# COMPARISON OF THE INTELLIGENCE MODELS USING STRUCTURAL EQUATION MODELING AND SELF-ORGANIZING FEATURE MAPS

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**ABSTRACT** – The problem of comparing hierarchical and nested intelligence factor models is under study. These models were developed according to existing theories of intelligence and enable to investigate latent factors of a general intelligence as well as factors of a verbal and nonverbal intelligence influences on observed parameters measured by the Wechsler intelligence test. Presented is a new technique for estimating goodness-of-fit measure in case of unrestricted factor models, which is based on the capabilities of self-organizing feature maps (Kohonen networks). This technique makes it possible to avoid tight restrictions imposed on observed data and factor model structure, which are inherent for the traditional factor model identification procedure. The procedure of estimating model components' statistical significance via comparison of goodness-of-fit measures for saturated and reduced models is also under consideration.

**KEYWORDS**
Model of intelligence, structural equation modeling, model goodness-of-fit, Kohonen networks.

## I. INTRODUCTION

The concept of intelligence is determined by quite diverse, but in general refers to individual characteristics, attributable to the cognitive sphere, above all - to thinking, memory, perception, attention, etc. Is intelligence a single entity or whether it consists of individual abilities of the particular potency? Could you define intelligence as a set of such potentials, the number and value of which depends on confronting the individual tasks of different difficulty levels? There were various theories formulated trying to answer these questions, among which we have a structural modeling approach.

## II. FACTOR MODELS OF INTELLIGENCE

The first attempt to analyze the structure properties of intelligence was made by Charles Spearman in 1904. Spearman found that schoolchildren's grades across seemingly unrelated subjects were positively correlated, and proposed that these correlations reflect the influence of a dominant factor, which he termed as **g** for "general" intelligence or ability. He developed a model in which all variability in intelligence test scores are explained by two factors: the first factor which is specific to an individual mental task: the individual abilities that would make a person more skilled at a specific cognitive task; and the second factor which is a general factor **g** that governs performance on all cognitive tasks. [9]

Also there is another classical factor model of intelligence which was created by L. Thurstone. Using his new approach to factor analysis, Thurstone found that intelligent behavior does not arise from a general factor, but rather emerges from some independent factors that he called as primary abilities. [10]

Thurstone's contribution to the development of factor analysis techniques was proved invaluable in establishing and verifying later psychometric factor structures, and has influenced the hierarchical models of intelligence which are used in intelligence tests such as WAIS and the modern Stanford-Binet IQ test.

The importance of a comprehensive analysis of different intelligence models and topicality of the best factor model structure identification is connected with increasing growth of interest to the problem of revealing the intelligence structure and caused by the emergence of new theories of intelligence and creation of new test methods that rely on it. [1, 3, 8]

An important task of comparing the hierarchical (Thurstone's model) and nested (Spearman's model) models of intelligence using results of twins' intellectual abilities study was posed by the professor D. Ushakov. The study involved 103 pairs of monozygotic (MZ) twins and 99 pairs of dizygotic (DZ) twins.

We constructed two factor models of intelligence according to the Thurstone's (see **Figure 1**) and Spearman's approach (see **Figure 2**). The results of Wechsler's test used as the observed parameters denoted as $\mathbf{S_1} - \mathbf{S_{11}}$. The test includes 11 subtests that cover the verbal and nonverbal aspects of intelligence.

These models have the following notation: factor **G** is a general factor, factor **V** is a factor of verbal intelligence, factor **N** is a non-verbal intelligence factor, and factors $\mathbf{E_1} - \mathbf{E_{11}}$ are measurement errors. We assessed hierarchical and nested models' goodness-of-fit measures using both average and difference values of the initial subtests results within twins' pair.

