Modelling macronutrients trajectories: Dynamics patterns and much more

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ABSTRACT

To our knowledge, attempts to directly model longitudinal change in macronutrients and energy intake of a population, with taking into account that individual change may not occur in the same fashion (i.e., develops at same growth rate), have never been practiced. In this respect, ambition of this paper is to propose the latent approach, by means of Latent Growth Curve Modeling (LGCM; Bollen & Curran, 2006) to the analysis of change in the nutritional status, namely fats, proteins and carbohydrates, and energy intake) of a target population in order to understand the time trend of the nutritional patterns at individual level. To this end, LGCM is able to outline the functional form of the individual growth trajectories and estimates the degree of individual variation and covariation around these just specified functions along with individualizing points of convergence and curvature. The subsequent application of multivariate LGCM allowed to check for gender invariance within people belonging to the same family and for multiple developmental trajectories while passing from urban to rural zone. The longitudinal data used as real example were taken from China Health and Nutrition Survey (CHNS) Household Food Inventory. From this survey a sample of 1229 households from urban and rural area, comprising of two adult family members of different gender, with having complete records of 3-day macronutrients and energy intake in 2000, 2004, 2006, 2009, 2011 was randomly selected. Interestingly, linear trajectories were found for fats and proteins at family level with convergence in 2009, and in 2006 and in 2012 respectively at rural and urban family level, whereas non-linearity was found for carbohydrates and energy intake. These nonlinearities were accommodated with polynomial functions and piecewise linear components with curvatures and knots for energy intake focalized respectively in 2006 and 2007. On the whole, the trajectories highlighted an equilibrium in the growth process with decreasing in the rate of change while passing from an initial heterogeneous amount of macronutrients and energy intake in 2000 to a more homogeneous status over the subsequent time period up to 2011. These results seemed in line with Chinese agricultural

reforms started in 2004-05, and 2008-09, from which Chinese families took benefit from by following a more balanced diet as well.

Keywords: Macronutrients, Latent Growth Curve Models, Structural Equation Models.

1. The nature of dynamics patterns

We define dynamics patterns as connected routes of repeated measures of variables at individual level. Repeated measures can be associated to time, as they usually do with typical longitudinal studies, or to different situations of repeated measurement such as the strength of an external stimulus (e.g., drug dosage). The main rationale of dynamics patterns is to have repeated measures "assessed or administered in a within-subject fashion and ordered in some logical way" (Preacher, 2010; p. 187). By simultaneously observing how these repeated measures vary across waves of measurement means studying how each individual behavior changes in terms of those measures. Hence, the study of dynamics patterns concerns the study of change in individual behaviors and how they deviate from a group-level change in common behaviors. This study is known as growth curve modeling (Muthén, 2001; p. 291). Despite of the fact that individuals may differ or not, in such repeated behaviors their connected routes outline trajectories. All these trajectories can follow a common average path or depart from it (Bollen & Curran, 2006). Further, they may have a theory of change behind, or take form of unspecified curves, but what is pretty sure is that they are ruled by a lawful, often unknown, developmental path that encompasses continuous and/or discontinuous phases. This effort to find out types of laws that rule over individuals, and group of individuals, change has already been faced over a century of research (see Bollen & Curran, 2006; p. 9-14), but it is still an ongoing challenge across scientific disciplines. Notwithstanding, what is of actual experiment is to understand this individual growth changing behavior as much as it does in the real world where individuals do not develop at the same rate and everything covaries. In this manner, a concrete starting point has been placed by the latent approach to the analysis of change. In this respect, the spirit of this paper is pioneering as it wants to propose such approach to an unusual area of research like nutrition and therefore making known potentialities and cutting edges.

