The May Model: A Proposed Model of the Mushroom Foray

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ALTHOUGH forays for the purpose of collecting and documenting mushroom species in an area have been conducted for centuries, I have been unable to find a published model of a foray that explains how mushrooms are distributed in their region and how the foray relates to its region, to other forays in that region, and to forays in other regions. The May Model is a tentative attempt, based largely on observations made in the course of Foray Newfoundland and Labrador, augmented by observations of other forays, digestion of published data, and discussions with mycologists and amateur mycophiles alike. This model applies to the "average" annual amateur club-organized foray, usually of 1–5 days' duration, carried out within the same season each year, and designed primarily to search out all species fruiting in a designated region at the time.

The basis of the May Model is a circle representing all the taxa of macromycota in the foray region. The position of taxa in the circle is not random; mushrooms are arranged according to their commonness from the centre outwards. Thus, common mushrooms are located in the centre of the circle and less and less common ones gradually fade outward to the circumference, which contains the rarest taxa in that region. This is illustrated by Figure 1, the black centre representing the commonest of taxa, gradually fading through lighter shades of gray to a white periphery occupied by the rarest.

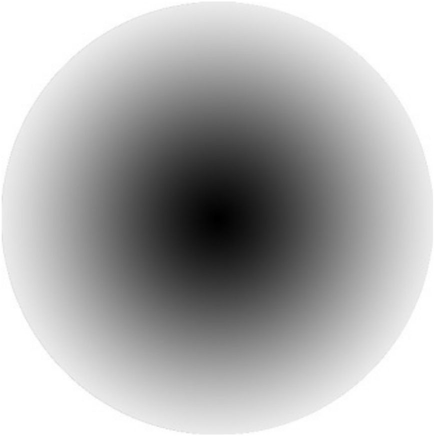

Figure 1. Distribution of mushroom taxa in their region. The commonest taxa are assigned a centre location in the circle, fading outwards toward increasingly more rare species.

By definition, the commonest mushrooms are recovered almost every year; thus the taxa collected on a foray assume the shape of a radially oriented tear-drop, the fat end extending beyond the centre to encompass most of the area of common taxa, looking somewhat like the hand of a clock. Because even the commonest taxon may be missed in any one year, be it due to an unusual climato-mycological aberration or human error of omission on behalf of the collectors, the fat end is shown with a small indentation—thus the heart shape of the foray. The size of this heart depends in part on the size of the area surveyed, the thoroughness with which it is surveyed, etc. The average amateur foray seems to retrieve less than 5% of the taxa in its region. Figure 2 illustrates the appearance of the mushroom taxa collected on a foray related to the total taxa of that region.

Crucial to the May Model is the centripetal gradation of taxal commonness, because this determines the relationship (position) of subsequent forays in the same region to each other. So long as the commonest taxa occupy the centre of the circle, the situation shown in Figure 3 is not possible for two forays in the depicted region. Both of those forays would have to have been conducted in totally different regions. Because common taxa are, by definition, present every year, the blunt ends of both foray lists must overlap the centre of the circle and, consequently, each other, as depicted in Figure 4. On the other hand, rare taxa are not collected each year, so the area away from the centre of two forays will not overlap. It is this area that accounts for the difference between foray lists from the same region and builds up the cumulative species list until, in theory, eventually all taxa have been recovered. As the number of forays in the region increases, there will be less and less uncommon and rare taxa to collect that have not been recorded previously. Thus, increasingly foray species lists will resemble the cumulative list. Figure 5 shows how the new foray resembles that of the aggregate of all previous forays on the 16th foray in the same region. It is important to understand that while each new foray is increasingly similar to the aggregate of previous forays, it is still considerably different from any individual previous foray.

Will we ever collect all the taxa in an area? The May Model suggests this is theoretically impossible. The centrifugally increasing taxal rarity extends to the rim, populated with the rarest taxa. In theory, the number of points along the circumference is infinite, so that it would take an infinite number of forays to recover them all. Even if the tip of the foray model were somewhat blunt, it is clear that the number of forays required to recover all taxa in an area is very large. To date, no region of the world has a complete list of macromycota, as exists, for example, for vascular plants. Our own preliminary experience, reconciled with the experience of others, suggests a reasonable time to collect all mushroom taxa in Newfoundland may be as much as 100 years of forays. Well, there will be many changes over 100 years, changes in climate, habitat, pollution, substrate, plant hosts, introduction and extinction of species, etc. Thus, the aggregate of 100 years' of forays would be very unlikely to be an accurate list of the total taxa in Newfoundland at that time—some will no longer be here while others may have adapted, evolved or been introduced that have not been collected yet.