By using the difference between subtests results

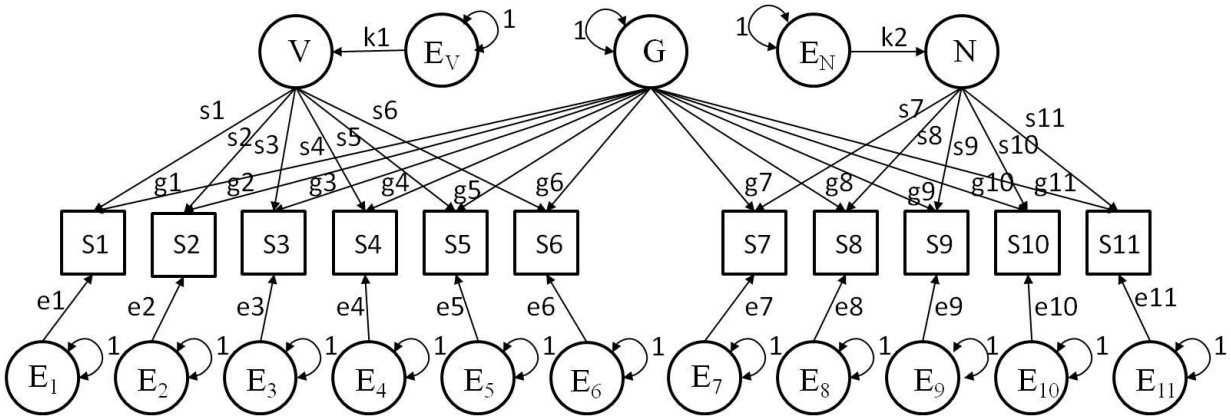


**Figure 1.** Nested intelligence factor model.

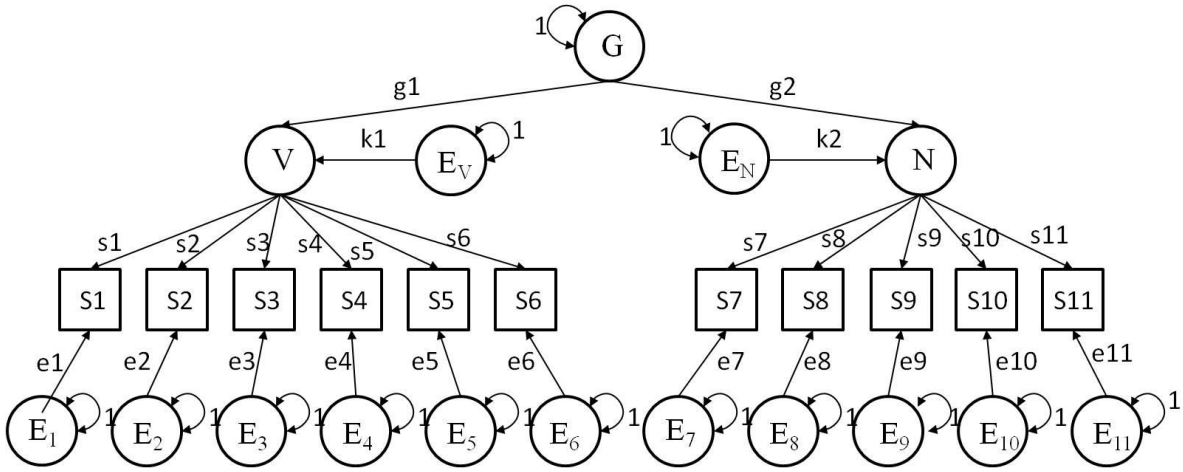


**Figure 2.** Hierarchical intelligence factor model.

we are trying to exclude a common genetic "portion of intelligence" while using of subtests averages obtained in the pair, guarantees that the influence of environment and genetic is not excluded.

Both nested and hierarchical complete models (as they are shown in **Figures 1** and **2**) were compared with their simplified variants without the factor **G**. Analysis scheme is shown in **Figure 3**. Comparison of the complete model and simplified performed for both types of models: hierarchical and nested, using the difference and average between subtests results of monozygotic (MZ) and dizygotic (DZ) twins.

Estimating of each model's goodness-of-fit measure is carried out by a new statistical method, which is a new technique for estimating a goodness-of-fit measure in case of unrestricted factor models, which is based on the capabilities of self-organizing feature maps and expands the approach described in [4].

