THE FUTURE OF AI IN PRECISION MEDICINE: ETHICAL, LEGAL, AND SOCIAL IMPLICATIONS

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CRANIAL EPIGENETIC TRAIT FREQUENCIES IN CROATIA: COMPARING MODERN AND ARCHAEOLOGICAL POPULATIONS

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To quantify cranial epigenetic (non-metric) traits in a contemporary Croatian MSCT sample and compare trait frequencies with an archaeological cranial series, overall and by sex. The modern dataset comprised 390 adult MSCT scans from Split (n=196) and Zagreb (n=194) and was balanced by sex (195 males and 195 females). The archaeological dataset comprised 140 adult crania (71 females, 69 males); trait-specific sample size varied due to missing observations. Traits were scored as present/absent (bilateral traits by side). Group differences were tested using χ^2/Fisher's exact tests, with Benjamini–Hochberg FDR adjustment (q-values). In the modern sample, 6/74 traits differed between Split and Zagreb, and 10/74 differed by sex after FDR correction ($q<0.05$), with higher frequencies consistently observed in Split and in males. In the archaeological series, no sex differences remained significant after FDR correction. Modern– archaeological comparisons across overlapping traits identified 35/72 traits with significant differences ($q<0.05$), consistent with secular change in cranial epigenetic trait frequencies. Contemporary MSCT- based profiling provides population-specific epigenetic trait reference data and, relative to archaeological material, indicates limited regional differentiation but pronounced sex-associated patterning in modern samples and substantial secular change across time.

Keywords: MSCT, cranial epigenetic traits, modern Croatian population, medieval period, secular changes

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BRIDGING THE GAP: A NATIONAL ROADMAP FOR IMPLEMENTING EHDS STANDARDS IN A NON-EU COUNTRY – THE CASE OF SERBIA

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The development of AI in precision medicine increasingly depends on access to high-quality, interoperable health data, positioning the European Health Data Space (EHDS) as a key regulatory and technological framework. While primarily designed for EU Member States, its implications for non-EU countries remain underexplored. This study aims to develop a national-level roadmap for aligning a non-EU healthcare system with EHDS standards, using Serbia as a case study, and to assess its broader ethical, legal, and social implications for AI deployment. The research applies a qualitative methodology combining normative legal analysis, comparative assessment with selected European models, and policy mapping of Serbia's existing digital health ecosystem, including legislation on medical documentation, national registries, and eHealth platforms. Findings indicate that Serbia has established a foundational legal and technical infrastructure, yet faces challenges related to interoperability, data governance, institutional capacity, and alignment with EU data protection and AI regulations. The proposed roadmap outlines phased alignment across legal harmonization, institutional design, and technical standardization, enabling integration into cross-border data ecosystems such as HealthData@EU. Importantly, the study highlights that such alignment extends beyond technical readiness, raising critical questions around data sovereignty, trust, algorithmic accountability, and equitable access to AI-driven healthcare. The paper concludes that adopting EHDS-compatible standards in non-EU contexts can accelerate innovation and international integration but must be accompanied by robust ethical and governance frameworks to ensure responsible and inclusive use of AI in precision medicine.

Keywords: EHDS, artificial intelligence, health data governance, digital health, Serbia

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MAPPING THE CROATIAN OPHTHALMIC DATA LANDSCAPE FOR INHERITED RETINAL DISEASES: A STEP TOWARD A NATIONAL FRAMEWORK

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To evaluate the availability of diagnostic procedures, access to genetic testing, and data management practices in tertiary ophthalmology centers in Croatia, with the goal of identifying needs for establishing a national framework for the care of patients with inherited retinal diseases (IRDs). A cross -sectional survey was conducted among ophthalmologists actively involved in IRD patient care across tertiary centers. Data were collected on the availability of diagnostic procedures, access to genetic testing, and local practices for data collection, storage, and integration of clinical and genetic information. Considerable variability was identified between centers in the availability of diagnostic methods and access to genetic testing. While core imaging modalities are widely available, advanced retinal function testing and genetic diagnostics are not uniformly accessible. Data are predominantly stored within local hospital systems, with limited standardization and minimal integration of clinical and genetic information. This study provides the first national overview of IRD -related diagnostic and data management practices in Croatia. Despite the establishment of a national Reference Center for inherited retinal dystrophies in 2022, its potential to coordinate care and enable centralized data collection remains underutilized. The identified gaps highlight the need for improved coordination, standardization, and data integration. Establishing a structured national framework, including a hub-and- spoke model and centralized data collection, could enhance patient care and support future therapeutic and research initiatives.