2. Latent growth curve modeling rationale and outcomes

Unfortunately, when a researcher is dealing with a large number of repeated observations and wants to understand their patterns it is impossible to capture an immediate functional form, or known rule, that summarizes all these individual dynamics at first glance. A researcher can hypothesize that the patterns may follow some growth theory in advance and therefore confirming, or disconfirming, this theory with imposing, more or less realistic, constraints on these paths. But, what happens when no theory is available at the outset? An opening simple answer rises up: *to leave the repeated measures free to covary and thus observing how they interplay each other over the waves of measurement*. By doing so, a researcher is indirectly postulating that a possible unobserved common pattern may rule over this longitudinal covariation among the repeated measures. This latter is the main rationale of the latent approach to the analysis of individual growth change: the unobserved common pattern is a latent trajectory outlined by latent common factors that gives rise to the way how the repeated measures covary across the waves of measurement. By *gambling* on this hypothesis, a researcher combines the study of growth curve modeling with structural equation modeling (SEM) that typically estimates relations between latent factors and observed variables. This fusion takes the name of latent growth curve modeling (LGCM; Bollen & Curran, 2006) whereas the aforementioned latent common factors take the name of latent growth factors.

The so-called unconditional LGCM is condensed in the following simple equation:

$$y_{it} = \alpha_i + \lambda_t\beta_i + \varepsilon_{it} \tag{2.1}$$

where y_{it} are the repeated measures of a variable y for each individual i across points in time t (t=0, n), α_i represents the i individual value of y at the initial time point (i.e., t=0) from which the change in y starts and needs to be compared with the following values $y_{it+1.}$ Hence, α_i is the well-known regression intercept for each individual value of y_i and thus it has a mean and a deviation from mean (i.e., variance): μ_α and $\sigma^2{}_\alpha$. Now, in the most common case that a change is occurring from the initial value α_i , and therefore $y_{it} \neq y_{it+n}$, a dynamic trajectory starts to take form with a slope β_i that defines the inclination (i.e., difference from the initial values) of the trajectory for each individual i and thus it also has a mean and a variance: μ_β and $\sigma^2{}_\beta$.

Granted that, α_i, and β_i are now a sort of covariates that want to commonly explain the dynamics patterns in the repeated measures y_{it} with controlling for the errors ε_{it} (with the usual assumptions of mean equal to zero for all i and t, uncorrelated with the covariates, non-autocorrelated and homoscedastic) from which these covariates depart to outline the dynamic change. This is the point at which SEM structure with latent factors takes action and the equation (2.1) gains, in turn, all the benefits of the SEM analytic technique. The covariates α_i, and β_i become common latent growth factors that vary and covary by means of the estimated growth parameters μ_α, $\sigma^2{}_\alpha$, μ_β, $\sigma^2{}_\beta$ and $\sigma_{\alpha\beta}$, respectively; λ_t are the factor loadings that represent the degree to which the latent growth factors are able to explain the dynamic change in the repeated measures or, in other words, the way how the progress of time (situation) influenced the change in the repeated measures. As a consequence, the simultaneity estimation of these SEM-based latent growth parameters permits to release the assessment of the compound symmetry and thus taking into account that individuals develop at different growth rate alike in the real world. Hence, LGCMs are more flexible than traditional ANOVA-like methods for longitudinal studies.

It is intuitive from the equation (2.1) that a researcher can outline many different functional forms starting from the basic linear function to high-order of polynomials until more complex known functions and their re-parametrizations (please refer to Preacher and Hancock, 2015) as well as hypothesizing high-order growth factors for modelling multiple measures and groups of respondents (e.g., multivariate and multilevel designs; Duncan, Duncan & Stryker, 2006). For example, should the function (2.1) not be linear, but depicting a known curvature it is still possible to select a new metric λ_t into the equation (2.1) that, in turn, advances via depending on the selected non-linear function. For example, for quadratic (2.2) and cubic (2.3) polynomials the function (2.1) respectively becomes:

$$y_{it} = \alpha_i + \lambda_t\beta_{1i} + \lambda^2{}_t\beta_{2i} + \varepsilon_{it} \tag{2.2}$$

$$y_{it} = \alpha_i + \lambda_t\beta_{1i} + \lambda^2{}_t\beta_{2i} + \lambda^3{}_t\beta_{3i} + \varepsilon_{it} \tag{2.3}$$