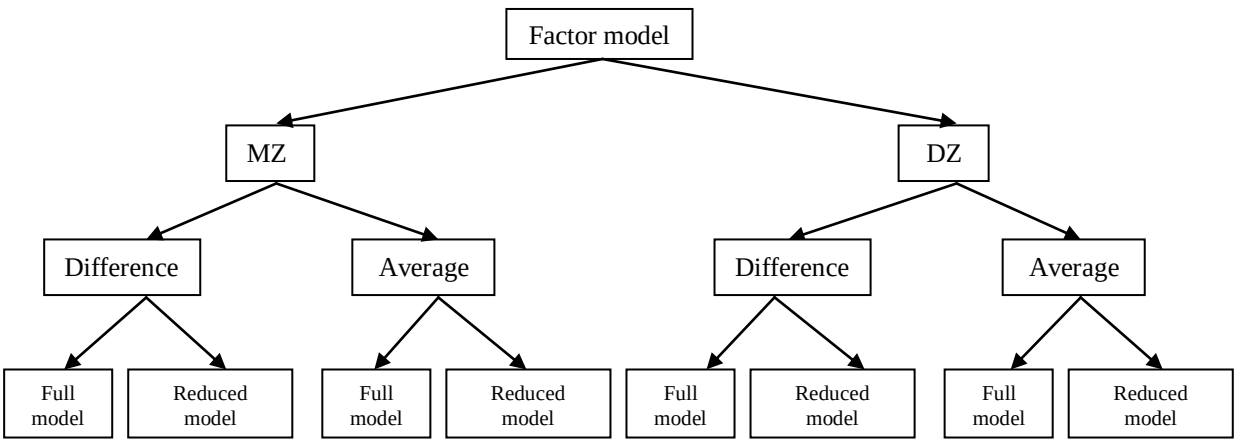


**Figure 3.** Scheme to assess the adequacy of the factor models.

## III. A NEW TECHNIQUE FOR ESTIMATING A GOODNESS-OF-FIT MEASURE

For each of the above-stated models we compose a corresponding overdetermined set of equations which can be expressed in the following way:

$$\mathbf{F(x)=b},$$

where $\mathbf{F(x)}$ - $n$-dimensional non-linear operator applied to $m$-dimensional vector $\mathbf{x}$ of unknown free model parameters of interest, which $n$ components are expected analytic expressions of variances and covariances for observed variables via $m$ free parameters of a factor model under consideration; $\mathbf{b}$ - column $n\times 1$ vector of variance and covariance sample estimates, which are determined using observation results.

The vector $\boldsymbol{\varepsilon}=\mathbf{F}(\mathbf{x}_*)-\mathbf{b}$ represents a residual of the pseudosolution $\mathbf{x}_*$, where

$$\| \mathbf{F}(\mathbf{x}_*) - \mathbf{b} \| = \min_{\mathbf{x}\in\mathbf{X}} \| \mathbf{F}(\mathbf{x}) - \mathbf{b} \|,$$

$\|\cdot\|$ - vector Euclidean norm, $\mathbf{X}$ – admitted region for $\mathbf{x}$.

To get this pseudosolution, any available numerical non-linear multivariate local optimization procedure with a minimization criterion represented by the residual Euclidean norm can be used. Gradient techniques are acceptable for this purpose. In particular, the authors employed a procedure called the Generalized Reduced Gradient.

To examine for the adequacy of the calculated pseudosolution to observations further development of the above-stated technique based on both the SOFM capabilities and the Monte Carlo method is suggested here. Its framework is shown in **Figure 4**. As before, calculation of goodness-of-fit measure is based on comparison of the pseudosolution residual vector $\boldsymbol{\varepsilon}=\mathbf{F}(\mathbf{x}_*)-\mathbf{b}$ and random samples of residual vectors $\boldsymbol{\varepsilon}_r=\mathbf{F}(\mathbf{x}_*)-\mathbf{F}(\mathbf{x}_r)$, where $\mathbf{x}_r$ is a generated random test vector belonging to a given neighborhood of the pseudosolution $\mathbf{x}_*$.

Any arbitrary distribution may be assigned to vectors $\mathbf{x}_r$, nevertheless for practical purposes it is convenient to produce them normally distributed, with the standard deviation being varied. If necessary, given averaged percentage of random vector components are placed beyond the given neighborhood intervals. Random samples of residual vectors $\boldsymbol{\varepsilon}_r$ are used to train SOFM of proper dimension and, as a result, to obtain samples of Euclidean distances between residual vectors $\boldsymbol{\varepsilon}_r$ used as network input cases and the centers of SOFM "winning" units. These samples are close to normally distributed ones owing to the afore-cited reasons. Estimation of their means and variances identifies the given distributions and yields the opportunity to calculate the probability of exceeding the distance between the pseudosolution residual vector $\boldsymbol{\varepsilon}$ and its corresponding "winning" unit center. This probability is considered as a factor model goodness-of-fit measure.

