many cases. However, TOST is based on the power while the CI approach is based on type I error, so the mixed up of these two methods may cause the confusion in some practical cases [12].

At the same time, the average bioequivalence approach and the log-transformation of pharmacokinetic data were also suggested [13]. Since then, there are several rules have been proposed to set the bioequivalence limit for the average bioequivalence assessment. This article focuses on two mainstream rules, ± 20 rule and 80/125 rule, which are generally used to assess raw data and log-transformed data, respectively.

Considering the study design, the FDA guideline suggested using the crossover design to conduct the comparison between two formulations or two test conditions while the parallel design may be more appropriate for the long half-life drug [14]. For parallel design, suppose $Y_{ik}, i=1, \dots, n_k, k=1,2$, where Y_{i1} and Y_{i2} are the response of the test lots and the reference lots, respectively. For crossover design, since we focus on the average bioequivalence approach, the replicated crossover design is not necessary [14]. Thus, 2×2 crossover design is the research subject of this article, and then use general linear model to calculate the confidence interval. Suppose $Y_{ijk}, i = \text{subject } 1, \dots, n_k, j = \text{period } 1, 2, k = \text{sequence } 1, 2$ are the response of two sequences RT and TR, respectively. For the confidence interval approach, let $[L, U]$ be the $(1-2\alpha) \times 100\%$ confidence interval for μ_T / μ_R or $\mu_T - \mu_R$. If confidence interval is entirely within BE limits or BS margin, then we claim that test formulation and reference formulation are bioequivalence/biosimilar [15]. Table 1 demonstrates the criteria of the confidence interval approach, where

$$S_p^2 = \frac{\sum_{k=1}^2 \sum_{i=1}^{n_k} \left(Y_{ik} - \frac{\sum_{i=1}^{n_k} Y_{ik}}{n_k} \right)^2}{n_1 + n_2 - 2}$$

Table1. BE/BS Limit of Confidence Interval Approach

| Hypothesis | Confidence Interval | BE/BS Limit |
|-------------------|---|--|
| Crossover | | |
| $\mu_T - \mu_R$ | $[L, U] = \hat{\mu}_T - \hat{\mu}_R \pm t_{1-\alpha, n_1+n_2-2} \sqrt{\hat{\sigma}_d^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)}$ | $[L, U] \subseteq (-20\% \hat{\mu}_R, 20\% \hat{\mu}_R)$ |
| μ_T / μ_R^* | $[L, U] = \exp \left[\hat{\mu}_T - \hat{\mu}_R - t_{1-\alpha, n_1+n_2-2} \sqrt{\hat{\sigma}_d^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)} \right]$ | $[L, U] \subseteq (80\%, 125\%)$ |
| Parallel | | |
| $\mu_T - \mu_R$ | $[L, U] = \hat{\mu}_T - \hat{\mu}_R \pm t_{1-\alpha, n_1+n_2-2} \sqrt{S_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)}$ | $[L, U] \subseteq (-20\% \hat{\mu}_R, 20\% \hat{\mu}_R)$ |
| μ_T / μ_R^* | $[L, U] = \exp \left[\hat{\mu}_T - \hat{\mu}_R \pm t_{1-\alpha, n_1+n_2-2} \sqrt{S_p^2 \left(\frac{1}{n_1} + \frac{1}{n_2} \right)} \right]$ | $[L, U] \subseteq (80\%, 125\%)$ |

* Log-transformation prior to data analysis

is pooled variance of the subjects from two treatments for parallel design, and

$$\hat{\sigma}_d^2 = \frac{\sum_{k=1}^2 \sum_{i=1}^{n_k} \left[\frac{1}{2} (Y_{i2k} - Y_{i1k}) - \frac{\sum_{i=1}^{n_k} \frac{1}{2} (Y_{i2k} - Y_{i1k})}{n_k} \right]^2}{n_1 + n_2 - 2}$$

is the pooled sample variance of period differences from both sequences for crossover design.

It seems reasonable to transform the confidence interval of the mean difference into the confidence interval of the ratio of two treatment mean by dividing the mean of the reference group and plus 1, which means $\frac{\mu_T - \mu_R}{\mu_R} + 1 = \frac{\mu_T}{\mu_R}$. However, these two methods are different because usually we could only use the sample mean estimate of the reference group instead of the true μ_R , which may lead to different conclusions [15].