Where β_{2i} and β_{3i} are further new growth parameters that take into account the new curvatures. Running these models by means of SEM and checking for the well-known diagnostics it is possible to confirm or disconfirm the hypothesized functions until reaching the one that fits better. In addition, SEM framework allows to explore for non-linearity of the repeated measures by leaving λ_t to be freely estimated for t = 2, .., n, with just setting $\lambda_o = 0$ and $\lambda_1 = 1$ or $\lambda_o = 0$ and the last $\lambda_n = 1$ for the latent factor metric. So that, the other un-standardized factor loadings are able to empirically estimate the type of non-linearity over the underling repeated measures. Furthermore, another very useful strategy for accommodating non-linearity in the trajectories is the so-called piecewise linear LGCM (Bollen & Curran, 2006). It simply consists in breaking the non-linear trajectories in the so-called breaking points, or transition (Bollen & Curran, 2006) or even discontinuity points (Hancock, Harring & Lawrence, 2013) and therefore connecting these points with linear functions till reaching a spline trajectory and thus looking into how it fits. Essentially, once λ_t are formalized, the functional form of the repeated measures is nearly outlined and the latent growth parameters μ_α, σ^2_α, $\mu_{\beta j}$, $\sigma^2_{\beta j}$ and $\sigma_{\alpha\beta j}$ (with j=1, n) can be estimated. The metric for α_i is always 1 because the intercept is the factor that simply blocks the initial amount of the repeated variable when there is no growth over time, $\beta_{it} = 0$.

The literature stipulates further useful statistics that can be inferred from the latent growth parameters. The first one is the so-called relative gradient for each slope $(RG_\beta)=\mu_\beta/\sigma_\beta$ (Hancock & Choi, 2006). The information it provides is about how many trajectories have a positive or negative inclinations. Furthermore, if a researcher assumes that the growth rates are distributed as $N(\mu_\beta, \sigma^2_\beta)$ the subsequent non-central standard normal distribution for RG can be re-written as N(RG,1) and it is possible to compute the proportion of positive and negative slopes with using the well-known non-central normal density curve table. A second statistical index is the so-called *aperture* (Hancock & Choi, 2006). Basically, the aperture is the point in time where the individual trajectories converge. It is noteworthy noticing that with a linear trajectory only just one aperture point is possible, with a piecewise linear-linear trajectory as many aperture points as the spline lines, but with nonlinear functions there might be multiple apertures. To our knowledge the math to locate multiple apertures in nonlinear scenarios and the related software commands have to be still worked out by academics. So then, we just report the three simple equations to determine the *aperture shift coefficient* a^{ap}, and its related moments, for a general linear time/situation interval metric of {a, b} (Hancock & Choi, 2006):

$$a^{ap}=a + (\sigma_{\alpha\beta}/ \sigma^2_\beta) \qquad (2.4)$$

$$\mu_a^{ap} = \mu_\alpha + (a-a^{ap})\, \mu_\beta \qquad (2.5)$$

$$\sigma^2_a{}^{ap} = \sigma^2_\alpha - [(\sigma_{\alpha\beta})^2 / \sigma^2_\beta] \qquad (2.6)$$

The aperture point and the moments permit, in turn, the estimation of the relative aperture location (RAL) and relative aperture variance (RAV) (Hancock & Choi, 2006):

$$RAL = - a^{ap} / (\lambda_p - \lambda_1) \qquad (2.7)$$

$$RAV = \sigma^2_a{}^{ap} / (\sigma^2_\alpha + b^2\sigma^2_\beta) \qquad (2.8)$$

RAL with values between 0 and 1 supplies information on the proportion of time span in which the aperture occurs (e.g., with RAL=0.30 the aperture occurs after 30% of the total time interval has passed) whereas with values of 0, below 0, 1 and over 1 it reveals that the aperture respectively occurs at the initial time point, below the investigated time span, on the final time point, over the investigated time span. RAV with values close to 0 indicates that the trajectories have a strong degree of convergence around the point a^{ap}, with exactly 0 there is perfect convergence. On the other hand, with RAV values close to 1 the aperture is wide and the convergence is weak since the trajectories tend to be parallel and distant each other; with exactly 1there is no convergence at all.

