Decisions on the selection of conservation units are often based on genetic inventories with genetic markers (Dudgeon et al. 2012; Boccacci et al. 2021). Further, the level of genetic relatedness of individuals is an important criterion for the evaluation of genetic resources (Welirnann and Bennewitz 2019). Relatedness can be estimated with the kinship-coefficient based on data of genetic markers (Han et al. 2020). In addition, genetic assignment is often used for conservation purposes, especially for law enforcement to protect species by checking the geographic origin or taxonomy of traded biological material such as seeds, timber, ivory or bush meat (Wasser et al. 2007; Degen et al. 2013).

GDA-NT stands for “Genetic data analysis and numerical tests”. The software computes various metrics of population fixation and differentiation using genetic data that are similar to other programmes, such as the Wright’s $F_{IS}$ and $F_{ST}$ indices computed by Alequin 3.5 (Excoffier and Lischer 2010). Or it provides different genetic assignment criteria to assign or exclude reference populations as implemented in GeneClass (Piry et al. 2004). It also computes
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as csv-files for further data visualisation and downstream data analyses such as a detailed analysis of spatial genetic structures, e.g., using the software SGS (Degen et al. 2001) or principal component analysis (PCA) and cluster analysis based on allele frequencies with the program PAST (Hammer et al. 2001). An overview of the program features is given in Table 1. The program can handle data of up to a few hundred populations and a few hundred genetic markers (see as an example Degen et al. (2021)). GDA-NT 2021 is well suited for conservation genetics studies, where typical datasets involve the screening of many populations with a specifically selected subset of informative genetic markers. It is not developed for applications with large SNP arrays comprising thousands or millions of SNPs, but it can be used for a genetic quality check of pruned SNP sets drawn from such large SNP arrays.

GDA-NT 2021 has been programmed in visual basic and compiled for the operating system Microsoft Windows (Windows 10 and earlier versions). The program, a zip-file with different input data files for demonstration, different videos that explain the use of the program and the user’s manual are available on our website:

allele and genotype frequencies on different aggregation levels as integrated in the R-package pegas (Paradis 2010). However, GDA-NT 2021 has more options to compute exclusion-probabilities in assignment tests, and does enable self-assignment tests for groups of individuals with variable group sizes. In addition, it allows the calculation of alternative measures of population differentiation, such as the standardized $F_{ST}$ (Hedrick 2005; Meirmans and Hedrick 2011) or $D_{j}$ (Gregorius and Roberds 1986; Gregorius et al. 2007), which can also integrate geographic location information to select sub-populations. The application of these alternative measures of genetic differentiation is particularly useful to address questions of conservation genetics (Prunier et al. 2017; Attu et al. 2022; Nguyen et al. 2022). Figure 1 shows the application of $D_{j}$ as an indicator to identify pedunculate oak populations in Germany that are likely of foreign origin and thus should be excluded from a conservation program.

ASCI text files with diploid genetic markers (e.g., nSNPs, nSSRs) or haploid genetic markers (e.g., cpSNPs, cpSSRs) are used as input files for GDA-NT. Alternative CSV files generated by other programs such as EXCEL and R can be imported, transformed and saved as input files. The results are automatically stored as text-files and optionally as csv-files for further data visualisation and downstream data analyses such as a detailed analysis of spatial genetic structures, e.g., using the software SGS (Degen et al. 2001) or principal component analysis (PCA) and cluster analysis based on allele frequencies with the program PAST (Hammer et al. 2001). An overview of the program features is given in Table 1. The program can handle data of up to a few hundred populations and a few hundred genetic markers (see as an example Degen et al. (2021)). GDA-NT 2021 is well suited for conservation genetics studies, where typical datasets involve the screening of many populations with a specifically selected subset of informative genetic markers. It is not developed for applications with large SNP arrays comprising thousands or millions of SNPs, but it can be used for a genetic quality check of pruned SNP sets drawn from such large SNP arrays.

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Table 1 Features, methods and measures implemented in the program GDA-NT 2021

| Feature                  | Method / Measure                  | Reference                      |
|-------------------------|-----------------------------------|--------------------------------|
| Genetic assignment      | Bayesian approach                 | Rannala and Mountain (1997)    |
|                        | Allele / haplotype frequencies    | Paetkau et al. (1995)          |
|                        | approach                          |                                |
|                        | Genetic distance                  | Gregorius (1974)               |
|                        | Exclusion probabilities           | Cornuet et al. (1999)          |

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