

Interactive Integrated Electronic Health Records

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Associate Editor: XXXXXXXX

Received on XXXXX: revised on XXXXX: accepted on XXXXX

Abstract

Motivation: The a

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Supplementary information: Supplementary data are available at *Bioinformatics* online.

1 Introduction

The widespread implementation of the electronic health record (EHR) has improved healthcare through reduced processing times and cost, improved quality of patient care and detailed clinical information through longitudinal storage Denny *et al.*, 2010. Longitudinal clinical data can be useful for applied clinical research like identifying drug adverse effects or repositioning of drugs. text follows.

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2 Approach

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3 Methods

3.1 Population

The clinical data modelling diabetes patients was generated using modules from Synthea, a synthetic patient generator. The population consisted of 1000 individuals originating from Massachusetts, MA. The selection criteria were that they suffered from a metabolic disorder. The wellness encounters module provide was used to generate useful observations including BMI, insulin resistance and glycated haemoglobin . Diabetes is stored in 2 modules namely metabolic syndrome disease and metabolic syndrome care. These contain diabetes specific measurements including hemoglobin levels.

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Genotypic data was extracted from the Gene Expression Omnibus. Montesanto et. al indicate that CAT, FTO and UCP1 are all associated with type 2 diabetes. Search each of these genes with type 2 diabetes directs me to the same series: GSE25462. To model the effect of medication on gene expression, the commonly prescribed drug Simvastatin 20 MG Oral Tablet (n = 46) was used in the search. The search term

was used to find gene expression variation associated with the disease and drug and the . The top result measured APOC3 levels in subgroups Type 2 diabetic and insulin-resistant but normoglycemic cohorts in skeletal muscle cells. The primary outcome of the search was to identify a suitable model for diabetes associated gene expression variation. Studies have suggested a linked between mitochondrial oxidative homeostasis and predisposition to diabetic vascular complications (Alberto Montesanto, 2018). Plasma APOC3 associates with almost half of HDL (Zvintzou E, 2017); HDL-associated apoA-I and lysosphingolipids protect against ATP reduction resulting from reverse cholesterol transport in mitochondria CR White, 2017). When sorting this by subset effect, TPM1 comes up as highest.

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3.3 Development of integrated genomic and clinical data

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Fig. 1. Caption, caption.

time. Efficiency is also improved by the elimination of issues associated with privacy including de-personalising the data and requesting new data privileges. Issue with Synthea is the discrepancies with demographic data that have been noted (ref). Synthea developers have addressed this and are continuously improving the likeliness to real data through their GitHub account (link).

Limitations of microarrays: limitations include cross-hybridisation induced high background limitations

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Normalisation prevents technical variation between assays from displaying as biological variation. The robust multi-array average (RMA) is used from the 'oligo' package to

5 Conclusion

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