The May Model needs to be altered a bit to allow a graphic representation of forays in different regions. While the easiest concept would be two separate "compasses," similar to the one in Figure 5, for each region, such radical difference is probably true only for diametrically different regions, e. g. Belize and Nunavut. The mycoflora of more similar regions will overlap. The model must allow for overlap of all segments, the periphery, the middle and the centre, because shared taxa for any two habitats occur throughout their distribution ranges. For many shared taxa, the frequency of occurrence will differ. What may be rare in one region may be common in another, and vice versa. Therefore, the areas of the commonest mushrooms need to be moved to an eccentric position near one edge, so that overlap of the total community also allows for overlap of their

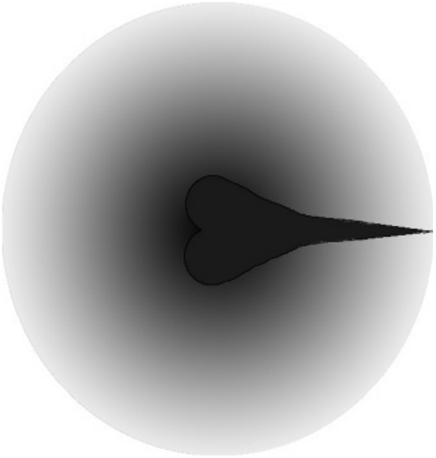

Figure 2. Appearance of a foray in its region. There is a fat, indented end overlapping the centre of common species with a projection tapering to a point at the circumference of the rarest of taxa.

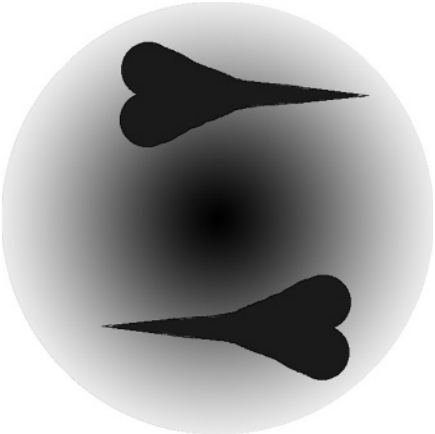

Figure 3. Two forays within a region will not look like this, because both should overlap in the area of common taxa. The depicted forays must have been conducted in totally different regions.

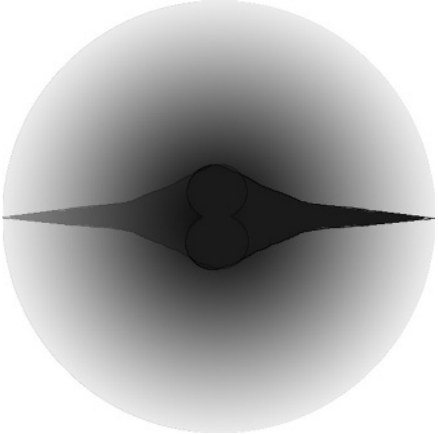

Figure 4. Correct appearance of two forays from the same region. There is an overlap of common mushrooms, but since there is such a large area of uncommon mushrooms, total species lists of the two will differ significantly from each other.

Figure 5. Appearance of the 16th foray in the same region. By now its species list resembles that of the aggregate of the previous 15 years. However, it will still differ significantly from any other single foray in the region. Note that although the centre of common and relatively common mushrooms has enlarged considerably, a very large portion of the uncommon and rare mushrooms are still not recorded.

respective areas of common species. Figure 6 is a graphic illustration of the May Model adjusted for two somewhat similar regions, A and B. Forays, a1, a2 and a3 are shown in region A and b1 in region B. The common mushrooms of foray a3 in region A, ($a3_c$) partly overlap those of foray b1 in habitat B ($b1_c$).

Differentiating regions on the basis of differences in their mycoflora is relatively simple after a large number of forays has been carried out in each region and most taxa have been recorded. As seen in Figure 5, comparing the aggregate of several forays from two regions should readily tell if the regions differ. Even if only one region has had several forays, a single foray should be sufficient to determine habitat difference: if the taxa collected during a single foray are similar to the aggregate of that region, the regions are the same or similar and if the taxa differ significantly, the single foray took place in a different region.

