mechanisms underlying their development, DNA methylation may be involved.

**Objectives:** The aim of this study was to estimate DNA methylation changes occurring secondary to psychotropic treatment and evaluate associations between 1-month metabolic changes and baseline DNA methylation or 1-month DNA methylation changes, using an epigenome-wide approach.

**Methods:** Seventy-nine psychiatric patients recruited as part of PsyMetab study, who started a treatment with either an antipsychotic, a mood stabilizer or mirtazapine were selected. Epigenome-wide DNA methylation was measured using the Illumina Methylation EPIC BeadChip at baseline and after one month of treatment.

**Results:** A global methylation increase was observed after 1 month of treatment, which was more pronounced in patients whose weight remained stable (i.e., <2.5% weight increase). Epigenome-wide significant methylation changes were observed at 52 loci in the whole cohort and at one site, namely cg12209987, located in an intergenic region within an enhancer, specifically in patients who underwent important early weight gain (i.e., ≥5% weight increase) during the same period of treatment (p<5*10^-8). Multivariable analysis confirmed an association between an increase in methylation at this locus and weight gain in the whole cohort (p=0.004). Epigenome-wide association analyses failed to identify any significant link between other metabolic changes (e.g. glucose or lipid levels) and methylation data.

**Conclusions:** These findings give new insight into the mechanisms of psychotropic drug-induced weight gain. With improved understanding of the metabolic side effects, the use of precision medicine with epigenetics may become possible.

**Disclosure:** No significant relationships.

**Keywords:** psychotropic drugs; Metabolic side effects; Precision Medicine; epigenetics

### Mental Health Care 2

**O0096**

**NeuroBlu: a natural language processing (NLP) electronic health record (EHR) data analytic tool to generate real-world evidence in mental healthcare**

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**Introduction:** EHRs contain a rich source of real-world data that can support evidence generation to better understand mental disorders and improve treatment outcomes. However, EHR datasets are complex and include unstructured free text data that are time consuming to manually review and analyse. We present NeuroBlu, a secure, cloud-based analytic tool that includes bespoke NLP software to enable users to analyse large volumes of EHR data to generate real-world evidence in mental healthcare.

![Image of NeuroBlu tool](https://www.neuroblu.ai/)

**Objectives:** (i) To assemble a large mental health EHR dataset in a secure, cloud-based environment.
(ii) To apply NLP software to extract data on clinical features as part of the Mental State Examination (MSE).
(iii) To analyse the distribution of NLP-derived MSE features by psychiatric diagnosis.

**Methods:** EHR data from 25 U.S. mental healthcare providers were de-identified and transformed into a common data model. NLP models were developed to extract 241 MSE features using a deep learning, long short-term memory (LSTM) approach. The NeuroBlu tool (https://www.neuroblu.ai/) was used to analyse the associations of MSE features in 543,849 patients.

**Results:** The figure below illustrates the percentage of patients in each diagnostic category with at least one recorded MSE feature.

![DISTRIBUTION OF MSE LABELS BY DISORDER](https://example.com/distribution.png)
Conclusions: Delusions and hallucinations were more likely to be recorded in people with schizophrenia and schizoaffective disorder, and cognitive features were more likely to be recorded in people with dementia. However, mood symptoms were frequently recorded across all diagnoses illustrating their importance as a transdiagnostic clinical feature. NLP-derived clinical information could enhance the potential of EHR data to generate real-world evidence in mental healthcare.

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Keywords: RWE; NLP; EHR; RWD