Table S1. Performance comparison of NCMHap and other methods on the Geraci's dataset with haplotype block length *l* *= 100*. Each element in this table is the average value of each 100 data samples.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Error | Coverage | SCGD | H-pop | FastHap | FCMHap | HGHap | AROHap | ALTHap | HRCH | NCMHap |
| 0.1 | 3 | 0.918 | 0.921 | 0.823 | 0.882 | 0.941 | 0.844 | 0.944 | 0.957 | 0.916 |
| 5 | 0.944 | 0.919 | 0.917 | 0.948 | 0.989 | 0.922 | 0.953 | 0.987 | 0.971 |
| 8 | 0.948 | 0.900 | 0.955 | 0.971 | 0.994 | 0.945 | 0.945 | 0.991 | 0.983 |
| 10 | 0.959 | 0.892 | 0.926 | 0.972 | 0.997 | 0.92 | 0.943 | 0.995 | 0.989 |
| 0.2 | 3 | 0.806 | 0.836 | 0.806 | 0.739 | 0.752 | 0.711 | 0.831 | 0.851 | 0.822 |
| 5 | 0.825 | 0.865 | 0.834 | 0.772 | 0.899 | 0.736 | 0.865 | 0.926 | 0.907 |
| 8 | 0.861 | 0.873 | 0.849 | 0.793 | 0.966 | 0.760 | 0.873 | 0.941 | 0.931 |
| 10 | 0.886 | 0.878 | 0.899 | 0.835 | 0.981 | 0.788 | 0.878 | 0.956 | 0.936 |
| 0.3 | 3 | 0.671 | 0.717 | 0.578 | 0.629 | 0.621 | 0.627 | 0.694 | 0.695 | 0.684 |
| 5 | 0.676 | 0.784 | 0.711 | 0.648 | 0.698 | 0.638 | 0.780 | 0.798 | 0.759 |
| 8 | 0.740 | 0.835 | 0.700 | 0.664 | 0.79 | 0.649 | 0.841 | 0.861 | 0.816 |
| 10 | 0.798 | 0.855 | 0.732 | 0.675 | 0.856 | 0.653 | 0.857 | 0.881 | 0.843 |

Table S2. Performance comparison of NCMHap and other methods on the Geraci's dataset with haplotype block length *l* *= 350*. Each element in this table is the average value of each 100 data samples.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Error | Coverage | SCGD | H-pop | FastHap | FCMHap | HGHap | AROHap | ALTHap | HRCH | NCMHap |
| 0.1 | 3 | 0.941 | 0.921 | 0.872 | 0.873 | 0.939 | 0.844 | 0.943 | 0.939 | 0.953 |
| 5 | 0.945 | 0.912 | 0.927 | 0.919 | 0.979 | 0.892 | 0.951 | 0.981 | 0.982 |
| 8 | 0.950 | 0.896 | 0.977 | 0.934 | 0.988 | 0.908 | 0.930 | 0.991 | 0.989 |
| 10 | 0.952 | 0.889 | 0.947 | 0.935 | 0.995 | 0.910 | 0.941 | 0.994 | 0.993 |
| 0.2 | 3 | 0.813 | 0.813 | 0.763 | 0.671 | 0.712 | 0.659 | 0.849 | 0.813 | 0.856 |
| 5 | 0.817 | 0.860 | 0.811 | 0.719 | 0.905 | 0.691 | 0.896 | 0.897 | 0.921 |
| 8 | 0.832 | 0.871 | 0.912 | 0.728 | 0.899 | 0.709 | 0.908 | 0.922 | 0.939 |
| 10 | 0.838 | 0.873 | 0.923 | 0.733 | 0.907 | 0.719 | 0.913 | 0.937 | 0.948 |
| 0.3 | 3 | 0.637 | 0.629 | 0.575 | 0.597 | 0.602 | 0.595 | 0.664 | 0.640 | 0.712 |
| 5 | 0.661 | 0.744 | 0.720 | 0.614 | 0.632 | 0.609 | 0.777 | 0.737 | 0.803 |
| 8 | 0.690 | 0.830 | 0.790 | 0.626 | 0.675 | 0.628 | 0.838 | 0.788 | 0.850 |
| 10 | 0.700 | 0.850 | 0.833 | 0.631 | 0.742 | 0.635 | 0.856 | 0.821 | 0.870 |

Table S3. Performance comparison of NCMHap and other methods on the Geraci's dataset with haplotype block length *l* *= 700.* Each element in this table is the average value of each 100 data samples.

