Functions

```
H[\theta_{-}] := H[\theta] = \frac{\theta}{1+\theta}
Ho[\theta_{-}, \rho_{-}] :=
                                                                      18 + 13 \rho + \rho^2 + 36 \theta + 22 \theta^2 + 4 \theta^3 + \rho(6 \theta + \theta^2)
     Ho[\theta, \rho] = -
                                                        (1+\theta)(18+13\rho+\rho^2+54\theta+40\theta^2+8\theta^3+\rho(\rho\theta+19\theta+6\theta^2))
H2[\theta_{-}, \rho_{-}] := H2[\theta_{-}, \rho_{-}] =
                                                                           \theta^{\,}2 (36 + 14 \rho + \rho^{\,}2 + 36 \theta + 6 \rho \theta + 8 \theta^{\,}2)
              (1+\theta)(18+13\rho+\rho^2+54\theta+40\theta^2+8\theta^3+\rho(\rho\theta+19\theta+6\theta^2))
H1[\theta_-, \rho_-] := H1[\theta, \rho] = 1 - Ho[\theta, \rho] - H2[\theta, \rho]
re[d_, g_, rbp_, L_] := rbp \left(d + 2\left(\frac{g}{rbp}\right)L\left(1 - e^{\Lambda}\left(\frac{-d}{L}\right)\right)\right)
H[\theta_{-}] := \frac{\theta}{1+\theta}
Ho[\theta_{-}, d_{-}, g_{-}, rbp_{-}, L_{-}] :=
     (18 + 13 \text{ re}[d, g, \text{rbp}, L] + \text{re}[d, g, \text{rbp}, L]^2 + 36 \theta + 22 \theta^2 + 4 \theta^2 
                        4 \theta^{3} + re[d, g, rbp, L] (6 \theta + \theta^{2})
            ((1+\theta)(18+13 \text{ re}[d, g, \text{rbp}, L]+\text{re}[d, g, \text{rbp}, L]^2+54\theta+40\theta^2+
                                     8 \theta^{3} + re[d, g, rbp, L] (re[d, g, rbp, L] \theta + 19 \theta + 6 \theta^{2}))
H2[\theta_{-}, d_{-}, g_{-}, rbp_{-}, L_{-}] :=
     (\theta^2 (36 + 14 \text{ re[d, g, rbp, L]} + \text{ re[d, g, rbp, L]}^2 + 36\theta + 6 \text{ re[d, g, rbp, L]}\theta +
                                    8 \theta^{2})/((1+\theta) (18 + 13 re[d, g, rbp, L]+re[d, g, rbp, L]^2 + 54 \theta +
                                    40 \theta^{2} + 8 \theta^{3} + re[d, g, rbp, L] (re[d, g, rbp, L] \theta + 19 \theta + 6 \theta^{2}))
H1[\theta_{-}, d_{-}, g_{-}, rbp_{-}, L_{-}] := 1 - Ho[\theta_{-}, re[d_{-}, g_{-}, rbp_{-}, L_{-}]] - H2[\theta_{-}, re[d_{-}, g_{-}, rbp_{-}, L_{-}]]
```