By the definition of $(1-2\alpha) \times 100\%$ confidence interval, there is $(1-2\alpha) \times 100\%$ confident that the true value of the difference of mean or the geometric mean ratio in the confidence interval. However, with limited sample size, this probability of confidence interval contain true value is unequal to the probability of the $(1-2\alpha) \times 100\%$ confidence interval within the BE/BS limit [15]. Let p be the probability that $(1-2\alpha) \times 100\%$ confidence interval within BE/BS limit. Select an appropriate sample size (i.e., n_1 and n_2 , without loss of generality, assume $n_1 = n_2 = n$) such that $p \geq p_0$ when p_0 is desired probability of concluding BE or BS. Based on this probability, next section will compare the difference between the analytical similarity assessment of US FDA and EU EMA.

$$1 - 2\alpha = P(\mu_T - \mu_R \text{ or } \mu_T/\mu_R \in [L, U]) > P([L, U] \subseteq (-20\% \hat{\mu}_R, 20\% \hat{\mu}_R) \text{ or } (80\%, 125\%)) = p$$

A Comparison between US FDA and EU EMA with Simulation Study

As the description in section 2, FDA suggested logarithmic transformation of pharmacokinetic data on the 2003 guidance [13]. Nowadays, the log-

transformation method is the only approach certified by FDA for analytical similarity assessment. However, the methods and standards of the assessment of generic drugs and biological products remain diverse around the world. For example, the procedures of two confidence interval approaches used by FDA and EMA have already been given in detail, however, these methods are based on different statistical models, measurements, confidence levels, and criteria as shown in the following table 2 [6]. The most obvious difference between these two methods is that they use different confidence interval approach with different significant level.

A simulation of AUC data with 1000 data sets each was used to demonstrate the comparison of the FDA approach and EMA approach under parallel design and 2×2 crossover design. Assume the AUC of test treatment and reference treatment are followed the normal distribution with true mean 80 and 82 with no period effect and carryover effect. The sample size for two treatments in parallel design and two sequences in 2×2 crossover design was considered to be the same, starting from 12 to 50, since 12 is the minimum number of evaluable subjects in BE study [3].

First, these data were used to show the relationship of the inequation mentioned in section 2, that is the probability $p < 1 - 2\alpha$. From the result in Table 3, the accuracy of the confidence interval approach to assess bioequivalence decreases as the variability increases.

Secondly, to give a more intuitive comparison, we compare the two methods in terms of the following theoretically, where FDA+ and EMA+ represent conclude bioequivalence/biosimilarity under FDA and EMA methods, respectively. Similarly, FDA- and EMA+ means reject the bioequivalence/biosimilarity under FDA and EMA methods, respectively. Table 4 shows four possible results of BE/BS assessment under FDA and EMA methods. Let p_1, \dots, p_4 be the probability of each result. Based on this, two conditional probabilities are generated to compare the FDA and EMA approaches.

$$p_A = P(\text{US FDA claim BE/BS} \mid \text{EU EMA claim BE/BS}) = P(\text{FDA} + \mid \text{EMA} +) = \frac{p_1}{p_1 + p_2}$$

$$p_B = P(\text{EU EMA claim BE/BS} \mid \text{US FDA claim BE/BS}) = P(\text{EMA} + \mid \text{FDA} +) = \frac{p_1}{p_1 + p_3}$$

Table 2 Comparison of analytical similarity assessment between US FDA and EU EMA

| Characteristics | US FDA | EU EMA |
|-----------------------------|--|---|
| Statistical Model | Log-transformed Model | Raw data Model |
| Official Method | TOST ($\alpha = 0.05$) | TOST ($\alpha = 0.025$) |
| Sample Size requirement | Based on TOST | Based on TOST |
| Interval Hypotheses Testing | $H_{01}: \mu_T/\mu_R \leq 0.8$ $H_{02}: \mu_T/\mu_R \geq 1.25$ | $H_{01}: \mu_T - \mu_R \leq -0.2\mu_R$ $H_{02}: \mu_T - \mu_R \geq 0.2\mu_R$ |
| Criteria of CI Approach | $(1-2\alpha) \times 100\%$ CI for μ_T/μ_R $\subset (80\%, 125\%)$ | $(1-2\alpha) \times 100\%$ CI for $\mu_T - \mu_R$ within $\pm 20\%$ of μ_R |