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Error | Coverage | SCGD | H-pop | FastHap | FCMHap | HGHap | AROHap | ALTHap | HRCH | NCMHap |
| 0.1 | 3 | 0.934 | 0.919 | 0.917 | 0.834 | 0.934 | 0.801 | 0.941 | 0.928 | 0.958 |
| 5 | 0.951 | 0.923 | 0.872 | 0.881 | 0.990 | 0.862 | 0.951 | 0.972 | 0.984 |
| 8 | 0.956 | 0.945 | 0.945 | 0.883 | 0.987 | 0.899 | 0.943 | 0.983 | 0.990 |
| 10 | 0.973 | 0.951 | 0.983 | 0.996 | 0.997 | 0.912 | 0.942 | 0.992 | 0.994 |
| 0.2 | 3 | 0.796 | 0.811 | 0.703 | 0.652 | 0.677 | 0.644 | 0.852 | 0.797 | 0.865 |
| 5 | 0.829 | 0.854 | 0.681 | 0.672 | 0.910 | 0.662 | 0.896 | 0.869 | 0.925 |
| 8 | 0.832 | 0.868 | 0.916 | 0.686 | 0.884 | 0.695 | 0.905 | 0.885 | 0.938 |
| 10 | 0.860 | 0.869 | 0.896 | 0.746 | 0.894 | 0.698 | 0.909 | 0.900 | 0.946 |
| 0.3 | 3 | 0.652 | 0.600 | 0.627 | 0.592 | 0.592 | 0.588 | 0.674 | 0.602 | 0.720 |
| 5 | 0.659 | 0.733 | 0.682 | 0.599 | 0.621 | 0.598 | 0.735 | 0.699 | 0.808 |
| 8 | 0.662 | 0.804 | 0.741 | 0.606 | 0.646 | 0.613 | 0.793 | 0.729 | 0.849 |
| 10 | 0.714 | 0.844 | 0.805 | 0.606 | 0.696 | 0.618 | 0.829 | 0.759 | 0.870 |

Table S4. The reconstruction rate for the proposed method, H-pop, SCGD, FastHap, HGHap, AROHap, FCMHap, ALTHap, and HRCH applied to the experimental dataset NA12878 dataset provided by 1000 genome project.

