

**Summary in English:**

Main result of studies included in this dissertation are about PGx-related bioinformatic software outcomes and the approaches to deal with less-studied pharmacogenes and pharmacovariants. Four publicly available PGx bioinformatics algorithms to assign PGx haplotypes were applied to nine selected very important pharmacogenes (VIP) and revealed a 45–70% concordance rate. To ensure availability of the results at point-of-care, actionable variants were stored in a web-hosted database and PGx-cards were developed for quick access and handed to the study subjects. Also, methods for deep computational filtration of large scale clinical PGx profiling introduced in order to perform functional assessment of not-interpreted pharmacovariants.