To get information about possible deviations of identified parameters from their estimations obtained with the aid of a given factor model, series of samples with both given different standard deviations of random components and their changing averaged percentages of going beyond the given neighborhood

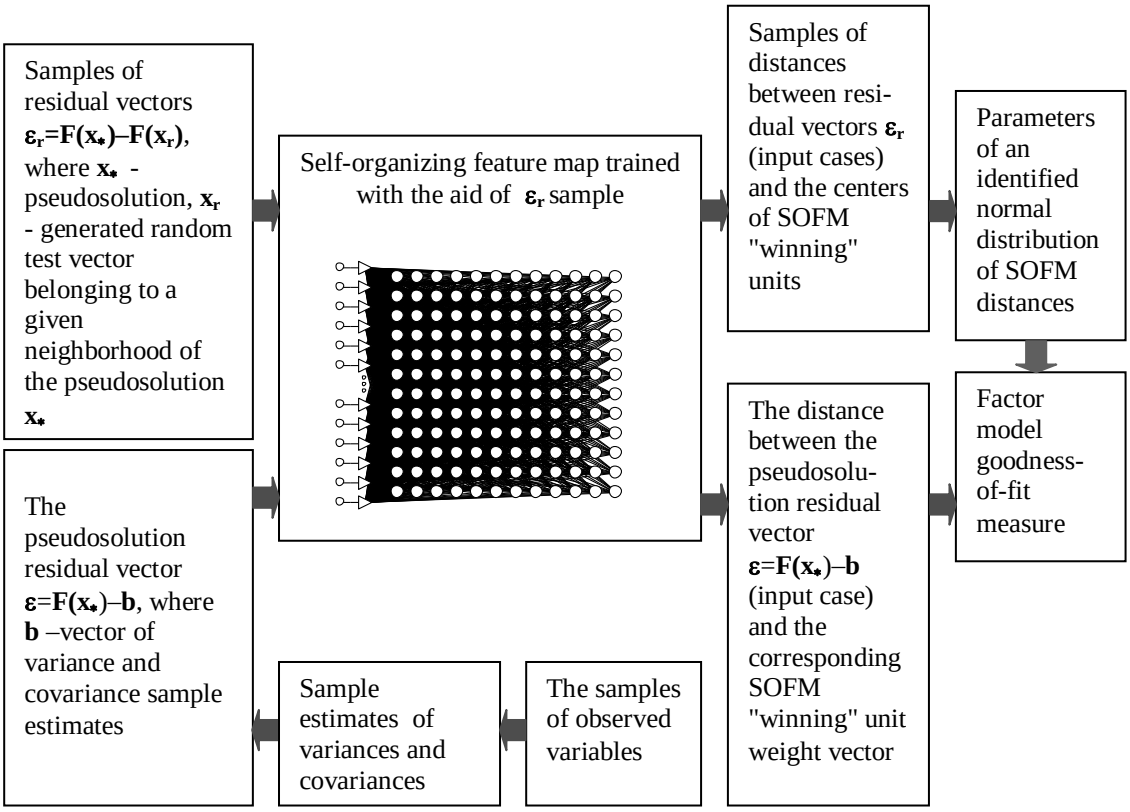


**Figure 4.** Calculation of arbitrary factor model goodness-of-fit measure with the aid of the self-organizing feature maps and the Monte Carlo method.