3. Real data example

In order to illustrate the strength of LGCM we used longitudinal real data from China Health and Nutrition Survey (CHNS) Household Food Inventory. From this survey a sample of 1229 households from urban and rural area, comprising of two adult family members of different gender, with having complete records of 3-day average macronutrients (fats, proteins and carbohydrates in grams) and 3-day average energy intake (in kcal) in 2000, 2004, 2006, 2009, 2011 was randomly selected. To simulate the growth change of the macronutrients and energy intake trajectories and to reflect the effective passage in time from 2000 (the reference point in time from which the change starts) to 2011the change in score per unit of time metric λ_t was fixed to the following unequal spaced units λ_{00}=0, λ_{04}=4, λ_{06}=6, λ_{09}=9, λ_{11}=11 so as to respect the yearly intervals {0,1}. The increasing sequence of numbers for λ_t hypothesizes how much an initial linear growth increases. For instance, the number 4 indicates that, on average, the change from 2000 to 2004 is 4 times as great as the change from 2000 to 2001 and so forth.

The analyses were initially conducted at member level in order to explore if there were similar functional forms for gender, separately. Successively, the final LGCMs were developed at family level both for the whole sample and territorial sites (i.e., urban vs rural) by applying multivariate representations of the growth process. These high-order levels of latent growth factors models accommodates for intra-class correlation occurring at members belonging to the same family (i.e., unique errors covariances free to covary) and for invariance of members trajectories (i.e., factor loadings between the first and the second order fixed to be equal over time of each family member; see Duncan, Duncan & Stryker, 2006; p. 69-74). In order to preserve space, we report results at family levels only since they are also the most relevant. Robust maximum likelihood (RML) estimation within LISREL 8.8 (Jöreskog & Sörbom, 2007) for fats and proteins individual trajectories provided good data-model fit (according to the main and well-known SEM fit indices and cut-off criteria: Chi-square not significant, Root Mean Squared Error of Approximation (RMSEA) under 0.05, Comparative Fit Index (CFI) over 0.95, Standardized Root Mean Squared Residual (SRMR) under 0.09) for common routes of linear growths in both gender and thus at family level (whole sample): Chi-square (df)=661.69(178), p<0.001, RMSEA=0.047 with 90 % Confidence Interval (CI) for RMSEA = (0.043 ; 0.051), CFI=0.94, SRMR=0.056. Latent growth factors parameter estimates and statistics are reported in table 1. Intercept and slope variances were statistically significantly different from zero with yielding to a significant individual difference of fats and proteins trajectories both at initial level and in the rate of change, although slope variances were smaller than intercept variances. These results would mean that fats and proteins patterns became even more similar in their rate of change. Interestingly, the covariance between the growth factors is significant and negative, and then the correlation is of -0.55. It means that the families with low fats and proteins score started to grow more, while the ones with high score to grow less. These latter were the most part since the RG provided 58% of family trajectories with negative slopes. Besides, the mean value over the time span was significant and negative as well. The statistics RAL and RAV showed a weak tight of convergence after 85.8% of the total time has passed, so then roughly 9.4 years after the initial 2000, in the first months of 2009.

A very interesting result was found when the sample was split in urban (i.e., n=362) and rural site (n=867). Although the dynamics patterns for fats and proteins were linear for both urban and rural families (i.e., for urban: Chi-square (df)=309.64(178), p>0.001(p=0.162), RMSEA=0.045, with 90 % CI for RMSEA = (0.037 ; 0.054), CFI=0.96, SRMR=0.066; for rural: Chi-square (df)=615.42(178), p<0.001, RMSEA=0.053, with 90 % CI for RMSEA = (0.049 ; 0.058), CFI=0.93, SRMR=0.064). For the former the trajectories were most negatively inclined (see table 1) with showing a decreasing across years with a convergence, although not very strong, above the time period and exactly slightly more than one year beyond 2011, in 2012. On the contrary, fats and proteins trajectories for rural families were pretty flat with a convergence, although pretty weak as well, after 55.6% of the time span has passed and therefore after 6.11 years, in 2006.

