Mendross: An open source Perl CLI and Web tool for computing classical Mendelian inheritance problems

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Abstract

The Internet lacks an integrated toolkit for calculating and representing the punnett square of the classical Mendelian inheritance crossings alongside a proper phenotype/genotype ratios system. Mendross is an Open-source tool that computes and represents the result of a simple Mendelian crossing including (Mono, Di and trihybrid cross) in a form of punnett square. It also computes the phenotype and genotype ratios of offspring with an added chi-square analysis functionality. Mendross is a User Experience-centered tool thats designed to provide ease in use for it's users. It's fully written in Perl language and is available online in two forms: The command-line interface (CLI) which is intended for programmers and developers and the Web application tool (Mendross.com) providing much easier user-experience for non-programmers and students coming from pure biological background with no prior experience in computer science. Mendross is a nucleus for a broader genetic toolkit that allows Multihybrid crossing in it's future releases. Mendross facilitates the process of teaching classical Mendelian inheritance to students and allows a more dynamic way of experiencing the Mendelian genetics.