(*Expectations replacing rho with re*)

```
Mean[#[[All, -1]]] & /@ (Values @ GroupBy [chrUnbinned [[All, All]], First]);
   chrUnbinned
  ];
BinnedChrCounts [chrUnbinned_ , binSize_] :=
 Module[{interval = binSize, binned1, binned2},
  binned1 = Table[\{\#[[1]] \& /@ \text{ chrUnbinned } [[\text{interval } (i-1)+1;; \text{ interval } (i)]],
      \#[[2]] \& /@ chrUnbinned [[interval (i - 1) + 1;; interval (i)]],
      \#[[3]] \& /@ chrUnbinned [[interval (i - 1) + 1;; interval (i)]],
      #[[4]] & /@ chrUnbinned [[interval (i - 1) + 1;; interval (i)]]},
     {i, 1, Floor@(Length[chrUnbinned]/interval)}];
  binned1 = SortBy[binned1, First];
  binned2 = {Mean[#[[1]]], Total[#[[2]]], Total[#[[3]]], Total[#[[4]]]} & /@ binned1;
  binned2
 1
BinnedChrProp [chrUnbinned_ , binSize_] :=
 Module[{interval = binSize, binned1, binned2},
  binned1 = Table[{#[[1]] & /@ chrUnbinned [[interval (i - 1) + 1;; interval (i)]],
      \#[[2]] \& /@ chrUnbinned [[interval (i - 1) + 1;; interval (i)]],
      #[[3]] & /@ chrUnbinned [[interval (i - 1) + 1;; interval (i)]],
      \#[[4]] \& @ \text{ chrUnbinned } [[\text{interval } (i-1)+1;; \text{ interval } (i)]]\},
     {i, 1, Floor@(Length[chrUnbinned]/interval)}];
  binned1 = SortBy[binned1, First];
  binned2 = {Mean[#[[1]]], Total[#[[2]]], Total[#[[3]]], Total[#[[4]]]} & /@ binned1;
  binned2 = {#[[1]], #[[2]] / Total[#[[2;; 4]]],
       #[[3]] / Total [#[[2;; 4]]], #[[4]] / Total [#[[2;; 4]]]} & /@ binned2;
  binned2
GetChrLikeFun [binnedChr_] := Module[{binned2 = binnedChr, binnedLike},
    binnedLike = Sum[binned2[[i, 2]] * Log[Ho[\theta, binned2[[i, 1]], g, rbp, L]] +
        binned2[[i, 3]] Log[H1[\theta, binned2[[i, 1]], g, rbp, L]] +
        binned2[[i, 4]] Log[H2[0, binned2[[i, 1]], g, rbp, L]], {i, 1, Length[binned2]}];
    binnedLike
  ];
CalculateLikeCounts [unbinnedChr_ , binSize_] := Module[
   {binnedCounts = GetChrLikeFun [BinnedChrCounts [unbinnedChr, binSize]],
     countEstimate , , propEstimate
   },
    countEstimate = NMaximize[{binnedCounts
        0.0001 < \theta < 0.1, 25 \le L \le 500, 0.0000000001 < rbp < 0.1, 0.0000001 < g < 0.1
      \{\theta, \text{ rbp}, g, L\}, \text{ MaxIterations } \rightarrow 2000, \text{ PrecisionGoal } \rightarrow 10];
   countEstimate
  ];
CalculateLikeCountsAndPropsBinned [unbinnedChr_, binSize_]:= Module[
```

```
{binnedCounts = GetChrLikeFun [BinnedChrCounts [unbinnedChr, binSize]],
   binnedProp = GetChrLikeFun [BinnedChrProp [unbinnedChr, binSize]],
  countEstimate , , propEstimate
 },
 countEstimate = NMaximize[{binnedCounts
      0.0001 < \theta < 0.1, 25 \le L \le 500, 0.0000000001 < rbp < 0.1, 0.0000001 < g < 0.1
    \{\theta, \text{ rbp}, g, L\}, \text{ MaxIterations } \rightarrow 2000, \text{ PrecisionGoal } \rightarrow 10];
 propEstimate = NMaximize[{binnedProp
      0.0001 < \theta < 0.1, 25 \le L \le 500, 0.0000000001 < rbp < 0.1, 0.0000001 < g < 0.1
    \{\theta, \text{ rbp}, g, L\}, \text{ MaxIterations } \rightarrow 2000, \text{ PrecisionGoal } \rightarrow 10];
 {countEstimate , propEstimate }
];
```

Data:

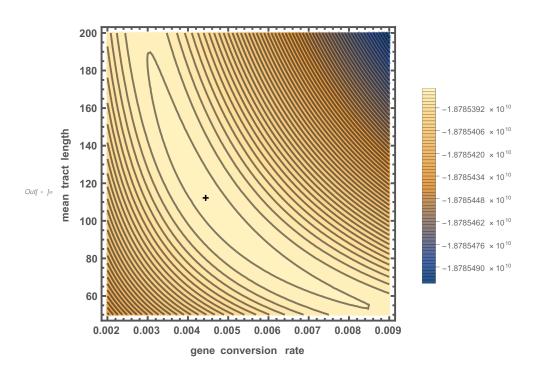
```
In[ • ]:= PoolIndividuals [chr_] := Module[{chrUnbinned},
         chrUnbinned = chr[[All, 3;;]];
         chrUnbinned = {#[[1]][[1]], Total[#[[All, 2]]], Total[#[[All, 3]]], Total[#[[All, 4]]],
              Mean[#[[All, -1]]]} & /@ (Values @GroupBy[chrUnbinned[[All, All]], First]);
         chrUnbinned
       ];
     GetChrLikeFun [binnedChr_] := Module[{binned2 = binnedChr, binnedLike},
         binnedLike = Sum[binned2[[i, 2]] * Log[Ho[binned2[i, 5], binned2[[i, 1]], g, rbp, L]] +
             binned2[[i, 3]] Log[H1[binned2[i, 5]], binned2[[i, 1]], g, rbp, L]] + binned2[[i, 4]]
              Log[H2[binned2[i, 5], binned2[[i, 1]], g, rbp, L]], {i, 1, Length[binned2]}];
         binnedLike
       1;
      data =
In[ • ]:=
         Import["~/Dropbox/projects/gene_conversion/mathematicaInputMice_unbinned .tsv" ,
          "Dataset", "HeaderLines" → 1];
       fullDataCountsByDistance = PoolIndividuals [data[Select[#chrom # "chrX" &]]];
 In[ • ]:= estimatesChr19MinDist100Python =
      {0.002673853733400405 , 0.004444332823674365 , 113.24025414204982 }
      (* kappa, gamma, L*)(*here, distance is actually 101,
       not 100, but should make little difference*)
Outf • J = \{0.00267385, 0.00444433, 113.24\}
```