Completely different situation was found for carbohydrates and energy intake dynamics patterns. In order to preserving space and due to similar results we present here just the results from energy intake (in kcalories). Since the observed variances for kcalories were extreme, the measures have been rescaled (i.e., multiplied by 0.1) in order to facilitate the model convergence (Hancock & Mueller, 2010) without affecting differences among the scores (Kline, 2011). The fit indices for linear trajectories of energy intake by gender suggested to explore potential forms of new curvatures that depart from linearity (i.e., for males: Chi-square (df)=94.86(10), p<0.001, RMSEA=0.083, with 90% CI for RMSEA=(0.068; 0.099), CFI=0.86, SRMR=0.051; for females: Chi-square (df)=68.12(10), p<0.001, RMSEA=0.069, with 90% CI for RMSEA=(0.068; 0.099), CFI=0.91, SRMR=0.038). By doing so, LGCMs for energy intake individual trajectories at family level were run with fixing the first λ_{00} and the last λ_{11} loadings respectively to 0 and 1 while leaving the others to be freely estimated (Bollen & Curran, 2006). This strategy permits to discover the proportion of cumulative change occurred from the initial time point to the specific time period in reference to the total change of the entire period. The trend was quite similar for both family members. By explaining it for males (M) the values of λ_{04}=0.19, λ_{06}=0.09, and λ_{09}=0.28 respectively reflected that 19%, 9%, 28% of the total change in energy intake occurred between 2000 and 2004, 2000 and 2006, 2000 and 2009. By computing the following differences (0.19-0.09=0.10) and (0.28-0.09=0.14) it yielded to 10% of the total change between 2004 and 2006 whereas 14% between 2006 and 2009. Similar results were found for females (i.e., λ_{04}=0.19, λ_{06}=0.09, and λ_{09}=0.26). As a consequence, it is straightforward noticing that most of change in the energy intake occurred after 2006 and these two trends seem to reflect an up and down growth process that departs from linearity to outline a cubic polynomial function with a potential curvature after 2006.

Table 1: *Estimates and statistics for fats and proteins common trajectories at family levels*

Whole sample

Parameter	σ^2_α	σ^2_β	$\sigma_{\alpha\beta}$	$\rho_{\alpha\beta}$	μ_α	μ_β
Estimate	149.55	1.27	-7.63	-0.55	77.99	-0.22
t-values	8.71	4.87	-4.32	-4.32	102.24	-3.44
Statistic	RG	N(RG;1) +	N(RG;1) -	ap	RAL	RAV
	-0.195	42%	58%	-6.01	0.858	0.988

Urban site

Parameter	σ^2_α	σ^2_β	$\sigma_{\alpha\beta}$	$\rho_{\alpha\beta}$	μ_α	μ_β
Estimate	327.63	3.36	-25.68	-0.77	88.37	-0.75
t-values	6.72	4.77	-5.08	-5.08	54.94	-5.02
Statistic	RG	N(RG;1) +	N(RG;1) -	ap	RAL	RAV
	-0.409	34%	66%	-7.64	1.09	0.975

Rural site

Parameter	σ^2_α	σ^2_β	$\sigma_{\alpha\beta}$	$\rho_{\alpha\beta}$	μ_α	μ_β
Estimate	106.95	0.91	-3.54	-0.36	73.88	-0.01
t-values	6.68	3.58	-2.15	-2.15	88.34	-0.13
Statistic	RG	N(RG;1) +	N(RG;1) -	ap	RAL	RAV
	-0.010	50%	50%	-3.89	0.556	0.990

Note: t-values <|2| are not significant.