Note: TOST = two one-sided tests, α = level of significance

Table 3: Comparison between the probability of CI contain 0 and within certain limit

| Study Design | Sample Size | $\sigma/\mu = 0.2$ | | $\sigma/\mu = 0.3$ | | $\sigma/\mu = 0.4$ | |
|--------------|-------------|--------------------|-------|--------------------|-------|--------------------|-------|
| | | $p_{0 \in CI}$ | p | $p_{0 \in CI}$ | p | $p_{0 \in CI}$ | p |
| Parallel | 12 | 0.947 | 0.322 | 0.945 | 0.009 | 0.942 | 0.000 |
| EMA | 16 | 0.943 | 0.565 | 0.946 | 0.035 | 0.948 | 0.001 |
| | 20 | 0.939 | 0.730 | 0.948 | 0.130 | 0.951 | 0.006 |
| | 30 | 0.931 | 0.918 | 0.936 | 0.443 | 0.944 | 0.064 |
| | 40 | 0.910 | 0.980 | 0.933 | 0.669 | 0.940 | 0.260 |
| | 50 | 0.928 | 0.997 | 0.940 | 0.823 | 0.947 | 0.451 |
| Parallel | 12 | 0.895 | 0.628 | 0.897 | 0.091 | 0.893 | 0.003 |
| FDA | 16 | 0.885 | 0.782 | 0.902 | 0.191 | 0.903 | 0.014 |
| | 20 | 0.878 | 0.870 | 0.887 | 0.328 | 0.906 | 0.044 |
| | 30 | 0.873 | 0.970 | 0.890 | 0.550 | 0.894 | 0.146 |
| | 40 | 0.842 | 0.993 | 0.888 | 0.735 | 0.901 | 0.296 |
| | 50 | 0.863 | 0.999 | 0.887 | 0.828 | 0.902 | 0.450 |
| Crossover | 12 | 0.931 | 0.795 | 0.939 | 0.233 | 0.943 | 0.027 |
| EMA | 16 | 0.923 | 0.942 | 0.943 | 0.455 | 0.950 | 0.099 |
| | 20 | 0.934 | 0.979 | 0.949 | 0.637 | 0.947 | 0.231 |
| | 30 | 0.897 | 0.999 | 0.938 | 0.894 | 0.941 | 0.605 |
| | 40 | 0.890 | 1.000 | 0.919 | 0.965 | 0.932 | 0.797 |
| | 50 | 0.866 | 1.000 | 0.904 | 0.993 | 0.913 | 0.878 |
| Crossover | 12 | 0.869 | 0.897 | 0.889 | 0.402 | 0.899 | 0.074 |
| FDA | 16 | 0.874 | 0.973 | 0.888 | 0.609 | 0.899 | 0.186 |
| | 20 | 0.866 | 0.989 | 0.885 | 0.698 | 0.890 | 0.269 |
| | 30 | 0.843 | 1.000 | 0.871 | 0.902 | 0.889 | 0.540 |
| | 40 | 0.803 | 1.000 | 0.861 | 0.956 | 0.893 | 0.719 |
| | 50 | 0.798 | 1.000 | 0.854 | 0.990 | 0.881 | 0.821 |

Note: $p_{0 \in CI}$ is the probability of CI contain 0, p is the probability of CI within BE/BS limit

Table 4: Probability of conclude BE/BS

| | FDA+ | FDA- |
|------|-------|-------|
| EMA+ | p_1 | p_2 |
| EMA- | p_3 | p_4 |

Then, these two conditional probabilities could be estimated through the same simulation data sets. From the simulation result in Table 5, when the sample size is small, $p_B < p_A$ for both two study designs, then with the increase of sample size, p_B get close to p_A and even larger than p_A . Therefore, EMA approach is more likely to approve the bioequivalence and

biosimilarity for the small sample size. While EMA approach and FDA approach have similar probabilities to approve the bioequivalence and biosimilarity for a large size. Table 6 shows the relationship between power and sample size of TOST for different study designs under fixed coefficient of variations.

Table 5: Simulation result

| Study Design | Sample Size | $\sigma/\mu = 0.2$ | | $\sigma/\mu = 0.3$ | | $\sigma/\mu = 0.4$ | |
|--------------|-------------|--------------------|-------|--------------------|-------|--------------------|-------|
| | | p_A | p_B | p_A | p_B | p_A | p_B |
| Parallel | 12 | 0.997 | 0.511 | 1.000 | 0.099 | NA | 0.000 |
| | 16 | 0.998 | 0.721 | 1.000 | 0.183 | 1.000 | 0.071 |
| | 20 | 0.997 | 0.837 | 0.962 | 0.381 | 1.000 | 0.136 |
| | 30 | 1.000 | 0.946 | 0.883 | 0.711 | 0.656 | 0.288 |
| | 40 | 1.000 | 0.987 | 0.948 | 0.863 | 0.669 | 0.588 |
| | 50 | 1.000 | 0.998 | 0.953 | 0.947 | 0.736 | 0.738 |
| Crossover | 12 | 0.999 | 0.885 | 0.940 | 0.545 | 0.741 | 0.270 |
| | 16 | 0.999 | 0.967 | 0.927 | 0.693 | 0.747 | 0.398 |
| | 20 | 0.998 | 0.988 | 0.929 | 0.848 | 0.671 | 0.576 |
| | 30 | 1.000 | 0.999 | 0.962 | 0.953 | 0.764 | 0.856 |
| | 40 | 1.000 | 1.000 | 0.987 | 0.996 | 0.867 | 0.961 |
| | 50 | 1.000 | 1.000 | 0.995 | 0.998 | 0.912 | 0.976 |