<code>ln[•]:= likeFunChr19 = GetChrLikeFun[chr19MinDist100]</code>

gc by L like surface

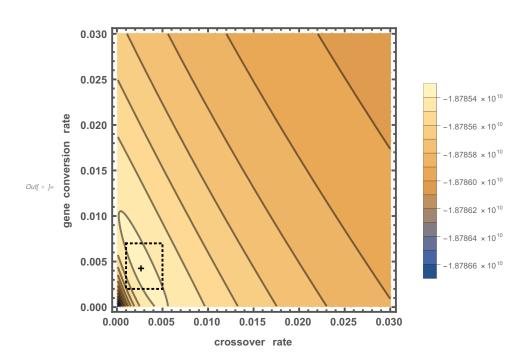
```
In[ • ]:= pGcByLBig = Show[
        ContourPlot[
         Evaluate[likeFunChr19 /. {rbp → 0.002673853733400405 }],
         {g, 0.0001, .035}, {L, 2, 800},
         ColorFunctionScaling → True,
         PlotLegends → Automatic,
         Contours → {Automatic, 20},
         ContourStyle → Thick,
         PerformanceGoal → "Quality",
         PlotRange → Full,
         PlotTheme → "Detailed",
         Frame → True, FrameStyle → Directive[12, Bold, Thick, Darker@Gray],
         FrameLabel → {"gene conversion rate", "mean tract length"},
         {\tt ImageSize} \ \rightarrow {\tt Automatic} \ , \ {\tt PlotRangePadding} \ \rightarrow {\tt Automatic} \ ,
         Epilog → {
            Inset[Graphics[{Black, Text[Style["+", 14, Bold]]}],
              {0.004444332823674365 , 113.24025414204982 }]}
       ],
        Graphics[
         {EdgeForm[{Thick, Dotted, Black}], FaceForm[], Rectangle [{0.002, 50}, {0.009, 200}]}]
      ]
         800
                                                                          -1.87854 \times 10^{10}
         600
                                                                          -1.87855 × 10<sup>10</sup>
     mean tract length
                                                                          -1.87856 \times 10^{10}
         400
                                                                          -1.87857 \times 10^{10}
                                                                          -1.87858 × 10<sup>10</sup>
                                                                          -1.87859 \times 10^{10}
         200
                                                                          -1.87860 \times 10^{10}
           0.000 0.005 0.010
                                 0.015 0.020 0.025 0.030
                             gene conversion rate
```

```
pGCByLSmall = Show[
  ContourPlot[
   Evaluate[likeFunChr19 /. {rbp → 0.002673853733400405 }],
   {g, 0.002, 0.009}, {L, 50, 200},
   ColorFunctionScaling → True,
   PlotLegends → Automatic,
   Contours \rightarrow {Automatic, 60},
   ContourStyle → Thick,
   PerformanceGoal → "Quality",
   PlotRange → Full,
   PlotTheme → "Detailed",
   Frame → True, FrameStyle → Directive[12, Bold, Thick, Darker@Gray],
   FrameLabel → {"gene conversion rate", "mean tract length"},
   ImageSize → Automatic, PlotRangePadding → Automatic,
   Epilog → {
     Inset[Graphics[{Black, Text[Style["+", 14, Bold]]}],
      {0.004444332823674365 , 113.24025414204982 }]}
 1
  (*,Graphics[
   {EdgeForm[{Thick, Dotted, Black}], FaceForm[], Rectangle [{0.0018,140}, {0.003,280}]]}*)
]
```