As a matter of fact, by applying equation (2.3) to the energy intake repeated measures we obtained excellent fit indices: Chi-square (df)=37.38(29), p>0.001(p=0.137), RMSEA=0.015, with 90% CI for RMSEA=(0.00; 0.028), CFI=1.00, SRMR=0.018. So then, the energy intake dynamics are definitely cubic. Nevertheless, in order to better detangle these nonlinear patterns, a piecewise LGCM strategy was applied here with splitting the curve into two linear trajectories and fixing the breaking point at year 2006 from which a second line departs. By doing so, the loadings λ_{06}, λ_{09}, and λ_{11} of the second linear slope β_{2i} were respectively fixed to 0, 3 and 5 according to the initial metric and thus simulating a new linear form departing from 2006. The piecewise linear model fitted well: Chi-square (df)=100.76(35), p<0.001, RMSEA=0.039, with 90% CI for RMSEA=(0.030; 0.048), CFI=0.97, SRMR=0.029. In the tables 2 and 3 are depicted the cubic and the piecewise linear LGCMs growth parameters for energy intake directly at family level (results about urban and rural area were not shown for preserving space. They can be requested, but they showed similar negative trends although more marked in the urban site families). Three slope factors (table 2) described the curvilinear function with showing significant variances in decreasing sequence indicating that the growth change in energy intake became more and more similar across individuals while passing time. This was a decreasing change since two factor means out of three were negative along with higher percentages of negative slopes as well. The covariances (correlations) indicated this decreasing growth process that already started from the linear part of the polynomial function (i.e., parameters of slope β), with a little increasing when passing to the quadratic part until decreasing again with a steeper acceleration down in the cubic part. These results were confirmed more clearly by piecewise linear model (table 3) with a decreasing of energy intake especially after 2006. Furthermore, a strong convergence point (i.e., $RAV_{\beta\beta 2}$=0.04) occurred when roughly 21.5% of time passed after 2006. It means after 1.07 years after 2006, in 2007.

Table 2: *Estimates and statistics for energy intake trajectories at family level*

Family whole sample cubic trajectories

Parameter	σ^2_α	σ^2_β	$\sigma^2_{\beta 2}$	$\sigma^2_{\beta 3}$	μ_α	μ_β	$\mu_{\beta 2}$	$\mu_{\beta 3}$	RG_β	$RG_{\beta 2}$	$RG_{\beta 3}$
Estimate	4214.72	1195.70	45.49	0.16	246.49	-6.15	1.61	-0.12	$^+$43%	$^+$59%	$^+$39%
t-values	22.50	8.33	5.21	4.97	143.31	-4.24	4.58	-5.47	$^-$57%	$^-$41%	$^-$61%

Parameter	$\sigma_{\alpha\beta}$ ($\rho_{\alpha\beta}$)	$\sigma_{\alpha\beta 2}$ ($\rho_{\alpha\beta 2}$)	$\sigma_{\alpha\beta 3}$ ($\rho_{\alpha\beta 3}$)	$\sigma_{\beta\beta 2}$ ($\rho_{\beta\beta 2}$)	$\sigma_{\beta\beta 3}$ ($\rho_{\beta\beta 3}$)	$\sigma_{\beta 2\beta 3}$ ($\rho_{\beta 2\beta 3}$)
Estimate	-1670.68(-0.74)	232.95(0.53)	-10.24(-0.39)	-218.01(-0.93)	11.66(0.84)	-2.64(-0.98)
t-values	-15.84	10.48	-7.80	-6.30	5.73	-5.02

Table 3: *Estimates and statistics for energy intake trajectories at family level*

Family whole sample piecewise linear-linear trajectories

Parameter	σ^2_α	σ^2_β	$\sigma^2_{\beta 2}$	$\sigma_{\alpha\beta}$ ($\rho_{\alpha\beta}$)	$\sigma_{\alpha\beta 2}$ ($\rho_{\alpha\beta 2}$)	$\sigma_{\beta\beta 2}$ ($\rho_{\beta\beta 2}$)	μ_α	μ_β	$\mu_{\beta 2}$
Estimate	635.75	24.37	103.53	-29.37 (-0.24)	35.30 (0.14)	-45.12 (-0.90)	246.04	-0.64	-3.35
t-values	2.45	2.16	3.57	-0.57	0.49	-2.74	145.78	-1.88	-5.30