Note: Sample Size: $n_1=n_2=n$, $p_A=1$ means $p_2=0$, $p_A=NA$ means $p_1=p_2=0$.

Table 6. Power of TOST for different sample size and study design under fixed coefficient of variations.

| Sample Size | FDA ($\alpha=0.05$) | | EMA ($\alpha=0.025$) | |
|-------------|-----------------------|-----------|------------------------|-----------|
| | Parallel | Crossover | Parallel | Crossover |
| 12 | 18.61 | 56.60 | 3.17 | 22.89 |
| 16 | 34.78 | 73.54 | 7.62 | 41.80 |
| 20 | 49.70 | 83.47 | 15.68 | 57.39 |
| 24 | 61.05 | 89.60 | 26.32 | 68.48 |
| 26 | 65.60 | 91.76 | 31.83 | 72.81 |
| 30 | 72.98 | 94.86 | 42.02 | 79.73 |
| 32 | 76.00 | 95.95 | 46.51 | 82.51 |
| 36 | 80.99 | 97.51 | 54.32 | 87.02 |
| 40 | 84.92 | 98.48 | 60.81 | 90.44 |
| 48 | 90.50 | 99.45 | 70.89 | 94.91 |
| 50 | 91.54 | 99.58 | 72.95 | 95.67 |
| 60 | 95.30 | 99.89 | 81.24 | 98.12 |
| 78 | 98.43 | 99.99 | 90.46 | 99.61 |

Note: Assume CV (coefficient of variations) = $\frac{\sqrt{MSE}}{\mu_R} \times 100\% = 20\%$.

Discussion and Conclusion

In this study, we take statistical approaches towards studying the properties of the confidence interval approach and comparing the differences between the EMA approach and FDA approach that were used to assess biosimilar. To investigate the statistical features of the confidence interval approach for assessing analytical similarity in biosimilar studies, we illustrated the criterion of the mean difference and geometric mean ratio confidence interval approaches based on parallel design and standard 2×2 crossover design. In addition, one of our primary aims was to compare the US FDA approach and the EU EMA. From the data requirement perspective, the EMA approach has an easier evaluation in data processing without log-transformation that is required by the FDA approach. However, the bioequivalence limit of the EMA approach contains the mean of the reference drug, which is unknown and has to be estimated by the sample, adding to the uncertainty of its result. Furthermore, the simulation results of the probability of concluding bioequivalence/biosimilar show that the FDA confidence interval approach has larger accuracy than the EMA approach with the same study design, sample size, and variability. In terms of false positive and false negative rates, the EMA approach and FDA approach have similar results in approving bioequivalence and biosimilarity for the large sample size, whereas the EMA approach has a higher probability of ratifying BE/BS for the small sample size, particularly for the parallel design, which requires a larger sample size to achieve desired power of demonstration bioequivalence with the same coefficient of variation. Therefore, the FDA method is more reliable for analytical similarity, especially when the bioequivalence is marginal.

However, in our attempt to uncover the differences between EMA and FDA CI approach, we find the comparison remains some limitations. Thereinto, this article focuses on the average bioequivalence, which is based on the population average of the bioequivalence measure and is recommended by both FDA and EMA. However, it does not consider the comparisons of the variances for the compared formulations. In addition, we discuss the FDA confidence interval approach and EMA confidence interval approach for analytical similarity assessment under two-arm parallel design and 2×2 crossover design. In practice, with the increased complexity of study designs, such as period effect, carryover effect, and replication, and

other uncontrollable factors such as unbalanced sample size, the average bioequivalence method maybe not be appropriate. In order to fill these gaps, FDA gave two new approaches, the population bioequivalence approach and the individual bioequivalence approach, which included total variability, within-subject variability, and the subject-by-formulation interaction [13]. Therefore, the availability of conclusions for more complex situations needs further study.

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