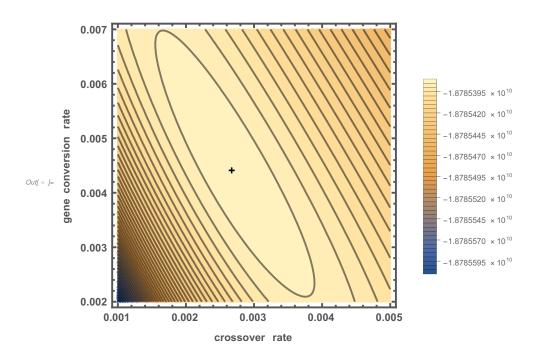


XO by GC like surface

```
pXoByGcBig = Show[
  ContourPlot[
   Evaluate[likeFunChr19 /. {L → 113.24}],
   {rbp, 0.0001, 0.03}, {g, 0.0001, 0.03},
   ColorFunctionScaling → True,
   PlotLegends → Automatic,
   Contours → {Automatic, 20},
   ContourStyle → Thick,
   PerformanceGoal → "Quality",
   PlotRange → Full,
   PlotTheme → "Detailed",
   Frame → True, FrameStyle → Directive[12, Bold, Thick, Darker@Gray],
   FrameLabel → {"crossover rate", "gene conversion rate"},
   {\tt ImageSize} \ \rightarrow {\tt Automatic} \ , \ {\tt PlotRangePadding} \ \rightarrow {\tt Automatic} \ ,
   Epilog →
     Inset[Graphics[{Black, Text[Style["+", 14, Bold]]}], {0.00267385, 0.00444433}]
  ],
  Graphics[{EdgeForm[{Thick, Dotted, Black}],
     FaceForm[], Rectangle [{.001, 0.002}, {0.005, 0.007}]]]
]
```

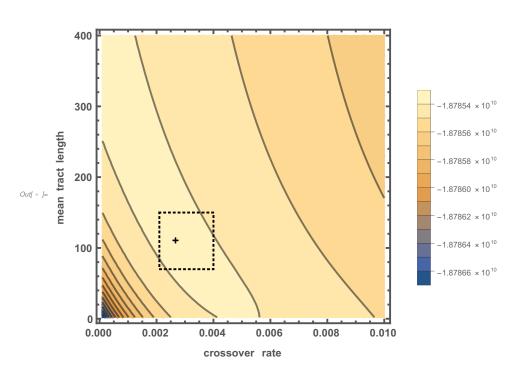


```
pXoByGcSmall = Show[
  ContourPlot[
   Evaluate[likeFunChr19 /. {L → 113.24}],
   {rbp, 0.001, 0.005}, {g, 0.002, 0.007},
   ColorFunctionScaling → True,
   PlotLegends → Automatic,
   Contours \rightarrow {Automatic, 60},
   ContourStyle → Thick,
   PerformanceGoal → "Quality",
   PlotRange → Full,
   PlotTheme → "Detailed",
   Frame → True, FrameStyle → Directive[12, Bold, Thick, Darker@Gray],
   FrameLabel → {"crossover rate", "gene conversion rate"},
   ImageSize → Automatic, PlotRangePadding → Automatic,
   Epilog →
    Inset[Graphics[{Black, Text[Style["+", 14, Bold]]}], {0.00267385, 0.00444433}]
  ]
]
```



xo rate vs tract length

```
pXoByLBig = Show[
  ContourPlot[
   Evaluate[likeFunChr19 /. {g → 0.00444433}],
   {rbp, 0.0001, .01}, {L, 2, 400},
   ColorFunctionScaling → True,
   PlotLegends → Automatic,
   Contours → {Automatic, 20},
   ContourStyle → Thick,
   PerformanceGoal → "Quality",
   PlotRange → Full,
   PlotTheme → "Detailed",
   Frame → True, FrameStyle → Directive[12, Bold, Thick, Darker@Gray],
   FrameLabel → {"crossover rate", "mean tract length"},
   {\tt ImageSize} \ \rightarrow {\tt Automatic} \ , \ {\tt PlotRangePadding} \ \rightarrow {\tt Automatic} \ ,
   Epilog → {
      Inset[Graphics[{Black, Text[Style["+", 14, Bold]]}],
       {0.002673853733400405 , 113.24025414204982 }]}
  ],
  Graphics[
   {EdgeForm[{Thick, Dotted, Black}], FaceForm[], Rectangle [{0.0021, 70}, {0.004, 150}]}]
]
```



```
pXoByLSmall = Show[
  ContourPlot[
   Evaluate[likeFunChr19 /. \{g \rightarrow 0.00444433\}],
   {rbp, 0.0021, 0.004}, {L, 70, 150},
   ColorFunctionScaling → True,
   PlotLegends → Automatic,
   Contours \rightarrow {Automatic, 71},
   ContourStyle → Thick,
   PerformanceGoal → "Quality",
   PlotRange → Full,
   PlotTheme → "Detailed",
   Frame → True, FrameStyle → Directive[12, Bold, Thick, Darker@Gray],
   FrameLabel → {"crossover rate", "mean tract length"},
   ImageSize → Automatic, PlotRangePadding → Automatic,
   Epilog → {
      Inset[Graphics[{Black, Text[Style["+", 14, Bold]]}],
       {0.002673853733400405 , 113.24025414204982 }]}
 ],
  Graphics[
   {EdgeForm[{Thick, Dotted, Black}], FaceForm[], Rectangle [{0.0013, 185}, {0.0016, 227}]}]
]
```

