Instruction and marking scheme for LR1 (due Nov. 2)

- use a publication format

Title
e.g., Five macrofungi from Ontario and DNA sequence identification

Author's name

Summary (5%)

Introduction (1/2 - 1 page) (5%)

Material and Methods (1/2 - 1 page) (5%)

Results and Discussion

Description and identification of five collections: 5 x 12% = 60%
- illustration (3%)
    Drawings, and picture(s) when available
- description (3%)
    Follow the description format in "*Fungi of Switzerland*", or in M. Kuo <e.g., <http://www.mushroomexpert.com/tricholoma_equestre.html> or mycoweb (e.g. <http://www.mykoweb.com/CAF/species/Tricholoma_flavovirens.html>); include collection number, date of collection, collector, locality, habitat, host, etc.
- comment (1/2 page) (6%)
    State here your source(s) of identification; how accurate do you think your identification is (genus accurate/tentative? Species epithet accurate/tentative?), and why; present and discuss relevant facts about the genus and/or species such as for instance its taxonomy, synonyms, related species, number of species in the genus, geographic distribution, ecology, economic importance, etc. Consult *Index Fungorum* < http://www.indexfungorum.org/names/names.asp> for taxonomic information. **Cite your sources**: a peer-reviewed scientific publication is generally preferable to a "free-lance" web resource (e.g. Wikipedia can be consulted but when so retrieve the original information from citation therein). **No plagiarism is tolerated.**
- provide dry (=herbarium) collection with lab report.

DNA sequence identification: 15%
    [imagine that you have created a start-up company that provide taxonomic identification service] To which genus this sequence belongs, and to what certainty? Can you possibly infer to which species, or group of species, it belongs. Is there any prediction you can make about the ecology, geographic distribution, habitat, host, toxicity, utility, etc. of the organism from which that sequence was derived?

Use half a page to 1 page. Add figures and/or tables as appropriate, including BLAST results and UNITE trees.

Bonus 3%: produce your own tree from BLAST results in GenBank that have at least 80% similarity to the query sequence, using alignment softwares (e.g., Clustal W and BioEdit) and a phylogenetic program (e.g. Phylip); describe the procedure you used in the Material and Methods section.

References (10%)