Is it possible to distinguish between two regions from the species list of only one foray in each (i. e. without having a large experience to fall back on in at least one of them)? The natural inclination might be to analyze the respective species lists according to principles of community ecology. This would work if the regions consisted of totally different habitats, such as Belize and Nunavut. In that case, their respective lists would be totally different, without overlap, and would clearly indicate differing regions as their source. However, for regions containing somewhat similar habitats, the May Model suggests comparing single foray lists will not tell them apart. A single foray recovers such a small proportion of the taxa in its region that the species list of a second foray will differ significantly from the first. In other words, collecting significantly different taxa on any two forays is the expected result even in the same habitat and, thus, does not necessarily indicate they were conducted in different habitats. The quantitative difference between the two forays in Figure 4 seems similar to that between forays a3 and b1 of Figure 6, yet the forays in Figure 4 are from the same habitat, while those in Figure 6 come from two entirely different habitats. Figures 4 and 5 show that the information about species in the mid and outer area of the community remains prominently incomplete for a large number of forays. Because single forays recover such a small fraction of the mushroom communities beyond the common taxa in the centre, there may be no mathematical way to determine whether forays a3 and b1came from the same or different habitats on the basis of analyzing differences in their total species lists.

The above suggests that it may not be not possible to tell from species lists of single forays whether they come from the same or different regions, yet we know empirically that such comparisons can be done in real life. An experienced mycologist can often tell within a few hours of foraging, if she's sampling a different mycoflora. How does she do it? Clearly not by comparing total species lists. People experienced at looking at mushrooms develop a sense for signature taxa, those taxa that are unique to a region and therefore serve to define it. Although signature taxa can occur throughout the commonness spectrum, for comparison purposes a mycologist focuses on the common mushrooms in the region. When first seen, an unusual species, something rarely or never seen before or elsewhere, is dismissed as an oddity, a fluke, a lucky chance encounter. However, if the same species is encountered repeatedly in a new region, it is noted as a signature species for the region. A collection of such taxa defines the new region as mycologically different from other regions previously encountered. In order to tell regions apart on the basis of a single survey of their mycoflora, we should ignore the complete foray lists and mimic what the mycologist does in real life—look only at the common mushrooms.

The May Model shows this approach in Figure 6, where the common taxa $a3_c$ and $b1_c$ of forays a3 and b1, conducted in the regions A and B, overlap. We no longer compare the total foray species lists a3 and b1, but only their respective common taxa. Using common taxa has two obvious advantages. First, as opposed to uncommon taxa, the vast majority of common taxa will be collected on the first foray, with very few additional taxa over the years. This allows a valid comparison to be made early. Second, there are only two variables to compare when comparing common taxa from two regions: either a species is unique to a region or it is shared with the other region. This allows for the use of a simple two-by-two table (Chi squared test) to test the significance of any observed difference, instead of the much more complex and "softer" analyses of richness and evenness used in normal community ecology.

This method mimics that used intuitively by a mycologist surveying a new region for the first time and is subject to the same disadvantages:

There is no satisfactory method of standardizing the determination of commonness for most amateur forays. Although a protocol to this effect can be implemented in theory, many participants may not follow it because:

- for many it will increase disagreeable paper work at the expense of much more enjoyable collecting in the field,
- concentrating on common mushrooms may seem unnatural to many seasoned mycophiles because it runs counter to their innate curiosity and the thrill of discovering the rare and unusual, and
- some participants may find such requirement an unpleasant conflict between their and somebody else's goals for a foray.

The number of common taxa is small, so that small differences may not achieve statistical significance. It is totally dependent on an arbitrary definition of commonness that is likely to vary from region to region and time to time, a source of potential confusion or error.These disadvantages must be understood and accepted as part of the price for this useful tool, a quick and relatively effective mycological fingerprint of its region. In some cases this fingerprint may be somewhat partial or smudged, but in most cases it will still serve to identify its region. Because of the above disadvantages, results of such comparisons should not be considered definitive and can always be revised after a greater amount of data is collected about the regions involved, allowing comparison of cumulative species lists.

Most forays take place in regions, which may contain within them many different habitats. Regions differ only to the extent that their habitats differ. Seasons, temperature, moisture, water, light, acidity, substrate, endemic plant and animal species are among the variables that define a habitat. Tolerance of and requirement for these variables differ for different mushrooms. Thus, each habitat has its own unique mycofloral portrait. While this discussion of the May Model was intended to describe the amateur foray conducted within a region of many habitats, the model can be adapted equally well to the use of professional surveys with standardized collection protocols or surveys of specific habitats. In fact, differences in