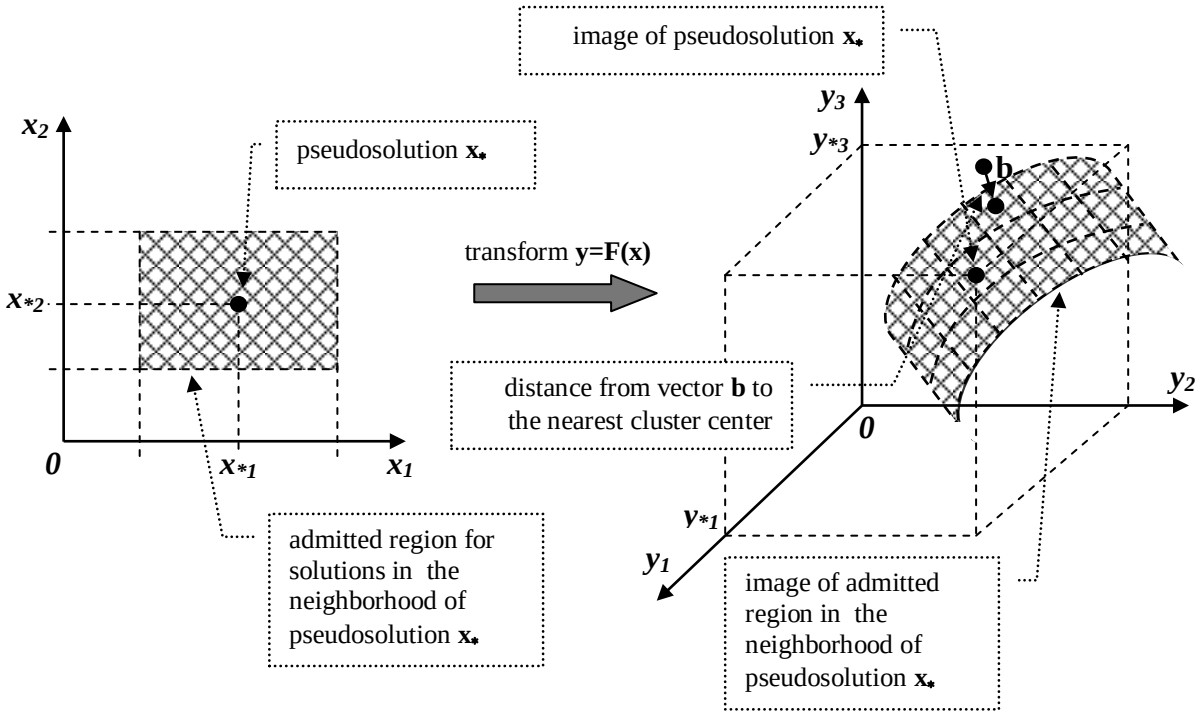


**Figure 5.** Geometric interpretation of the admitted solution region non-linear transform.

intervals are generated for SOFM training. For ease of analysis standard deviation of each test vector component is assumed to be equal to a certain constant percentage of the corresponding component mean value. Comparison of the above-stated SOFM distance distributions for different standard deviations and percentages makes it possible to reveal the maximum likelihood combination of the obtained pseudosolution precision presented by the estimated standard deviation and the component-wise structure of significant deviations for the pseudosolution components.

Geometric illustration clarifying the above-stated procedure, which is non-linear in general case, is given in **Figure 5**.

The suggested approach allows making conclusions on statistical significance of differences between two most probable factor model patterns under study using certain probability tests. Specific parameters of these model patterns can be identified by the foregoing technique. To compare patterns one should consider their maximum likelihood ratios $r=\sigma/m$, where $\sigma$ is the most probable standard deviation for generated normally distributed values of free model parameters and $m$ – corresponding distribution mean value. Since standard deviations of these generated values are assumed here to be equal to a certain constant percentage of relevant mean values, these ratios are kept constant for all model pattern parameters, but can differ for various patterns which allow, in general case, diverse averaged percentages going beyond the given parameter neighborhood intervals.

Let the ratios of compared patterns equal to $r_1=\sigma_1/m_1$ and $r_2=\sigma_2/m_2$, correspondingly, and $r_1 \le r_2$. Comparison is carried out for the same relative standard deviation $\sigma_*=r_1=r_2m_2$ when the mean value $m_1$ equals to $1$. In this case probability of the obtained deviation of reduced mean $m_2=r_1/r_2$ is estimated, viz.: probability $P(m_2 \le X \le 1)=\Phi(1)-\Phi(m_2)$ of being within the limits $[m_2;m_1=1]$ is calculated for random quantity $X$, where $\Phi$ is the normal distribution function with a mean of $1$ and a standard deviation of $\sigma_*$. If this probability is greater than the given significance level that is usually equal to $0.05$, the pattern difference is recognized as significant, otherwise it is considered as negligible.