Keywords: inherited retinal diseases (IRDs), genetic testing, diagnostic techniques, data management, health care organization

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EVALUATION OF TRUST AND PERSPECTIVES ON ARTIFICIAL INTELLIGENCE INTEGRATION AMONG MEDICAL AND PHARMACEUTICAL PROFESSIONALS: A SURVEY STUDY

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This study evaluated the level of trust, risk perception, and expectations of the medical and pharmaceutical community regarding the implementation of artificial intelligence (AI) tools in professional practice. A cross-sectional survey was conducted among 71 healthcare professionals, including 36 pharmacists (50.7%) and 35 physicians (49.3%). The questionnaire addressed AI tool usage frequency, trust in generated recommendations measured on a 5-point Likert scale, and assessment of privacy risks. Statistical analysis involved calculating mean values and frequency distributions. The results demonstrated an average level of professional trust in AI recommendations of 3.14 points. The highest level of concern related to patient confidentiality and data security risks, which were rated at 3.24 points. While the hypothesis of complete human replacement by AI technology was decisively rejected (1.8 points), forecasts for deep AI integration into professional workflows over the next decade remained very high (3.89 points). A significant "educational vacuum" was identified, with 67.6% of respondents acquiring AI skills through self-study, whereas university curricula lacked such knowledge for all participants. In conclusion, specialists view AI as an intelligent digital assistant rather than a replacement for human expertise. Despite a high readiness for professional transformation, barriers such as data security risks and the absence of systemic education must be addressed through secure local AI solutions and modernized medical curricula.

Keywords: artificial intelligence, digital medicine, healthcare, professional trust, medical education

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DEVELOPING REFERENCE DATA BASES FOR MEGALOPOLISES BY DNA-MARKERS TAKING INTO ACCOUNT DYNAMICS OF GENE POOL UNDER ACTION OF MIGRATION

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Megalopolises represent specific historically new type of population structure for which adequate models and methods of study have not yet been developed. Megalopolises are characterized by ethnically mixed population (1 million or over) with territorial subdivision, high level of migration and reproduction of population due to migration preferentially. Migration is the main factor of gene pool dynamics of megalopolises. The goal of the study was to characterize the gene pool of three megalopolises by, DNA markers of Y-chromosome and mtDNA, by autosomal STR and to estimate influence of migration on their dynamics using standard statistical approaches, Material and methods. In the samples from Saint- Petersburg, senior generation of Novosibirsk, senior and young generations from Moscow, the genetic differentiation by 18 STR and haplogroups of Y-chromosome and haplogroups (detected by 18 STR haplotypes by Internet-predictors) of mtDNA detected by Internet-predictor basing on nucleotide sequences of HVSI and HVSII (Moscow samples by 27 autosomal STR, additionally) was studied. Migration parameters were calculated by analysis of questionnaire data. Results. Differentiation by DNA markers of Y-chromosome demonstrates a more prominent influence of migration processes compared to other markers. Accumulation of "southern origin" haplogroups of Y-chromosome in the gene pool of Moscow was demonstrated under action of modern migration flows. Autosomal STR frequencies demonstrate the less influence of migration in generations. Territorial ethnic subdivision of the megalopolises population was demonstrated by 2010 Census data. Conclusion. Observed statistically significant differences between samples by DNA-markers mostly mediated by modern migration (especially from North Caucasus. Transcaucasia and Middle Asia) evidence of necessity of developing separate reference data bases for each megalopolis (considering territorial subdivision) including molecular and genetic demographic data.

Keywords: megalopolis, population, migration, reference database