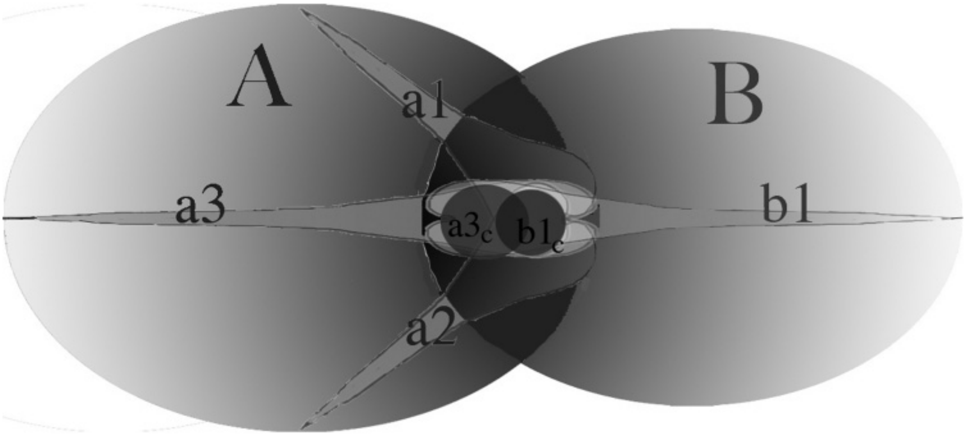

Figure 6. Modification of the May Model to depict forays in two different but not totally dissimilar regions. To show some overlap of mushrooms in all areas, the centres of common taxa had to be placed in an eccentric position. Note the similarity of forays a3 and b1 to the two forays depicted in Figure 4. Although the latter come from the same region and the former from two different regions, they look quite similar. Comparison of whole foray species lists are unable to determine whether two forays were held in the same or in different areas; to do that, the respective centers of common taxa must be analyzed. Please see text for detail.

the variables making up habitats may not be obvious; where plants and trees do not tell habitats apart, it is possible that the mycoflora does. In the absence of species lists for several years, the mycological fingerprint of common taxa may find its greatest application in distinguishing between such seemingly similar habitats.

A certain similarity of this graphic model to a mushroom should not have escaped the notice of most mycophiles. The circle of taxa in a region is the pileus, darker on the disc than the edge, possibly even with some veil remnants hanging from it. The foray looks like a stipe with a bulbous cleft foot. This essay may be viewed as the formal description of a newly discovered mushroom species. I have eschewed the Latin description in the beginning, but have preserved the right to name this newly discovered species. It is named in the memory of my good friend Barry May. Barry was an accomplished outdoorsman, naturalist, athlete, physician and volunteer all his life. He has made very significant contributions to both the outdoors and naturalist movements in Newfoundland. Knowledgeable about all fields of natural history, for many years his favorite pastime was birding. In the last few years he became fascinated with mushrooming, which became his new passion. He was an active participant and organizer of our annual mushroom week-end, Foray Newfoundland and Labrador, He has traveled on forays to Europe and had made plans for many more mushrooming trips in the future. Barry also became a committed mushroom cook. For at least two years, not a day went by that he did not sauté some mushrooms on toast and during the Forays he took responsibility for our mushroom cookouts. Barry died suddenly November 1, 2005, at the age of 62.

There is another and quite obvious reason for naming the model. Clearly, I should like to see it tested by individuals and organizations with large collections of data against their experience. Corrections, alterations and refinements should produce a robust model that can accurately predict the relationship of the common mushroom foray to the taxa of its region. Should such testing occur and be reported in the literature, this original description would likely be referred to as "the Voitk model," "the model proposed by Voitk" or, worst choice of all, "Voitk's model." These sound quite awkward and are singularly unappealing because of an inherent lack of phonetic aesthetics of my last name. In contrast, "May Model" sounds quite pleasing. I am sure Barry would have been glad to do me this favour of making my newly discovered model more attractive, increasing the chance that others may go on to test it and thereby provide those hundreds of mycophiles, who, like Barry, love to go on forays, some insight into their activity.

In summary, a model of the mushroom foray, the “May Model,” is described that gives a seemingly realistic graphic depiction of

- distribution of mushroom commonness in a region,
- the relationship of a foray to the mushrooms of the region,
- the relationship of other forays in the same region to each other and to all the taxa of the region,
- the likelihood of collecting all taxa of a region,
- the relationship of different regions to each other,
- the relationship of forays in different regions to each other,
- the long way for comparing regions from mycological data, and
- a quick fingerprint by which mycoflora could differentiate habitats.

ACKNOWLEDGMENTS

In developing this model, I owe thanks to Dr. Dave Malloch, whose ideas provided much of the original stimulus to pursue this concept and whose criticism and comments forced me to think it through to a somewhat unexpected end result that seemed to fit my own real life experience.