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chr | H-pop | SCGD | FastHap | HGHap | AROHap | FCMHap | ALTHap | HRCH | NCMHap |
| 1 | 0.957 | 0.925 | 0.919 | 0.937 | 0.935 | 0.913 | 0.974 | 0.954 | 0.972 |
| 2 | 0.956 | 0.926 | 0.922 | 0.929 | 0.943 | 0.908 | 0.953 | 0.943 | 0.959 |
| 3 | 0.912 | 0.919 | 0.923 | 0.928 | 0.940 | 0.913 | 0.933 | 0.944 | 0.969 |
| 4 | 0.970 | 0.927 | 0.933 | 0.923 | 0.949 | 0.923 | 0.969 | 0.960 | 0.961 |
| 5 | 0.966 | 0.939 | 0.914 | 0.932 | 0.942 | 0.912 | 0.972 | 0.952 | 0.957 |
| 6 | 0.952 | 0.930 | 0.938 | 0.935 | 0.948 | 0.929 | 0.949 | 0.958 | 0.977 |
| 7 | 0.924 | 0.935 | 0.921 | 0.925 | 0.951 | 0.904 | 0.970 | 0.954 | 0.971 |
| 8 | 0.947 | 0.907 | 0.906 | 0.906 | 0.934 | 0.903 | 0.962 | 0.949 | 0.950 |
| 9 | 0.910 | 0.971 | 0.940 | 0.901 | 0.966 | 0.937 | 0.971 | 0.921 | 0.956 |
| 10 | 0.945 | 0.926 | 0.923 | 0.940 | 0.945 | 0.913 | 0.968 | 0.954 | 0.956 |
| 11 | 0.915 | 0.932 | 0.931 | 0.939 | 0.942 | 0.923 | 0.933 | 0.963 | 0.964 |
| 12 | 0.903 | 0.923 | 0.923 | 0.945 | 0.935 | 0.908 | 0.921 | 0.954 | 0.963 |
| 13 | 0.941 | 0.970 | 0.941 | 0.930 | 0.935 | 0.925 | 0.970 | 0.946 | 0.965 |
| 14 | 0.971 | 0.911 | 0.934 | 0.917 | 0.934 | 0.932 | 0.903 | 0.949 | 0.970 |
| 15 | 0.974 | 0.991 | 0.917 | 0.920 | 0.937 | 0.905 | 0.972 | 0.951 | 0.959 |
| 16 | 0.935 | 0.930 | 0.932 | 0.932 | 0.946 | 0.924 | 0.967 | 0.962 | 0.973 |
| 17 | 0.911 | 0.967 | 0.944 | 0.931 | 0.951 | 0.920 | 0.975 | 0.963 | 0.973 |
| 18 | 0.976 | 0.903 | 0.926 | 0.924 | 0.949 | 0.919 | 0.910 | 0.954 | 0.973 |
| 19 | 0.978 | 0.972 | 0.930 | 0.949 | 0.942 | 0.923 | 0.976 | 0.960 | 0.968 |
| 20 | 0.950 | 0.968 | 0.931 | 0.945 | 0.946 | 0.922 | 0.973 | 0.957 | 0.971 |
| 21 | 0.970 | 0.943 | 0.919 | 0.933 | 0.941 | 0.915 | 0.974 | 0.960 | 0.960 |
| 22 | 0.983 | 0.941 | 0.926 | 0.951 | 0.941 | 0.914 | 0.973 | 0.964 | 0.976 |

Table S5. The average of running time of NCMHap and other methods on the Geraci's dataset with haplotype block length *l* *= 100* (In seconds).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Error | Coverage | SCGD | H-pop | FastHap | FCMHap | HGHap | AROHap | ALTHap | HRCH | NCMHap |
| 0.1 | 3 | 0.094 | 0.425 | 0.091 | 0.065 | 0.357 | 1.301 | 0.043 | 7.757 | 0.176 |
| 5 | 0.173 | 0.471 | 0.174 | 0.139 | 0.443 | 2.002 | 0.060 | 6.272 | 0.272 |
| 8 | 0.773 | 0.541 | 0.440 | 0.334 | 0.682 | 2.324 | 0.088 | 6.161 | 0.613 |
| 10 | 2.660 | 0.567 | 0.772 | 0.561 | 0.744 | 3.027 | 0.136 | 5.578 | 0.925 |
| 0.2 | 3 | 0.097 | 0.437 | 0.083 | 0.059 | 0.425 | 1.840 | 0.039 | 7.571 | 0.179 |
| 5 | 0.157 | 0.485 | 0.183 | 0.137 | 0.650 | 2.096 | 0.060 | 8.275 | 0.232 |
| 8 | 0.537 | 0.527 | 0.518 | 0.307 | 0.834 | 2.017 | 0.094 | 8.525 | 0.510 |
| 10 | 3.050 | 0.570 | 0.723 | 0.441 | 1.040 | 2.632 | 0.135 | 6.822 | 0.776 |
| 0.3 | 3 | 0.102 | 0.350 | 0.114 | 0.061 | 0.350 | 1.919 | 0.041 | 9.448 | 0.162 |
| 5 | 0.205 | 0.400 | 0.192 | 0.131 | 0.474 | 1.303 | 0.063 | 9.844 | 0.229 |
| 8 | 0.643 | 0.454 | 0.461 | 0.283 | 0.720 | 1.930 | 0.093 | 9.462 | 0.493 |
| 10 | 3.005 | 0.470 | 0.963 | 0.427 | 0.955 | 2.488 | 0.133 | 10.155 | 0.713 |

