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Academic Degree	prof. dr hab. inż. (Prof.)
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UPWr Base of Knowledge - link	<a href="https://bazawiedzy.upwr.edu.pl/info/autor/UPWr0b20a261b6864df1b93c3a1feb84e5cc/Joanna+Szyda?affil=&amp;r=phd&amp;tab=phd&amp;lang=en&amp;cid=492636">https://bazawiedzy.upwr.edu.pl/info/autor/UPWr0b20a261b6864df1b93c3a1feb84e5cc/Joanna+Szyda?affil=&amp;r=phd&amp;tab=phd&amp;lang=en&amp;cid=492636</a>
Researchgate:	
Personal website / Working group website:	
Projects in last 5 years (chronological; with distinction into PI (kierownik) and RF (wykonawca)):	2020 - 2024 PreludiumBis (NCN) "The application of deep learning methods in the analysis of livestock genomes", kierownik 2017-2021 ReDiverse (ERA NET SusAn) "Biodiversity within and between European Red dairy breeds – conservation through utilization", wykonawca 2017-2020 COST "Functional Annotation of Animal Genomes - European network", wykonawca 2016-2019 Opus (NCN) "A bioinformatic analysis of leg and hoof disease in cattle with the emphasis on epistasis", kierownik 2015-2018 Opus (NCN) "Resolving genetic predisposition to clinical mastitis based on whole genome sequences of 32 cows", kierownik
<b>Research topic and funding</b>	
1) PhD topic:	Breeding value prediction in dairy cattle using a single step model
2) Research discipline in Doctoral School	Animal Science and Fisheries
3) Short description of the research problem to be solved in the PhD:	The evaluation of additive genetic merit of animals, called Estimated Breeding Values (EBVs), has for many decades been a standard element of dairy cattle breeding programs. Currently, in many countries this process is carried out in two steps. First, a Genomically Enhanced Breeding Value (gEBV) is predicted for young selection candidates based on SNP (Single Nucleotide Polymorphism) genotypes and the information from ancestors' data. Prior to this procedure the effects of SNPs need to be estimated based on the reference bull data set. Second, a Conventional Estimated Breeding Values are predicted based on own or daughter phenotypes. In practice, two separate evaluations are needed - one for young animals without own or daughter information and one for older animals with own or daughter phenotypes. Such approach has been successfully applied up to date, but has several disadvantages. Combining SNP information, relatives' information and own phenotypic data is sub-optimal because effects of the particular models are not estimated simultaneously. As a result, information from SNPs is not propagated to un-genotyped animals, SNP effect estimates may be confounded with effects estimated based on relatives' data. A few years ago, a theoretical solution of this problem has been proposed, in the form of a single step genetic evaluation model. The most important advantage of such a model is simultaneous utilization of SNP and phenotypic information sources. Such solution allows for using both genotyped and non-genotyped animals in one EBV prediction procedure. Recently, also the major computational issues have been resolved and the first few commercial software packages are available. The application of the one-step model, the analysis of its predictive quality and the differences in prediction between the one-step and the two-step models is at the heart of the doctoral project.
4) Professional skills for PhD candidate (e.g. master program, specializations, softwares, language, analytical techniques):	The ability to work in the Linux operating system using the command line, the ability to create scripts in the bash shell, the ability to work with various software developed in open-source mode, the ability to program in C or Fortran languages at an intermediate level. Good knowledge of mathematical statistics. Very good working knowledge of English. Engagement in scientific work. Completed technical studies: bioinformatics, animal science, computer science, or related.
5) Details of the project to support PhD research	
a) Project title:	0
b) Agreement number:	0
c) Number of months in the project to support PhD (in months; starting from 1st of October 2021):	0
6) Project website:	