Michael Newton <wiscstatman@gmail.com>

probabilities for alternative orders

2 messages

Eleftheria Palkopoulou   **Thu, Jan 14, 2010 at**
<Eleftheria.Palkopoulou.4200@student.uu.se>   **7:57 AM**
To: Multiple Recipients of <angenmap@animalgenome.org>

> [AnGenMap Discussion Mailing List - Mail distributed to 1756 members
>]
> [INFO: http://www.animalgenome.org/community/discuss.html]
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>
> Hi all,
>
> I am working with linkage maps and I want to estimate the probability
> (e.g. p-value) of an order of loci against alternative orders, given the
> LOD score for each alternative order. For markers that could not be
> ordered significantly in the framework map, the software CRIMAP
> provides
> the LOD scores for the alternative positions of these markers. What I
> need to estimate is: how more likely is one order compared to an
> alternative one (p-value or odds). So given the example below, we can
> see
> that marker x is more likely positioned between markers C and D (since
> this order gives the least negative LOD score), but how much more
> likely
> is this order against the other two alternative positions (between marker
> pairs A and B and between marker pairs B and C)? Please let me know
> if
> you have an idea about how to estimate this probability.

A   B   C   D   E
  x   x   x

1.LOD score = -139,5
2.LOD score = -142,83
3.LOD score = -132,6

Thank you very much in advance.
Kind regards,

Eleftheria

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-o NRSP8 National Animal Genome Project - Sponsored by
USDA/CSREES
-o http://www.animalgenome.org <> bioinfo-team@animalgenome.org
-o Unsubscribe: angenmap-request@animalgenome.org

**schnabelr@missouri.edu   Thu, Jan 14, 2010 at
<schnabelr@missouri.edu>   8:52 AM**
Reply-To: schnabelr@missouri.edu
To: Multiple Recipients of <angenmap@animalgenome.org>

[AnGenMap Discussion Mailing List - Mail distributed to 1756 members
]
[INFO: http://www.animalgenome.org/community/discuss.html]
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I assume your chromosome has more than just these 6 markers on it.
Just add
your marker X to your ordered loci where you want it and run a flips.

The
number of markers you can flip will be determined by the size of your
pedigree, number of markers, computer hardware and your patience.
Flips4
may be a good place to start. This will tell you the change in likelihood
between all permutations of the markers.

By the way, those are not LOD scores you mention below. Those are
the
difference between the likelihood of the ordered loci and the likelihood
with the marker inserted at position X. What do you have
PUK_LIKE_TOL and
PK_LIKE_TOL set to in the par file?

Bob

------Original Message------
.From: Eleftheria Palkopoulou
.To: Multiple Recipients of
.Subject: probabilities for alternative orders
.Sent: Jan 14, 2010 6:57 AM

Hi all,

I am working with linkage maps and I want to estimate the probability
(e.g.
p-value) of an order of loci against alternative orders, given the LOD
score for each alternative order. For markers that could not be ordered
significantly in the framework map, the software CRIMAP provides the
LOD
scores for the alternative positions of these markers. What I need to
estimate is: how more likely is one order compared to an alternative one

(p-value or odds). So given the example below, we can see that marker x is
more likely positioned between markers C and D (since this order gives the
least negative LOD score), but how much more likely is this order against
the other two alternative positions (between marker pairs A and B and
between marker pairs B and C)? Please let me know if you have an idea about
how to estimate this probability.

A   B   C   D   E
 x   x   x

1.LOD score -139,5 2.LOD score -142,83 3.LOD score -132,6

Thank you very much in advance. Kind regards,

Eleftheria

Sent on the SprintŽ Now Network from my BlackBerryŽ

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