Table S6. The average of running time of NCMHap and other methods on the Geraci's dataset with haplotype block length *l* *= 350* (In seconds).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Error | Coverage | SCGD | H-pop | FastHap | FCMHap | HGHap | AROHap | ALTHap | HRCH | NCMHap |
| 0.1 | 3 | 0.403 | 0.707 | 1.444 | 0.772 | 2.263 | 6.013 | 0.210 | 14.62 | 1.517 |
| 5 | 1.255 | 0.906 | 4.823 | 1.959 | 5.500 | 8.557 | 0.447 | 13.00 | 3.496 |
| 8 | 19.750 | 1.150 | 18.061 | 5.55 | 12.935 | 17.679 | 0.818 | 11.48 | 7.940 |
| 10 | 22.836 | 1.300 | 35.922 | 10.10 | 19.192 | 28.498 | 1.962 | 11.27 | 17.16 |
| 0.2 | 3 | 0.417 | 0.762 | 1.494 | 0.792 | 2.226 | 4.948 | 0.220 | 13.37 | 1.610 |
| 5 | 1.506 | 0.924 | 4.872 | 1.974 | 5.750 | 8.512 | 0.456 | 14.38 | 3.318 |
| 8 | 16.070 | 1.175 | 14.786 | 5.437 | 14.370 | 17.478 | 0.843 | 17.94 | 8.466 |
| 10 | 26.652 | 1.331 | 32.024 | 9.212 | 21.356 | 26.242 | 1.843 | 20.37 | 14.11 |
| 0.3 | 3 | 0.432 | 0.916 | 1.255 | 0.813 | 2.559 | 5.161 | 0.226 | 12.48 | 1.607 |
| 5 | 1.600 | 0.997 | 2.553 | 2.096 | 6.311 | 8.914 | 0.481 | 14.46 | 3.706 |
| 8 | 15.684 | 1.022 | 11.857 | 5.356 | 15.607 | 17.695 | 0.809 | 19.69 | 8.597 |
| 10 | 33.916 | 1.330 | 19.952 | 8.621 | 23.727 | 26.004 | 1.948 | 22.53 | 13.78 |

Table S7. The average of running time of NCMHap and other methods on the Geraci's dataset with haplotype block length *l* *= 700* (In seconds).

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Error | Coverage | SCGD | H-pop | FastHap | FCMHap | HGHap | AROHap | ALTHap | HRCH | NCMHap |
| 0.1 | 3 | 1.520 | 1.178 | 4.324 | 4.241 | 13.159 | 24.843 | 1.037 | 31.82 | 6.770 |
| 5 | 7.319 | 1.886 | 29.161 | 12.28 | 35.123 | 60.621 | 2.062 | 34.37 | 17.55 |
| 8 | 61.88 | 3.765 | 141.98 | 41.164 | 85.829 | 164.708 | 4.817 | 43.35 | 72.80 |
| 10 | 101.5 | 5.316 | 257.77 | 77.432 | 136.267 | 226.777 | 11.38 | 40.05 | 151.4 |
| 0.2 | 3 | 1.320 | 1.238 | 4.871 | 4.567 | 14.453 | 29.882 | 0.901 | 29.21 | 7.460 |
| 5 | 5.744 | 1.979 | 36.862 | 12.368 | 37.972 | 64.612 | 1.938 | 38.73 | 19.36 |
| 8 | 64.51 | 3.922 | 110.93 | 37.862 | 100.422 | 157.694 | 4.375 | 55.19 | 65.15 |
| 10 | 87.71 | 5.763 | 222.89 | 67.696 | 153.434 | 264.44 | 10.13 | 72.24 | 133.3 |
| 0.3 | 3 | 1.348 | 1.260 | 4.726 | 4.92 | 16.483 | 27.922 | 0.997 | 25.67 | 7.590 |
| 5 | 5.216 | 2.082 | 38.79 | 13.785 | 43.084 | 57.402 | 2.056 | 44.44 | 20.83 |
| 8 | 79.42 | 4.035 | 127.97 | 39.386 | 117.87 | 128.85 | 4.455 | 70.66 | 71.74 |
| 10 | 117.2 | 5.324 | 210.343 | 68.927 | 178.775 | 225.696 | 9.028 | 75.12 | 137.2 |

Table S8. The average of running time for the proposed method, H-pop, SCGD, FastHap, HGHap, AROHap, FCMHap, ALTHap, and HRCH applied to the experimental dataset NA12878 dataset provided by 1000 genome project (In seconds).

