Diabetology

Extended Abstract

The Use of Artifical Intelligence in Assessing Glucose Variability in Individuals with Diabetes Type 2 from Routine Primary Care Data - Ljiljana Trtica Majnarić - JJ Strossmayer University Osijek, Croatia

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Abstract

Background

The continuous glucose monitoring technique is recommended for follow-up of individuals with diabetes type 1. For those with diabetes type 2, glucose variability measures, either performed automatically or by visit-to-visit method, can be used to complement glycosylated haemoglobin (HbA1c) in predicting long-term outcomes.

The main constraint in making the choices of medication therapy is the lack of relevant information on diabetes control. For example, a tight diabetes control in older individuals with DM2 and comorbidities and target organs involvement is difficult to achieve, as the precise knowledge on factors influencing glycaemic control in these individuals is scarce [2]. Some of the mechanisms may include increased inflammation and oxidative stress, by which inflamed target organs tissues may worsen insulin resistance [3]. The recent reports suggest an inflammatory marker, neutrophil/lymphocyte ratio, as a new measure of diabetes control [4]. Some non-diabetic drugs, acting alone, or in the concert with other drugs, can interfere with the blood glucose levels [5].

Glycosylated haemoglobin (HbA1c), a measure of average blood glucose in the past three months, has been historically used as a measure of the overall glycaemic control, and as a surrogate marker for the development of long-term diabetes complications [6]. According to the current guidelines, HbA1c values below 7% indicate optimal glycaemic control [2]. A limitation of this measure is a lack of information on acute glycaemic variations, and an inability to predict acute hypoglycaemic events [7]. In addition, individuals with the same HbA1c value may have different mean glucose concentrations [8]. In the era of personalised medicine, HbA1c, if taken alone, is not sufficient to guide decisions on treatment

Methods

A-proof-of-concept study, conducted in primary care. A total of 63 variables were used from electronic health records to describe clinical characteristics of 110 individuals with diabetes type 2 of both gender, 40-86 years old (average 62.69), and on treatment with oral hypoglycaemic drugs. The artificial neural networks (ANN) of machine learning techniques was used to model inter-day glucose variability based on the estimation of variances (the square of the standard deviation) of sporadically recorded fasting and postprandial (2h after breakfast) glucose measurements as the outcome measures. Model of increased HbA1c (≥ 7%) was used as the benchmark. The number of variables for modelling was reduced by using the pre-processing method. Multiple linear regression (MLR) models were performed on the prepared subsets to compare to the predictive accuracy of ANN models. This was a retrospective observational and analytical pilot study conducted from October 1, 2016, to January 31, 2017, in two PC practices, in eastern Croatia. Participants were individuals diagnosed with DM2. The number of participants included in the study exceeded 100 (N = 110), which is the minimal number of subjects recommended for data modelling [15]. They were of both gender, and 40-86 years old (average 62.69). Data was collected during encounters, in a four-month lasting recruitment process. This was a sufficiently long period that all individuals who adhere to treatment with oral hypoglycaemic drugs (OHDs) rotate. During this period, participants were invited several times for blood glucose measurements. They were informed about the purpose of the study and all signed their informed consent for participation in the study and for the possible publication of the study results.

Results

A higher glucose variability, for both fasting and postprandial glucose variances, was associated with higher HbA1c values

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(Q1-Q4 differences, p = 0.002 and 0.006, respectively). The two top-ranked variables in ANN models of glucose variability were the same, indicating HbA1c and glomerular filtration rate, a measure of chronic renal impairment. MLR models of glucose variability did not give the significant predictors.

Conclusion

For created models of glucose variability, to become practically useful, their outcome measures should be dichotomised and standardised according to the thresholds of HbA1c or some standardised measures of glucose variability, such as the coefficient of variation. The Q4 of fasting or postprandial glucose variance, compared to Q1, is considered as a higher level of glucose variability.

A considerable part of subjects in Q1 of fasting glucose variance had HbA1c values which are within the range of normal HbA1c values, while a majority of subjects in Q4 had increased HbA1c values (≥ 7%). The Q1-Q4 difference was statistically significant (p = 0.002) (Figure 1, left).

An association between Q1-Q4 of postprandial glucose variance and HbA1c, also showed statistically significant difference (p = 0.006) (Figure 2, right). Compared to Q4 of fasting glucose variance, in Q4 of postprandial glucose variance, more subjects had HbA1c values which are within the range of normal HbA1c values. In this terms, results of QQ analysis showed that the principle, the higher variances of fasting and postprandial glucose, the higher HbA1c, is only partly true, as there are participants with a higher glucose variability (Q4) who do not have increased HbA1c, and *vice versa*, a considerable part of those with increased HbA1c are at a lower level of glucose variability (Q1) (Figure 1). In addition, from models indicating increased HbA1c, it can be seen that HbA1c might be influenced by other factors than the level of glucose exposure (Table 1 and Figure 3). And oppositely, glucose variability measures are likely to be influenced by a wide range of factors, each having a small contribution but neither reaching a power as an independent predictor, thus demonstrating a behaviour as a complex system (Table 1 and Figure 2). Among these factors, HbA1c plays an important role (ANN models of glucose variability) (Figure 2) but still not as a dominating, independent predictor (MLR models of glucose variability)

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