Statistic	RG_β	$RG_{\beta 2}$	$ap^{\alpha\beta}$	$ap^{\beta\beta 2}$	$RAL^{\alpha\beta}$	$RAV^{\alpha\beta}$	$RAL^{\beta\beta 2}$	$RAV^{\beta\beta 2}$
	-0.130 ($^+$45%; $^-$55%)	-0.329 ($^+$47%; $^-$63%)	-1.20	-0.43	0.171	0.96	0.215	0.04

4. Wrap-up and conclusion

At present, we do believe that by attempting to detangle the complexity of nutritional growth processes in the human over a time span, or different situations of intervention, requires of inspecting variations at individual level. In this respect, what is needed is of a statistical technique that is able to estimate variations and shared-variations among individual trajectories, simultaneously. Advances in this direction have been made by latent growth curve models. Latent growth parameters of such curves permit to catch a lot of detailed information that deserve to be further investigated. The real data example concerning fats, proteins, carbohydrates and energy intake individual trajectories of Chinese people collected in unequal blocks of years from 2000 to 2011 showed different growth functions. Nevertheless, all the individual trajectories tended to be negatively inclined with also reducing the high discrepancies occurred before Chinese agricultural reforms took place in 2004-05 and 2008-09. The former introduced direct subsidies to farmers, agricultural tax reduction, support to seed and machinery purchases whereas the latter introduced investments to housing, to rural constructions and infrastructure so as to enhance domestic demand and people’s livelihood . These reforms presumably encouraged people to follow a more balanced diet since the general reducing of macronutrients and energy intake discrepancies yielded to many convergence points (in 2006, 2007, 2009, 2012) and interesting curvatures in 2006 occurred both after and throughout the corresponding aforementioned time intervals of such reforms.

REFERENCES

Bollen K. A. & Curran P. J. (2006) *Latent curve models: A structural equation perspective*. New York: Wiley.

Duncan T. E., Duncan S. C. & Stryker L. A. (2006) *An introduction to latent variable growth curve modeling: Concepts, issues, and applications (2nd ed.).* Mahwah, NJ: Lawrence Erlbaum.

Hancock G. R. & Choi J. (2006) A vernacular for linear latent growth models, *Structural Equation Modeling: A multidisciplinary journal*, 13:3, 352-377.

Hancock G. R., Harring J. R. & Lawrence F. R. (2013) Using latent growth models to evaluate longitudinal change, in: *Structural equation modeling: A second course (2nd ed.)*, Hancock, G. R. Mueller, R. O. (Eds.), Charlotte, NC: Information Age Publishing, Inc., 309-341.

Hancock G. R. & Mueller R. O. (2010) *The reviewer's guide to quantitative methods in the social sciences*. New York: Routledge.

Jöreskog K. & Sörbom D. (2007) *LISREL 8.80 for Windows*. Scientific Software International Inc., Chicago, IL

Kline B. R. (2011) *Principles and Practice of Structural Equation Modeling (Third edition)*. New York: The Guildford Press.

Muthén B. (2001) Second-generation structural equation modeling with a combination of categorical and continuous latent variables: New opportunities for latent class-latent growth modeling, in: *New methods for the analysis of change*, Collins, L. M. & Sayer, A. G. (Eds), Washington DC: APA, 291-322.

Preacher K. J. (2010) Latent Growth Curve Models, in: *The reviewer's guide to quantitative methods in the social sciences*, Hancock, G. H. & Mueller, R. O. (Eds), New York: Routledge, 185-198.

Preacher K. J. & Hancock G. R. (2015) Meaningful aspects of change as novel random coefficients: A general method for re-parameterizing longitudinal models. *Psychological Methods*, 20, 1, 84-101.