The goodness-of-fit measures under consideration give the opportunity to determine the sample sizes required for testing hypotheses of equality of the distance between the pseudosolution residual vector $\varepsilon$ and its corresponding SOFM "winning" unit center to the certain value with both the given significance level and given test power. A formula of interest is derived from the comparison of corresponding acceptance region limits[1]:

$$N = \left( \frac{z_{1-\alpha/2} + z_{1-\beta}}{d_{norm}} \right)^2,$$

where $z_{1-\alpha/2}$ and $z_{1-\beta}$ are standard normal distribution quantiles of orders $1-\alpha/2$ and $1-\beta$, correspondingly; $\alpha$ is significance level; $\beta$ is probability of type 2 error; $d_{norm}$ is the ratio of deflection of true distance expectation from the tested certain value to the standard deviation of distance distribution.

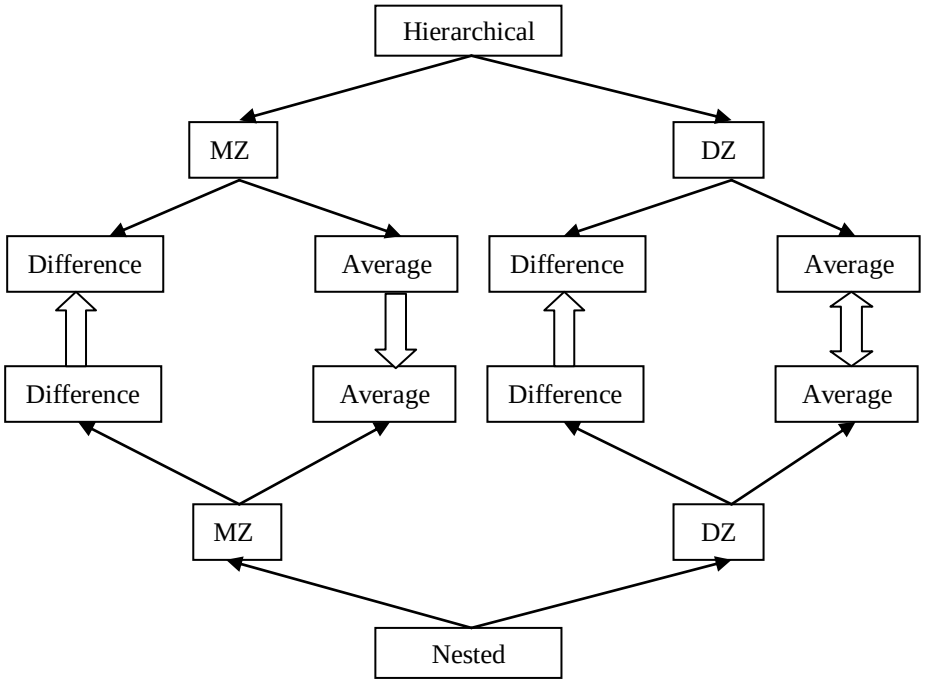


**Figure 6.** Result of comparison of factor models.

The presented techniques were software implemented on the base of the *LabVIEW* graphical programming environment [6]. The work of self-organizing feature maps was simulated with the aid of the STATISTICA Neural Networks software package [2, 5].

## IV. MAIN RESULTS AND CONCLUSIONS

The analysis expose that the hierarchical and nested models showed its adequacy for all investigated data from dizygotic and monozygotic twins with the differences and the average values of the subtests in the pair. The significance of factor G was confirmed in the comparison of full and simplified models.

Developed is a new technology estimated for factor models which advanced are:

- No need to test multivariate normalcy of distributions of either observed variables or residual vector components
- Higher reliability of obtained goodness-of-fit measures because of unrestrictedness of generated random samples of the pseudosolution components and the following unlimited goodness-of-fit estimation accuracy.

**Figure 6** shows the comparison of two types of models between them, where arrows indicate the best models, which show the best match to the observed parameters. Comparison of models using the average in dizygotic twin's pair revealed no significant differences between the models.

The nested model better describes the observed parameters by using the average values of the subtests in the twin's pair. This type of model considers the influence of environment and genetics. The hierarchical model is more responsive to the influence of environment than genetics.

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