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Chr | H-pop | SCGD | FastHap | HGHap | AROHap | FCMHap | ALTHap | HRCH | NCMHap |
| 1 | 5.22 | 3.62 | 5.90 | 1.54 | 20.28 | 1.09 | 11.26 | 10.40 | 2.593 |
| 2 | 5.65 | 4.41 | 6.72 | 1.30 | 18.03 | 1.04 | 12.22 | 12.34 | 1.585 |
| 3 | 6.99 | 3.40 | 7.54 | 1.17 | 18.45 | 1.91 | 10.38 | 12.75 | 4.116 |
| 4 | 5.24 | 5.47 | 5.24 | 1.20 | 18.06 | 1.68 | 12.16 | 13.07 | 4.137 |
| 5 | 4.67 | 3.54 | 6.10 | 1.24 | 15.09 | 1.27 | 9.96 | 14.98 | 2.827 |
| 6 | 4.93 | 8.70 | 6.82 | 1.22 | 15.60 | 1.04 | 14.17 | 13.58 | 2.227 |
| 7 | 4.24 | 3.95 | 7.30 | 1.26 | 16.34 | 1.03 | 11.19 | 12.53 | 1.642 |
| 8 | 4.14 | 2.18 | 8.11 | 1.25 | 16.62 | 1.07 | 9.63 | 13.03 | 2.641 |
| 9 | 3.36 | 2.94 | 8.63 | 1.30 | 15.25 | 1.04 | 6.42 | 12.63 | 1.874 |
| 10 | 3.67 | 2.56 | 7.76 | 1.21 | 15.73 | 1.28 | 7.97 | 13.14 | 3.300 |
| 11 | 3.71 | 2.95 | 5.90 | 1.17 | 14.34 | 1.18 | 7.45 | 10.46 | 2.101 |
| 12 | 3.46 | 2.03 | 6.21 | 1.19 | 14.26 | 1.14 | 7.12 | 11.33 | 2.430 |
| 13 | 2.89 | 3.31 | 9.75 | 1.22 | 15.72 | 1.43 | 4.42 | 14.12 | 2.918 |
| 14 | 2.54 | 1.36 | 7.22 | 1.52 | 15.42 | 1.11 | 9.53 | 14.03 | 1.959 |
| 15 | 2.40 | 1.21 | 7.50 | 1.02 | 16.65 | 1.04 | 9.42 | 12.24 | 2.030 |
| 16 | 2.47 | 1.79 | 6.82 | 1.11 | 15.27 | 1.35 | 5.40 | 11.01 | 3.052 |
| 17 | 1.98 | 2.61 | 6.55 | 1.25 | 15.86 | 1.11 | 4.58 | 11.35 | 1.991 |
| 18 | 2.51 | 1.16 | 6.70 | 1.86 | 15.66 | 1.01 | 4.54 | 13.02 | 2.402 |
| 19 | 1.82 | 3.25 | 5.23 | 1.60 | 14.58 | 1.40 | 3.32 | 10.46 | 2.976 |
| 20 | 2.00 | 1.38 | 6.88 | 1.90 | 15.49 | 1.12 | 3.53 | 11.31 | 2.235 |
| 21 | 1.70 | 0.63 | 7.82 | 1.52 | 15.12 | 1.08 | 2.51 | 12.77 | 2.034 |
| 22 | 1.44 | 0.74 | 5.52 | 1.16 | 14.34 | 1.33 | 1.98 | 9.64 | 2.749 |